PROCEEDINGS

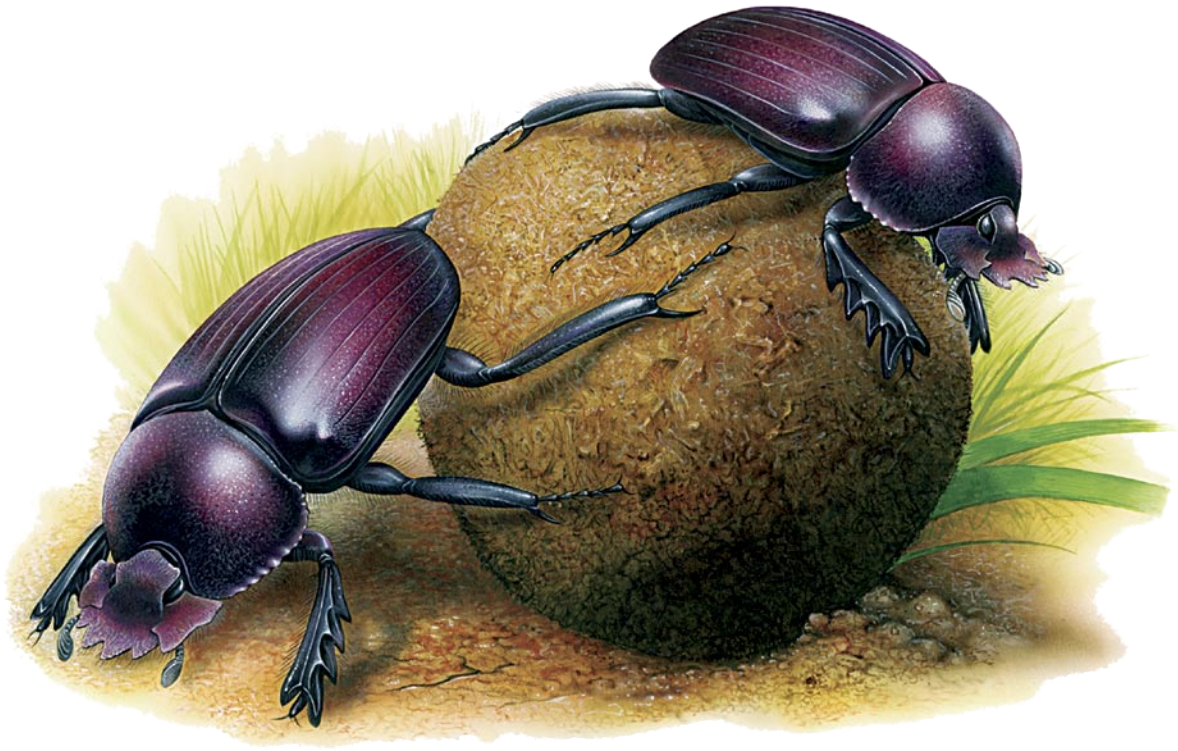
ICE 2008

XXIII International Congress of Entomology

6 - 12 July, 2008: International Convention Centre, Durban

"Celebrating Entomology: Contributions to Modern Science"

ICE 2008: TABLE OF CONTENTS



ICE2008 ORGANIZING COMMITTEES

SOUTH AFRICAN MANAGEMENT COMMITTEE

Congress President

Robin Crewe

Chairman

Gerhard Prinsloo

Deputy Chairman

Schalk Louw

Members

Marcus Byrne
Ahmed Hassanali
Jannette Mitchell
Shirley Hanrahan
John Hoffmann
Margaret Kieser (Secretary)

SCIENTIFIC PROGRAMME COMMITTEE

John Hoffmann (Chair)
Brian Barnes
Jan Giliomee
Cliff Moran

SOCIAL EVENTS COMMITTEE

Marcus Byrne (Chair)
Shirley Hanrahan

FINANCIAL AND SPONSORSHIP COMMITTEE

Jannette Mitchell (Chair)
Steve Mitchell

AFRICAN LIAISON COMMITTEE

Ahmed Hassanali (Chair)
Johnnie van den Berg

DURBAN ORGANIZING COMMITTEE

Des Conlong (Chair)
Various staff members from the following institutions:

ARC-Plant Protection research Institute, Cedara.
Natal Museum, Pietermaritzburg.
Natural Science Museum, Durban.
South African Sugarcane Research Institute, Mount Edgecombe.
University of KwaZulu-Natal, Pietermaritzburg and Durban.

ICE COUNCIL MEMBER

Shirley Hanrahan

The Council - ICE International

The purpose of the Council is to provide continuity and direction for the International Congresses of Entomology, and to serve as the Entomology Section of the International Union of Biological Sciences (IUBS). It may also encourage the holding of smaller inter-Congress meetings.

The Council consists of not more than twenty-three (23) members, who shall represent as wide a field as possible both geographically and by entomological discipline. Membership of the Council shall be limited to distinguished entomologists who are interested in the welfare and future of the International Congresses of Entomology. Members are elected for one term of 8 years. Members can be re-elected for a second term but are not permitted to serve more than two consecutive terms.

Council is able to appoint Honorary members as prescribed in the Constitution. Honorary Members are appointed from among entomologists who have made outstanding contributions to entomological knowledge, who have influenced entomology substantially both within and outside their own countries or regions, and who have made important contributions to the International Congresses of Entomology.

Officers of the Council:

Chairman: Professor Frantisek Sehnal (appointed to Council 1992; Chairman 2004)
Deputy Chairman: Professor Robert Lane (appointed to Council 1998; Deputy Chair 2004)
Secretary/Treasurer: Professor Willem Takken (appointed to Council 1998; Secretary/Treasurer 2004)

Past Chairman: Professor Lynn Riddiford (appointed to Council 1988; Past Chair 2004)

Members of the Council (as of August 2004):

Name	Country	Date of Birth	Year Appointed	Field of Interest
Cheng, Jiaan	China	12 Jul 1942	2000	Pest management, Ecology
Ekbom, Barbara	Sweden	1950	2004	Insect ecology
Hanrahan, Shirley, A	South Africa	11 Jul 1939	2004	Ecophysiology
Hassanali, Ahmed	Kenya (ICIPE)	12 Dec 1941	2000	Chemical Ecology & Physiology
Hoy, Marjorie A	USA	n	2004	Biological Control & Acarology
Kim, Byung-Jin	Korea	25 Apr 2005	2004	Taxonomy & Molecular Phylogeny of ants
Lane, Richard	UK	16 May 1951	1992; 2000	Medical Entomology & Biosystematics
Lane, Robert	USA	07 Mar 1944	1988	Medical & Veterinary Acarology
Moscardi, V.F	Brazil	26 May 1949	1992; 2000	IPM
Napompeth, Banpot	Thailand	20 Feb 1941	1996	IPM, Disease Control
Riddiford, Lyn M	USA	18 Oct 1936	1988;2000	Physiology, Devpt, Biology
Ridsdill-Smith, James	Australia	31 Mar 1942	2004	Experimental ecology, Feeding
Sasaki, M	Japan	27 Jan 1948	2000	Behaviour
Sehnal, Fratisek	Czech Republic	11 Sep 1938	1992; 2000	Physiology, Ecophysiology
Sharma, Hari C	India	15 Jun 1954	2004	IPM
Takken, Willem	The Netherlands	05 Jan 1951	1998	Medical & Veterinary Entomology
Waage, Jefferey	UK	13 Mar 1953	1998	Biological control, Parasitoids
Wysoki, M	Israel	27 Apr 1936	2000	IPM, Acarology, Thrips
Zalukcki, Myron P	Australia	26 May 1954	2004	Ecology, Insect-plant interaction

Honorary Members of the Council:

Member	Country	Date of Birth	Year of Appointment
Adkisson, P	USA	11 Mar 1929	1992
Bacetti, B.	Italy	07 May 1931	1988
Freeman, P.	UK	26 May 1912	1988
Galun, R.	Israel	03 Apr 1926	1996
Hafez, M	Egypt	10 Jan 1912	1992
Ishii, S.	Japan	12 Feb 1915	1996
Lioying, Li.	China	10 Mar 1932	1984
Oliver, J.H.	USA	10 Mar 1931	1992
Pal, R.	Switzerland	10 Oct 1919	1988
Rothschild, M	UK	05 Aug 1908	1984
Sabrosky, C.W.	USA	03 Apr 1910	1984
Saito, T	Japan	29 Sep 1924	1992
Smith, R	USA	20 Jan 1919	1992
Waterhouse, D.F.*	Australia	03 Jun 1916	1988
Whitten, M.J.	Australia	29 Mar 1940	2004

*Doug Waterhouse was elected Honorary Chairman of Council at the August 2000 Congress of Entomology in Iguacu, Brazil. He was awarded this unique honour in recognition of this outstanding contribution to the Congress of Entomology and the cause of international entomology. He died on 7 December 2000 (Obituary in "Historical Records of Australian Science", Vol 13 (4) Pp495 - 519) by M Day, M J Whitten and D Sands.

ICE 2008 recognises the following sponsors for their valued contribution

PREMIER SPONSORS	
agriculture Department: Agriculture REPUBLIC OF SOUTH AFRICA	Department of Agriculture
ARC • LNR	Agricultural Research Council
science & technology Department: Science and Technology REPUBLIC OF SOUTH AFRICA	Department of Science & Technology
E OPPENHEIMER & SON SOUTH AFRICA	E Oppenheimer and Son
	Entomological Society of Southern Africa
Durban Africa's Sporting & Events Capital	The City of Durban
VALUE SPONSORS	
EVERARD READ JOHANNESBURG	Everard Read Gallery
MONSANTO	Monsanto
Leica MICROSYSTEMS	Leica Microsystems
Council for International Congresses of Entomology	Council for International Congresses of Entomology
Dow AgroSciences TM	Dow AgroScience

Section & Symposium Information

SECTION 1	PEST MANAGEMENT: PERENNIAL CROPS	
Convenors	Vaughan Hattingh, Citrus Research International, RSA Jerry Cross, East Malling Research, UK	
Symposium Organisers	**No.**	**Symposium Titles**
Jerry Cross (UK) & Tim Grout (RSA)	**1.1**	IPM on perennial crops
Jim Hardie (UK) & David Hall (UK)	**1.2**	Semiochemicals in IPM on perennial crops
Mark Brown (USA) & Viktor Marko (Hungary)	**1.3**	Functional biodiversity in perennial crops for pest management
Joerg Samietz (Switzerland)	**1.4**	Phenology models and their use in IPM on perennial crops
Nilsa Bosque-Perez (USA) & Sanford Eigenbrode (USA)	**1.5**	Coffee entomology: an international perspective
Paula Shrewsbury (USA) & Rob van Tol (The Netherlands)	**1.6**	Advances in implementing biological control for perennial ornamental crops grown outdoors
Johannes Jehle (Germany) & Patricia Stock (USA)	**1.7**	Microbial and nematode biocontrol agents for pests of perennial crops

SECTION 2	PEST MANAGEMENT: ANNUAL CROPS	
Convenors	Johnnie Van Den Berg, North-West University, RSA Huib van Hamburg, North-West University, RSA John D Mumford, Centre for Environmental Policy, UK	
Symposium Organisers	**No.**	**Symposium Titles**
Megha N. Parajulee (USA), Robert Mensah (Australia) & Lewis Wilson (Australia)	**2.1**	Ecological approaches to cotton IPM: a global perspective
Samuel Waladde (RSA), Johnnie Van den Berg (RSA) & Zeyaur Khan (Kenya)	**2.2**	Pest management: prospects, successes and failures
Sam Cook (UK) & Zeyaur Khan (Kenya)	**2.3**	Habitat management strategies for controlling insect pests of crop plants
Joop van Lenteren (The Netherlands)	**2.4**	Can boundaries between biocontrol and GMOs be overcome?
Mark Stevens (Australia) & Mike Way (USA)	**2.5**	Ecology and management of key rice pests
Vicki Tolmay (RSA) & K.A. Shufran (USA)	**2.6**	Russian wheat aphid management
Joop van Lenteren (The Netherlands) & Martin Hill (RSA)	**2.7**	Critical analyses of successes and failures of biological control in Africa
Malcolm Keeping (RSA) & M.N. Sallam (Australia)	**2.8**	Sugarcane IPM: tough challenges - sweet outcomes
Dionyssios Perdikis (Greece) & Oscar Alomar (Spain)	**2.9**	Predatory Heteroptera: recent advances and future needs
Sunday Ekesi (Kenya) & M. Knapp (Kenya)	**2.11**	IPM in horticultural crops in the tropics

SECTION 3	PESTICIDES, RESISTANCE & TRANSGENICS	
Convenors	Graham Head (USA)	
Symposium Organisers	**No.**	**Symposium Titles**
John Stark (USA)	**3.1**	New pesticides and pest control technologies
Rafael Martinez Pardo (Spain) & Ralf Nauen (Germany)	**3.2**	Insecticide resistance in sucking insects in agriculture
William Moar (USA) & Joseph Huesing (USA)	**3.3**	Development, barriers and use of insect resistant transgenic crops in developing countries
Joerg Romeis (Switzerland) & Tony Shelton (USA)	**3.4**	Integration of insect-resistant GM crops within IPM programs
Srinivas Parimi (India) & Blair Siegfried (USA)	**3.5**	Coffee entomology: an international perspective
Noubar Bostanian (Canada) & J.M. Hardman (Canada)	**3.6**	The effects of pesticides on non-target arthropods

SECTION 4	FOREST ENTOMOLOGY	
Convenors	Andrew Liebhold, USDA Forest Service, USA Michael J. Wingfield, Forestry and Agricultural Research Institute (FABI), RSA Dan Robison, North Carolina State University, USA	
Symposium Organisers	**No.**	**Symposium Titles**
Daniel Doucet (Canada) & Qili Feng (China)	**4.1**	Forest entomology in the era of genomics and post-genomics
Diana Six (USA) & Bernard Slippers (RSA)	**4.2a**	Consequences of environmental change and globalization on insect-microbe symbioses: anthropogenic effects on symbioses
Naoto Kamata (Japan) & Jean-Claude Grégoire (Belguim)	**4.2b**	Consequences of environmental change and globalization on insect-microbe symbioses: ambrosia beetles as affected by environmental factors
Kier Klepzig (USA), Francois Lieutier (France) & Timothy D. Paine (USA)	**4.3**	Mediation of tree-insect interactions by micro-organisms
Joseph Elkinton (USA), Nancy Gillette (USA) & Bernard Slippers (RSA)	**4.4**	Use of molecular techniques to identify and to trace the origin and spread of invasive forest insects
John Spence (Canada), Jari Niemelä (Finland) & Johan Kotze (RSA)	**4.5**	Ecological and conservation implications of linkage between arthropod biodiversity and forestry practices
Patrick Tobin (USA), Brian Aukema (Canada) & Hugh Evans (UK)	**4.6**	Insect invasion dynamics in forest ecosystems
Fred Stephen (USA) & Robert Coulson (USA)	**4.8**	Impacts of insects on forest landscapes: implications for forest health management

SECTION 5	URBAN, STORED PRODUCT & POST HARVEST ENTOMOLOGY	
Convenors	Frank Arthur, Grain Marketing & Production Research Center, USA Frikkie Kirsten, Agricultural Research Council, RSA Michael K. Rust, University of California, Riverside, USA	
Symposium Organisers	**No.**	**Symposium Titles**
Tom Phillips (USA) & Frank Arthur (USA)	**5.1**	Ecology and management of stored-product insects in large-scale facilities
Paul Flinn (USA) & Cornell Adler (Germany)	**5.2**	Biological control of stored product insects
James Campbell (USA) & Marcé Lorenzen (USA)	**5.3**	The stored product pest Tribolium castaneum as a model organism
James Throne (USA) & Brighton Myumi (Zimbabwe)	**5.4**	Ecology of stored-product insects for improving pest management
Brian Forschler (USA) & Vernard Lewis (USA)	**5.5**	Economical, environmentally sensitive termite management: a global perspective

SECTION 6	ECOLOGY	
Convenors	Melodie McGeoch, University of Stellenbosch, RSA Stig Larsson, Swedish University of Agricultural Sciences, Sweden	
Symposium Organisers	**No.**	**Symposium Titles**
Robert Denno (USA) & Matthew Thomas (Australia)	**6.1**	Multiple natural-enemy interactions in natural and managed systems
Robert Knell (UK), Sheena Cotter (UK) & Ken Wilson (UK)	**6.2**	Ecological immunity of insects
Marcel Dicke (The Netherlands) & Louise Vet (The Netherlands)	**6.3**	Omics and ecology and evolution of multitrophic interactions
Jeff Harvey (The Netherlands) & Paul Ode (USA)	**6.4**	Plant chemistry and insect ecology: a multitrophic perspective
Takayuki Ohgushi (Japan), Oswald Schmitz (USA) & Robert Holt (USA)	**6.5**	Trait-mediated indirect effects in insect communities
Nuria Roura-Pascual (Spain/RSA) & Joaquin Hortal (UK)	**6.6**	Sampling and modelling the spatial responses of insects across spatial scales
Connal Eardley (RSA) & Carolin Mayer (Germany)	**6.7**	Pollinators in full bloom
Pedro Barbosa (USA) & Markus Rantala (Finland)	**6.8**	Insect outbreaks revisited
Louise Vet (The Netherlands) & Brian Smith (USA)	**6.9**	Ecology, evolution and application of learning in insects
Jeff Harvey (The Netherlands) & Martijn Bezemer (The Netherlands)	**6.10**	Linking aboveground and belowground multitrophic interactions

SECTION 7	GENETICS, GENOMICS, TRANSGENICS & EVOLUTIONARY BIOLOGY	
Convenors	Ary Hoffmann, University of Melbourne, Australia J. Nagaraju, Centre for DNA Fingerprinting and Diagnostics, India	
Symposium Organisers	**No.**	**Symposium Titles**
J. Nagaraju & H.A. Ranganath (India)	**7.2**	Insect genetics
K. Mita (Japan) & J. Nagaraju (India)	**7.3**	Insect genomics
Chris Klingenberg (UK) & James S. Patterson (UK)	**7.4**	Insect morphometrics
Steve Sinkins (UK)	**7.7**	Wolbachia endosymbionts in invertebrates

SECTION 8	INSECT PATHOLOGY	
Convenors	Justin Hatting, ARC-Small Grain Institute, RSA Patricia Stock, University of Arizona, USA	
Symposium Organisers	**No.**	**Symposium Titles**
Sean Moore (RSA)	**8.1**	Success and failure of microbial control products and businesses: determining factors
Eda Reinot (USA)	**8.2**	Biopesticides: development, formulations, applications
Jørgen Eilenberg (Denmark) & Patricia Stock (USA)	**8.5**	Ecology of insect host-pathogen interactions
Trevor Jackson (New Zealand)	**8.6**	Microbial control of concealed and soil-dwelling pests
Sarjeet Gill (USA)	**8.7**	Microbes: pathogenicity and host interactions

SECTION 9	MEDICAL & VETERINARY ENTOMOLOGY	
Convenors	Maureen Coetzee, National Institute for Communicable Diseases, RSA Theuns C. van der Linde, University of the Free State, RSA Willem Takken, Wageningen University, The Netherlands	
Symposium Organisers	**No.**	**Symposium Titles**
John Hargrove (RSA) & Rajinder Saini (Kenya)	**9.1**	African Trypanosomiasis
Richard Hunt (RSA) & John Githure (Kenya)	**9.2**	Malaria in Africa - ecology and control of vectors
Bart Knols (The Netherlands)	**9.3**	Novel control strategies
Hilary Ranson (UK) & Lizette Koekemoer (RSA)	**9.4**	Insecticide resistance in vectors
Larry Zweibel (USA) & Alan Clements (UK)	**9.5**	Olfaction and physiology
Abdalla Latif (RSA) & Ahmed Hassanali (Kenya)	**9.6**	Ticks and tick-borne diseases
Theuns van der Linde (RSA) & Gail Anderson (Canada)	**9.7**	Forensic entomology
Wayne Hunter (USA) & George Christophides (UK)	**9.8**	Genetics, bio-informatics and genomics
Mustapha Debboun (USA) & Rajendra Maharaj (RSA)	**9.9**	Global repellent research
Willem Takken (The Netherlands) & Tom Scott (USA)	**9.10**	Emerging vector-borne diseases

SECTION 10	REPRODUCTION & DEVELOPMENT	
Convenors	Lynn Riddiford, University of Washington, USA Klaus Hoffmann, University of Bayreuth, Germany	
Symposium Organisers	**No.**	**Symposium Titles**
Marek Jindra (Czech Republic)	**10.1**	From embryo to metamorphosis: genes of insect development
Lynn Riddiford (USA), Klaus Hoffmann (Germany), Jozef vanden Broeck (Belgium) & Hans Ferenz (Germany)	**10.4a** **10.4b**	Hormonal control of development and reproduction: Insulin signalling and development (Neuro) hormonal control of reproduction
Goggy Davidowitz (USA), Elizabeth Jockusch (USA) & Lisa Nagy (USA)	**10.6**	Evolution and development of integrated phenotypes
Francesco Pennacchio (Italy) & Michael Strand (USA)	**10.7**	Developmental strategies in parasitoids

SECTION 11	PHYSIOLOGY & BIOCHEMISTRY	
Convenors	Frances Duncan, University of the Witwatersrand, RSA Laura Fielden, Truman State University, USA	
Symposium Organisers	**No.**	**Symposium Titles**
Thorsten Burmester (Germany) & Stefan Hetz (Germany)	**11.1**	It's not the heat - it's the humidity? Challenges and tradeoffs in insect respiration
Gerd Gäde (RSA)	**11.2**	Regulation of metabolism, growth, development and reproduction: from molecule to organismal research
Jadwiga Giebultowicz (USA) & David Denlinger (USA)	**11.3**	Biological clocks: from genes to physiology and behaviour
Wolfram Kutch (Germany)	**11.4**	Insect flight: new traits
Andrew Li (USA) & Glen Needham (USA)	**11.5**	New approaches toward understanding vector physiology and control
William Symondson (UK)	**11.7**	Trophic interactions using molecular approaches
Maciej Pszczolkowski (USA) & Sonny Ramaswamy (USA)	**11.8**	Juvenile hormone in adult physiology and behaviour: the roads less travelled

SECTION 12	BEHAVIOUR AND NEUROBIOLOGY	
Convenors	James W. Truman, University of Washington, USA Giovanni Galizia, Universität Konstanz, Germany	
Symposium Organisers	**No.**	**Symposium Titles**
Wolfgang Blenau (Germany), Arnd Baumann (Germany) & Patricia Pietrantonio (USA)	**12.1**	Signalling by G Protein-coupled receptors in arthropods
Silke Sachse (Germany) & Mattias Larsson (Sweden)	**12.2**	Neurobiology of sensory systems
Mike Adams (USA) & Sabine Kreissl (Germany)	**12.3**	Peptides and behaviour
Friedrich Barth (Austria) & Michael Hrncir (Brazil)	**12.4**	Stingless bees
Greg Holwell (Australia)	**12.6**	Behaviour and evolution of Mantodea
Ian Meinertzhagen (Canada)	**12.7**	Neural circuits in the insect brain

SECTION 13	SOCIAL INSECTS	
Convenors	Robin Crewe, University of Pretoria, RSA Theresa Wossler, University of Stellenbosch, RSA Klaus Hartfelder, Universidade de Sao Paulo, Brazil	
Symposium Organisers	**No.**	**Symposium Titles**
Vivienne Uys (RSA), Paul Eggleton (UK) & Jo Darlington (UK)	**13.1a** **13.1b**	Termite phylogeny and nest structure: Taxonomy and molecular phylogeny Nest structure, ventilation and homeostasis
David Nash (Denmark) & Koos Boomsma (Denmark)	**13.2**	Cooperation and conflict in insect societies: novel concepts and newly discovered mechanisms
Michael Schwarz (Australia)	**13.3**	Origins and losses of sociality: new insights that address big questions
Andy Suarez (USA) & Theresa Wossler (RSA)	**13.4**	The biology of a global invader: the Argentine ant
Gro Amdam (USA/Norway)	**13.5**	Endocrine and genetic network regulation of social life histories
Robin Moritz (Germany) & Theresa Wossler (RSA)	**13.6**	Genes and pheromones: the molecular basis of social parasitism in insect societies
Asha Rao (USA) & Bradleigh Vinson (USA)	**13.7**	Current advances in ant physiology and behaviour
Duur Aanen (The Netherlands)	**13.8**	Social insects and their symbionts: from mutualism to parasitism
Theo Evans (Australia)	**13.9**	Termites as beneficial insects
Ed Vargo (USA) & Claudia Husseneder (USA)	**13.10**	Breeding systems in social insects: causes and consequences of within colony genetic diversity

SECTION 14	SYSTEMATICS, PHYLOGENY & ZOOGEOGRAPHY	
Convenors	Martin Villet, Rhodes University, RSA Chris Simon, University of Connecticut, USA	
Symposium Organisers	**No.**	**Symposium Titles**
John La Salle (Australia)	**14.1**	New technologies and global initiatives in arthropod systematics
Thomas Pape (Denmark)	**14.2**	Names and naming in Entomology
Jim Whitfield (USA)	**14.3**	Ancient rapid radiations in insects: strategies and prospects for resolution
Mikhail Mostovski (RSA)	**14.4**	Insects in palaeoenvironments
Mike Picker (RSA) & Jeyaraney Kathirithamby (UK)	**14.6a** **14.6b**	Enigmatic Orders: Mantophasmatodea advances and controversies - 7 years after the discovery Biodiversity and systematics of Strepsiptera
Mike Sharkey (USA)	**14.7**	Hymenoptera: assembling the tree of life
Thomas Simonsen (Canada), Akito Kawahara (USA) & Charles Mitter (USA)	**14.8**	Lepidoptera phylogeny and evolution

SECTION 15	CONSERVATION, BIODIVERSITY & CLIMATE CHANGE	
Convenors	Michael Samways, University of Stellenbosch, RSA Tim New, La Trobe University, Australia	
Symposium Organisers	**No.**	**Symposium Titles**
Sacha Spector (USA)	**15.1**	Insect species conservation
Sujaya Rao (USA)	**15.2**	The pollinator crisis: native bees in native habitats and agricultural landscapes
Tim New (Australia) & Michael Samways (RSA)	**15.3**	Insect conservation in practice
Mattias Jonsson (New Zealand) & Marco Jacometti (New Zealand)	**15.4**	Insects and ecosystem services

SECTION 16	INVASIVE SPECIES	
Convenors	Helen Roy, CEH Monks Wood, UK Marc Kenis, CABI Europe, Switzerland Julie Coetzee, Rhodes University, RSA	
Symposium Organisers	**No.**	**Symposium Titles**
Franz Bigler (Switzerland) & Joop van Lenteren (The Netherlands)	**16.1**	Environmental benefits and risks of biological control
Remy Ware (UK) & Helen Roy (UK)	**16.2**	Harmonia axyridis: a model invasive insect
Alain Roques (France) & Andrea Battisti (Italy)	**16.3**	Insect invasions and climate change
Marc Kenis (Switzerland) & Sandy Smith (Canada)	**16.4**	Ecological impact of invasive insects
Craig Phillips (New Zealand) & James Ridsdill-Smith (Australia)	**16.5**	Defending national and internal borders against invasive insects
Michael Schauff (USA) & Michael Gates (USA)	**16.7**	Global impact of invasive Hymenoptera
Julie Coetzee (RSA)	**16.8**	Insect invasions in Africa
Julie Coetzee (RSA) & Martin Hill (RSA)	**16.9**	Insects as weed biological control agents

SECTION 17	INSECT PLANT INTERACTIONS	
Convenors	Peter Price, Northern Arizona University, USA Ingrid Nanni, South African Biodiversity Institute, RSA John Donaldson, South African National Biodiversity Institute, RSA	
Symposium Organisers	**No.**	**Symposium Titles**
Teja Tscharntke (Germany) & Jason Tylianakis (New Zealand)	**17.1**	Multitrophic-level interactions under climate change
Netta Dorchin (USA) & Joseph Shorthouse (Canada)	**17.2**	Gall inducing insects
Steve Johnson(RSA), Rob Raguso (USA) & Sue Nicolson (RSA)	**17.3**	Floral rewards and advertising
Philippe Giordanengo (France), Yvan Pelletier (Canada) & Charles Vincent (Canada)	**17.4**	Insects of solanaceous crops
Joe Bailey (USA) & Jennifer Schweitzer (USA)	**17.5**	Ecological and evolutionary consequences of insect plant interactions: a genes to ecosystems approach
Myron Zalucki (Australia)	**17.6**	Traversing a treacherous landscape: caterpillar movement and behaviour on whole plants at multiple scales
Wilson Fernandez (Brazil)	**17.8**	Comparison of tropical and temperate plant-insect interactions

SECTION 18	SPECIAL ISSUES	
Convenors	Vivienne Uys, Plant Protection Research Institute, RSA	
Symposium Organisers	**No.**	**Symposium Titles**
Marcel Dicke (The Netherlands) & Arnold van Huis (The Netherlands)	**18.1**	Insects and society
Jacques Brodeur (Canada) & Joop van Lenteren (The Netherlands)	**18.3**	What are ecology's contributions to biological control and vice versa?
Michael Schmitt (Germany) & Beth Grobbelaar (RSA)	**18.4**	Biology of the Chrysomelidae (Coleoptera)
Dawid Jacobs (RSA) & Ernst Heiss (Austria)	**18.5**	The true bugs (Heteroptera) with emphasis on the Afrotropical fauna
Jan-Hendrik Venter (RSA)	**18.6**	Developing sanitary and phytosanitary (SPS) capacity in Africa
Des Conlong (RSA) & Norman Leppla (USA)	**18.7**	Education and training in rearing insects for private and public ventures

WORKSHOPS		
Fabian Haas (Kenya) & Bernhard Löhr (Germany)	**W18.1**	Invasive species, biological control and the Convention on Biological Diversity

PLENARY SPEAKERS

Prof. Louise E.M. Vet
Netherlands

Director of the Netherlands Institute of Ecology (NIOO-KNAW) and Professor of Evolutionary Ecology, Wageningen University, Wageningen.

"Insect-plant interactions in a multitrophic world."

Dr. Zeyaur Khan
Kenya

Principal Scientist and leader of the Habitat Management Programme, International Centre of Insect Physiology and Ecology (ICIPE), Nairobi.

"Push-Pull" - a chemical ecology-based IPM strategy for smallholder farmers in Africa.

Dr. Walter R. Tschinkel
USA

Department of Biological Science, Florida State University, Tallahassee.

Exotic fire ants and native ants: a cautionary tale.

Prof. Maureen Coetzee
South Africa

National Institute for Communicable Diseases and the University of the Witwatersrand, Johannesburg.

Malaria and mosquitoes: will insecticide resistance be our downfall ?

Prof. H. Charles J. Godfray
United Kingdom

Hope Professor of Entomology, Department of Zoology, Oxford University, Oxford.

What structures the communities of plant-feeding insects ?

Prof. Raghavendra Gadagkar
India

JC Bose National Fellow, Centre for Ecological Sciences, Indian Institute of Science, Bangalore.

The functional organization of a tropical insect society.

ABSTRACTS

ORAL PRESENTATIONS

To Search, preferably use the Adobe search facility (under the ‘binoculars’ icon), otherwise press “CTRL” and “F” on your keyboard, type in the keyword(s) or phrase, then press “ENTER”

ABSTRACTS TO TALKS AND POSTERS THAT WERE NOT PRESENTED AT THE CONGRESS
(INCLUDING ABSENTEES AND ‘NO-SHOWS’)
ARE NOT INCLUDED IN THE CONFERENCE PROCEEDINGS

Whitefly resistance potential in different genotypes and cultivars of *Mentha* species

Dwijendra Singh

Central Institute of Medicinal and Aromatic Plants, Lucknow, India

Introduction: *Mentha* species are cultivated commercially as major natural sources of menthol both in tropical and temperate regions globally. Menthol is widely used in the cosmetics, perfumery, beverage, soft drink and pharmaceutical industries etc. The introduction of new chemo-types of mint species is regularly found associated with sweet potato whitefly during last two decades in India.

Methods: Whitefly (*Bemisia tabaci*) adult populations were sampled by applying yellow sticky traps in different plant genotypes of mint species. However, pupae population on menthol-mint leaves was counted with the help of a microscope in laboratory. The *Begmovirus* infection was recorded per m^2 area over healthy twigs during growth and development of mint.

Results: Among 26 entries of *M. arvensis*, 13 entries of *M. piperita*, and seven entries of *M. cardiaca,* two, one, and two entries were found comprising significantly higher resistant potential against whitefly resistance, respectively. Whitefly population build up was found maximum during Ist week of April and mid May in all the menthol-mint genotypes in northern Indian plain conditions. Among ten genotypes and cultivars of menthol mint, variety *Kushal* was found significantly ($P<0.05$) whitefly resistant over other cultivars. The infection of *Begomovirus* was found significantly low in field plots of Kushal and synthesized high oil content in fresh herb over other mint genotypes.

Conclusion: *Mentha* species genotypes and cultivars possessing significant potential resistant to whitefly and *Begomovirus* possibly be recommended further to use in integrated pest management programmes to develop new varieties and studies on insect plant interaction.

The landscape ecology of trophic interactions: Trait- and density-mediated effects

Peter Hambäck

Stockholm University, Stockholm, Sweden

It is becoming increasingly apparent that indirect interactions among species may be caused by changes not only in the abundance of intermediate species but also in their behaviour. This has been observed in a diverse array of interactions, both as behavioural changes in herbivores and as chemical changes in plants. The research on trait-mediated effects has however largely neglected the spatial dimension of species interactions, and how predators may affect the residence time of prey in local habitats. Predators may both cause a freezing behaviour and increased movements in herbivores, which both have direct effects on dispersal rates from host plant patches. Similarly, the spatial dynamics of herbivore-induced chemicals may affect immigration rates of both herbivores and predators into patches. In this talk, I will utilize a recently derived model that accounts for the scaling of migration rates for patches of different size and combine this model with a predator-prey model. In the original model, scaling rules for migration rates depend on the search mode by individuals and the model has successfully predicted variability in density-area relationships for broad groups of insect herbivores. In the predator-prey model, I aim to predict the relative distribution of predator and prey in a patch size gradient and to compare the relative importance of direct mortality and predator-induced changes in herbivore behaviour. This is done both by including different search behaviours by predator and prey but also by including feed-backs between the local predator density and the herbivore movement behaviour.

Population dynamics and management of the mango seed weevil, *Sternochetus mangiferae* (F.) (Coleoptera: Curculionidae), in South Africa

Johan de Graaf

Westfalia Technological Services, Duiwelskloof, Limpopo Province, South Africa

Introduction: *Sternochetus mangiferae* (F.) is quarantine pest of mango in South Africa, preventing exports to several countries. The aim of the study was to investigate the population dynamics and chemical control of the insect.

Methods: The population dynamics were monitored in mango orchards from the onset of weevil egg laying until harvest of fruit. Fruit were sampled randomly every two weeks from trees located in stratified plots. The infestation levels and proportion of infested fruit were recorded for each life stage. The chemical trials used a replicated block design with three replicates. The efficacy of fenthion, fenvalerate, fipronil and thiamethoxam was determined by a similar sampling procedure as the population dynamics trial series, but also noted scale insects on the fruit surface. Analysis of variance (*post hoc* Tukey HSD test) was used to analyse the data
.

Results: Eggs were observed over 12 weeks and showed a long peak through November and December. Small larvae, large larvae, pupae and adults mainly occurred in mid November, early December, mid December and early January. Fruit was the most vulnerable to infestation by eggs laid 4-5 weeks after the onset of oviposition. The weevil was only susceptible to chemical control before larvae entered the seed and the most effective chemicals were thiamethoxam and fipronil, resulting in less than 1% and 10% infestation at harvest, respectively. Fipronil caused the greatest number of fruit infested with scales.

Conclusion: Insecticides is an important control measure as part of a systems approach to manage the mango seed weevil.

Facing the problems of predicting insect distributions

Jorge M. Lobo[1], Alberto Jiménez-Valverde[1], Joaquín Hortal[2]

[1]Museo Nacional Ciencias Naturales, Madrid, Spain, [2]NERC Centre for Population Biology, Imperial College London, London, United Kingdom

Predictive modelling methodologies are commonly thought as being reliable enough to improve significantly the limited information on the distribution of species. However, studies predicting the distribution of insect species are scarce. Here, we review some of the basic problems of predictive modelling, analyzing how they apply to the particular case of insects. First, we discuss the essence and dynamics of the potential and realized distribution of species, making a critic assessment of how predictive models could provide a consistent picture of such dynamic phenomenon. Then, we examine the effects of the quality and bias of distributional data used to feed the models on their performance. In addition, we analyze the influence of the choice and use of predictors in the results and utility of the obtained models as well as the applicability of standard validation procedures. The negative effects of data quality are amplified in the case of insects; information on the distribution, taxonomy and ecological requirements of insect species is scarce and hard to access. This problem is aggravated by the high diversity that insects represent. We provide clues and practical choices for the entomologists to (a) improve the quality of their predictive maps for insect distributions, and (b) assess the limitations and utility of these predictions derived from limited data quality and knowledge about their ecology.

Structure and diversity of dung beetles communities (Coleoptera: Scarabaeoidea) in Southern Larzac (France)

Jean-Philippe Deguine[1], Eric Goze[2], Jean-Pierre Lumaret[3]

[1]CIRAD, Saint-Pierre, La Réunion, France, [2]CIRAD, Montpellier, France, [3]CNRS, Montpellier, France

Introduction: The ecosystems of Southern Larzac (France) have experienced an evolution of pastoral practices which progressively led to a change of landscape structure. With the disappearance of transhumance and the decrease of grazing, the landscape tends to close up and it ancestral equilibrium is changed. Thus, the role of dung beetles (Coleoptera: Scarabaeoidea) and the organization of their communities are strongly modified. The aim of this work is to analyse the structure of these communities and their diversity according to this global evolution.

Methods: The study was carried out during the year 2005. The insects were collected with attractive baited pitfall traps in six sites during four periods of the year. The Motomura model was used to analyse the diversity and the organization of communities. The distribution of the main species was described with correspondence analysis taking into account climatic parameters and pastoral practices.

Results: 4582 insects were collected. The study of the communities showed a wide range of 46 species belonging to four families (Aphodiidae, Scarabaeidae, Geotrupidae, Trogidae). The functional groups differed depending on the seasons, the pedoclimatic characteristics and their breeding requirements.

Conclusion: These preliminary results on the seasonal and spatial structure of the populations of dung beetles highlight the significant role of dung beetle communities in Larzac ecosystems. From a Biological Conservation point of view, our results can help to take decisions for a sustainable management of these ecosystems.

Microorganisms as mediators of tree-insect interactions: Pathogens, saprogens and cofactors

Kier Klepzig

USDA Forest Service, Southern Research Station, Pineville, LA, United States

Introduction: Oleoresin flow is an important factor in resistance of pines to attack by southern pine beetle and its associated fungi. However, little is known of the effects of inoculation with beetle associated fungi on oleoresin flow.

Methods: We measured how constitutive and induced resin yield in loblolly pine was affected by mass fungal inoculation with the southern pine beetle associated fungus *Ophiostoma minus*.

Results: As long as 105 days post-treatment, mass inoculated trees produced higher induced resin yields than control or wounded-only trees. This indicated a localized induced response to fungal inoculation. We noted no systemic induction of host defenses against fungal colonization. Despite mass inoculations, *O. minus* did not kill any host trees. It is unlikely that this fungus functions as a virulent plant pathogen.

Conclusions: While some bark beetle associated fungi can kill trees, numerous inoculation studies have failed to demonstrate a similar role for *O. minus*. Rather, the role of bark beetle associated fungi may be that of 'co-factors' - biotic agents that are not pathogenic in and of themselves but do function in compromising host defenses.

In the bark beetle system, the primary role of the associated fungi may be to aid in exhausting tree defenses and thereby allow beetle establishment. The moderately virulent habit of *O. minus* may, ultimately, be the best strategy for SPB. This allows the beetle to successfully mass attack the tree, but limits the extent to which the fungus can grow during the process of beetle development.

The ubiquity of indirect effects

Peter Price

Northern Arizona University, Flagstaff, United States

An indirect effect occurs when the influence of one species, the donor, is transmitted through a second species, the transmitter, to a third species, the receiver. Since the first food webs about 100 years ago, indirect effects have been evident, and more common than direct effects. This is because species share resources and consumers on each trophic level, so the impact of one influences the other species. Bottom-up and top-down effects cascade through food webs impacting all trophic levels, and “the balance of nature” is tightly linked to indirect effects conceptually, making the subject of central importance in ecology. Apparent competition, multiple-trophic-level interactions, trophic cascades, induced chemical and structural changes, and above and below ground interactions, all contribute to knowledge on indirect effects. Moving from food webs to include indirect interaction webs provides a more holistic and synthetic concept of nature. Because predators kill prey, they influence the density of one species A, and thus indirectly affect the density of another species B interacting with A through competition. This is a density-mediated indirect interaction. But, small herbivores usually act more as parasites on large host plants, seldom killing host plants but altering host traits, such as rolling leaves, or inducing chemical defenses. These traits affect other herbivore species, resulting in trait-mediated indirect interactions. The conceptual development of this large field, and the empirical evidence, contribute importantly to the development of community ecology.

Scolytine beetles and *Ceratocystis* fungi: a deadly interaction for tree health in Africa

Jolanda Roux, Gilbert Kamgan Nkuekam, Ronald Heath, Michael Wingfield

DST/NRF Centre of Excellence in Tree Health Biotechnology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa.

Various insect species have associations with fungal tree pathogens. These associations can be very specific, such as those involving the tree pathognenic fungus *Ceratocystis laricicola* and the bark beetle *Ips cembrae*, or casual as is found in the case of Diptera (*Drosophila melanogaster)* and the oak wilt pathogen, *Ceratocystis fagacearum*. The insects provide the fungi with transport to new trees and also wounds, necessary for infection. Ambrosia beetles (Coleoptera: Playtypodidea), which have very specific associations with fungi, maintain pure cultures of their symbionts, thereby protecting the fungi from competitors and providing food for the vectors. Little is known regarding bark and ambrosia beetles and their fungal associates on hardwood tree species in the Southern Hemisphere. More specifically, studies on *Ceratocystis* spp. and their insect associates in Africa, are limited to a few recent examples. These recent studies have specifically considered the role of wounds emerging from anthropogenic activity, such as pruning and harvesting of bark for medicinal purposes. Insect infestation was found to be common on these wounds and the insects involved included nitidulids (Coleoptera: Nitidulidae), bark (Coleoptera: Scolytinae) and ambrosia beetles. Several species of *Ceratocystis* and other fungi have been isolated from these insects and their tunnels. These included known tree pathogens as well as several previously undescribed species. The results of a small number of studies clearly illustrate the need for further and more detailed investigations on the Coleoptera and their fungal associates in Africa.

Ant use of antibiotics in agriculture

Michael Poulsen, Cameron Currie

University of Wisconsin, Madison, Madison, WI, United States

The dynamics of host-pathogen associations are believed shaped at least in part by evolutionary arms races, in which pathogens evolve to overcome host defenses and hosts are selected to counter-act these through the evolution of new defense mechanisms. Fungus-growing ants appear to have successfully employed antibiotic-producing actinomycete bacteria in the genus *Pseudonocardia* for millions of years to defend their mutualistic fungus gardens from specialized microfungal *Escovopsis* parasites. Here we explore host-pathogen dynamics in the fungus-growing ant symbiosis by evaluating inhibitory capacities of *Pseudonocardia* originating from different ant colonies against a variety of *Escovopsis* strains, in addition to examining the link between *in vitro* inhibition and *in vivo* defense by the *Pseudonocardia* symbionts. Our results suggest that antibiotic resistance has evolved repeatedly in the parasite and that resistant strains are substantially more virulent to fungus-growing ant nests than strains susceptible to the antibiotics. Counteracting antibiotic resistance is the apparent continuous evolution of novel antibiotic compounds in the bacteria. The diversity and specificity in the antibiotics suggest ongoing antagonistic co-evolutionary arms race dynamics in the fungus-growing ant–microbe symbiosis. These dynamics are characterized by defense release of the immediate host (the fungal cultivar), while selection on antibiotic resistance and novel defenses appear to occur between alternative parties in the association (*Pseudonocardia* and *Escovopsis*). Fungus-growing ant use of actinomycete-derived antibiotic production may thus mirror many human pharmaceutical and agricultural practices, where the challenge of maintaining efficient antibiotics against continuously evolving antibiotic-resistance in parasites persists.

Conflict and cooperation in fungus-growing ant mutualisms

Michael Poulsen

University of Wisconsin, Madison, Madison, WI, United States

Potential conflict between partners involved in mutually beneficial associations is predicted to destabilize cooperative relationships. Theoretical and empirical work exploring such conflict has provided significant insight into how it influences relationship dynamics. Here I present results exploring the complexity of conflict within the ancient and coevolved mutualistic associations between attine ants and their fungal cultivar (*Leucoagaricus*) reared for food and actinomycetous bacteria (*Pseudonocardia*) reared to obtain antibiotics against potentially virulent microfungal *Escovopsis* parasites. Both ant-mutualist associations occasionally experience horizontal transmission, potentially decoupling the reproductive interests of host and symbionts and incurring competition between mixed symbiont strains. However, it appears that i) default vertical symbiont transmission aligns the reproductive interests of the partners, and that ii) single symbiont rearing within individual colonies prevents the expression of competitive symbiont-symbiont conflict. The rearing of a single fungal clone within a colony is not expected to pose a cost to the ants in relation to increased colony susceptibility to infection, because the cultivar itself does not have efficient defense against *Escovopsis*. However, the rearing of a single strain of actinomycetes could constrain the effectiveness of the ant-*Pseudonocardia* symbiosis, because rearing multiple strains of antibiotic-producing bacteria would increase antibiotic diversity. The findings presented suggest additional layers of complexity of conflict expression within the fungus-growing ant microbe–symbiosis, through the presence of antagonism between genetically different mutualistic symbionts maintained by different ant colonies, but also through the presence of additional symbiont lineages (*Escovopsis*) that adjust conflict dynamics within an association previously examined in a bipartite framework.

Symbiotic relationships of an invasive psyllid colonizing eucalyptus in California, USA

Allison Hansen, Richard Stouthamer, Timothy Paine

Department of Entomology, University of California, Riverside, Riverside, California, United States

Two endosymbionts, an obligate primary symbiont and facultative secondary symbiont are harbored within the invasive red gum (eucalyptus) lerp psyllid, *Glycaspis brimblecombei*, in California. An extensive survey of diversity and frequency of *G. brimblecombei*'s secondary symbiont was conducted in multiple populations throughout the state of California using PCR detection, restriction enzymes, cloning, and sequencing. A total of 380 *G. brimblecombei* individuals were screened for secondary symbionts among 19 populations. Based on molecular screening results, only one type of secondary symbiont was present among *G. brimblecombei* populations in California. Secondary symbiont infection frequencies among *G. brimblecombei* populations varied dramatically from 0-75%, and were significantly related to parasitism pressure by *Psyllaphaegus bliteus*, a solitary endoparasitoid of the psyllid. *G. brimblecombei* is also associated with a phage which has an intimate relationship with the secondary symbiont. This phage may be a key mechanism in providing potential resistance to parasitism in secondary symbiont infected psyllids.

A new look at beetle-fungus-tree interactions

Timothy Paine

University of California, Riverside, CA, United States

Scolytid bark beetles that colonize living conifers are frequently associated with specific fungi that are carried in specialized structures or on the body surface. These fungi are introduced into the tree during the attack process. The continuing association suggests that there is mutual benefit to the fitness of both beetles and fungi. Extensive research has been directed towards characterizing the interactions of beetle-fungal complexes with live host conifers and determining the advantages for maintaining the associations. The fungal species may benefit from the association with the beetles by transport to new host trees. Beetle species may benefit from the association with fungi by feeding on the fungi, by limiting the impact of potentially detrimental fungi, or by the fungi contributing to the death of the host trees through mycelial penetration of host tissue, toxin release, interactions with preformed and induced conifer defenses, or the combined action of both beetles and fungi during colonization. However, differences among systems and how species interact under different population and environmental conditions make it difficult to generalize about the importance of the separate biological components in successful host colonization. The objective of this evaluation is to describe the paradigms of beetle-fungal-host tree interactions over the last five decades and to establish the historical research context for current efforts.

Genetic identification of forensically important flies

Judith Smith

University of Central Lancashire, Preston, United Kingdom

Insects, in particular members of the Calliphoridae (blowflies) and Sarcophagidae (fleshflies) can be important indicators in a forensic investigation.

Blowflies are attracted to a corpse within minutes of death and the stages and species identified on a body can provide important evidence. Most importantly the stages of the particular species identified can help determine time since death. In addition, the location of maggots on a body can in some cases help determine the cause or manner of death or provide evidence of abuse and the identification of particular insect species may provide evidence as to whether a body has been moved.

Forensic entomology requires and understanding of the ecology, behaviour, developmental biology, and genetics of the species involved. Rates of development can vary even between closely related species thus accurate species identification is critical for an accurate calculation of time since death. Morphological identification is time consuming, complex and highly subjective to the untrained eye, genetic identification could provide a quick and unambiguous way to identify species. We present an analysis of the use of mitochondrial genes for species identification of forensically important blowfly species in the UK.

Induced host-plant volatiles with the aphid sex pheromone using a specific trap design create a highly selective attractant for the male aphid *Dysaphis plantaginea*

Rob van Tol[1], Herman Helsen[2], Frans Griepink[1], Willem Jan de Kogel[1]

[1]Plant Research International, Wageningen, Netherlands, [2]Applied Plant Research, Randwijk, Netherlands

Introduction: All aphid species studied so far share the same sex pheromone components nepetalactol and nepetalactone. Variation by different enantiomers and blends of the two components released by different aphid species is limited and can only partially explain species-specific attraction of males to females. While some host-plant odours are known to enhance more specific attraction of aphid species, herbivore-induced plant volatiles that attract male aphids more specifically to female infested host-plants are unknown.

Methods: Relevant odours of infested apple trees were identified by GC-MS and GC-EAD techniques. Different mixtures of identified plant volatiles and aphid pheromone were tested in an apple orchard on attraction of aphids to different trap types.

Results: We demonstrate that for the host-alternating rosy apple aphid (*Dysaphis plantaginea*) specificity of attraction of males to females on the primary host plant, *Malus* sp. is enhanced by female-induced tree odours in combination with the pheromone. Female aphid infestation induce increased release of four butyrates from apple leaves. These butyrates increase the number of male *D. plantaginea* and decrease the number of other aphid species caught in water traps in the presence of the pheromone components. The butyrate blend alone was not attractive. A further 90% reduction in by-catch of other aphid species was achieved by using an adapted trap allowing aphids to walk after landing. Odour-mediated orientation of male aphids after landing during walking appears to be an important next step in selective attraction to conspecific females.

Conclusions: The demonstration that sexual aphid species use herbivore-induced plant volatiles as a species-specific attractant for mate finding adds a new dimension to our understanding of insect species using or manipulating chemical cues of host plants for orientation.

Populations of lacewings, *Chrysoperla carnea* (Stephens), in relation to sucking insect pests in cotton ecosystems

J.M.Mari, S.M.Nizamani, M.K.Lohar

Sindh Agriculture University Tandojam Pakistan, Hyderabad, Pakistan

The results on population of lacewing in relation to sucking insects pests in cotton ecosystem through direct plant count method was recorded in the vicinity of Sindh agriculture University Tando Jam Pakistan from 8th May to 25th September, at weekly intervals. The consolidated data showed that the sucking insect pest population was highest on 19th July. The regression equation showed that the population growth with time interval was highly significant. The slope rate of population increase was 0.950X. The R-square was 0.98 which explained that about 98 percent variation in population increase was observed by weeks. Thereafter, population decreased and reached its minimum with a declining curve-0.434X it also showed a highly significant relation among population and dates. The R-square was r^2= 0.66. The predator population increased gradually and linearly it was on their peak (6.74) per leaf on 21st September. The regression analysis indicated that the population was highly significant with time interval. The slope of line with increasing trend was 0.4278X. The R-square of model was estimated to be 85. The highest population of predators could be due to easy access of sucking insect pests. The population of lacewing was associated with the sucking insect pests. Lacewing population were positive and highly significant (r=0.863) with aphid. It may be concluded that the population of sucking insect pests was more during the month of July and August, aphid appeared late than the other pests. It was found that increasing population of aphid progressively increased the population of lacewing. For effective control of aphid in cotton spray of any kind of agro-chemicals in and around the cotton crop may be avoided.

Critical analyses of successes and failures of biological control in Africa

Peter Neuenschwander

International Institute of Tropical Agriculture, Cotonou, Benin

Classical biological control has been practiced in Africa since the 19th century. Introductions of insect natural enemies peaked in the 1980s (at around 150). Percentage establishment peaked at 65% in the 1990s, with about 10% contributing to control. Biological control of weeds by insects and later pathogens was practiced mainly in South Africa. Since the 1980s, international collaboration in Africa-wide projects, starting with the control of cassava mealybug and cassava green mite by arthropod predators and followed by a mycopesticide against grasshoppers, brought a new surge in foreign exploration, research, releases, impact assessment and training at all levels.

Documented benefits in crop loss prevention alone – without the concomitant environmental and human health benefits – are huge. Despite these successes, biological control remains controversial and often the last option, when other choices like pesticides and crop varieties have failed to give the expected results. We attribute this reluctance to place resources into biological control to the following factors: 1- continued occurrence of short-term and local pest outbreaks even in successful projects, 2- incomplete coverage of ecological niches by biological control agents, 3- interference with other agricultural techniques (pesticides, but also bad soil and water management), 4- unreasonable requirements on efficiency through low economic thresholds, while full costs of other options are not taken into account, 5- too stringent requests concerning non-target impacts, based on comparisons with the status before the accidental introduction of the pest, instead of the status quo. Priority actions concern foreign exploration, biological control in IPM and public awareness.

Managing mosquito threats using personal protection strategies: Living with mosquitoes in northern New South Wales, Australia

David Durrheim[1], Cameron Webb[3], Richard Russell[3]

[1]Hunter New England Population Health, Hunter New England Area Health Service, Newcastle, Australia, [2]School of Medical Practice and Population Health, University of Newcastle, Newcastle, Australia, [3]Department of Medical Entomology, University of Sydney and ICPMR, Westmead Hospital, Sydney, Australia

The transmission of the disease-causing pathogens, Ross River virus and Barmah Forest virus, results in over 5000 notified cases of mosquito-borne disease annually in Australia. There has been a steady increase in notifications during recent years in northern NSW, as residential and recreational land uses encroach on productive mosquito habitats. Local vector biology and legislative requirements limit the possibility of large scale mosquito control programs, and a newly developed region-wide mosquito awareness strategy emphasises personal protection measures.

The 'Living With Mosquitoes' strategy was developed in conjunction with local, state and federal agencies, and represents the first regionally specific approach to mosquito-borne disease management in NSW. The first stage of this strategy is a coordinated mosquito awareness program with the key element being effective communication of accurate information on personal protection measures, including the appropriate selection and application of insect repellents.

An innovative communications strategy has been developed that addresses the issues of public health and nuisance-biting risks with personal protection measures to complement the overall environmental education messages of the region.

A natural bridged tricyclic sesquiterpene, (–)-Isolongifolenone, is a repellent against ticks and mosquitoes

Aijun Zhang[1], Shifa Wang[2], Jerome Klun[1], John Carroll[3], Mustapha Debboun[4]

[1]Invasive Insect Biocontrol and Behavior Laboratory, Beltsville Agriculture Research Center-West, USDA, Agriculture Research Service, Beltsville, Maryland 20705, United States, [2]College of Chemical Engineering, Nanjing Forestry University, Nanjing, Jiangsu 210037, China, [3]Animal Parasitic Diseases Laboratory, Beltsville Agriculture Research Center-East, USDA Agricultural Research Service, Beltsville, Maryland 20705, United States, [4]US Army Medical Department Center & School, Academy of Health Sciences, Department of Preventive Health Services, Medical Zoology Branch, Fort Sam Houston, TX 78234, United States

Introduction: Human diseases transmitted by blood-feeding mosquitoes represent a serious threat to public health worldwide. More than 700 million cases of mosquito-transmitted diseases have been reported annually. Over 3 billion people live under the threat of malaria, which kills millions annually. Consequently personal protection from mosquitoes is of great importance. A synthetic compound, Deet, is the most widely used insect repellent worldwide. However, it is a synthetic compound and a plasticizer, perceived by as some safety and environmental concerns regarding human usage and water pollution. Therefore, there is clear and good reason to pursue discovery of new chemical tools that might help alleviate above suffering.

Methods: Efficacy of the compound against mosquitoes and ticks was evaluated using the in vitro K&D module bioassay and fingertip bioassay systems.

Results: We discover that (–)-isolongifolenone deters the biting of the yellowfever mosquito, *Aedes aegypti* and *Anopheles stephensi*, a mosquito vector of malaria, more effectively than Deet. We also found that (–)-isolongifolenone repelled the blacklegged tick, *Ixodes scapularis*, and lone star tick, *Amblyomma americanum*, as effectively as Deet. However, at lower concentrations, the (–)-isolongifolenone was more effective against *I. scapularis* than Deet.

Conclusions: Inasmuch as derivatives of isolongifolenone have routinely been used in topically applied cosmetics, we believe that newly discovered properties of the compound give it good potential as a natural product for further development and eventual safe-clinical usage for protection of humans, especially, for military and general public usage against mosquito, tick, and sand fly bites.

Impacts of honeybees on native bumblebees in northern Europe

Dave Goulson

University of Stirling, Stirling, United Kingdom

Honeybees are well known to be non-native organisms in large parts of the globe, but in Europe they are generally regarded at native species. However, in northern Europe they are unlikely to be native and exist at artificially high densities due to assistance from man. I present data that demonstrate a clear effect of honeybees on worker size in a range of bumblebee species in Scotland. Since worker size reflects food return to the colony, and small workers bring back less food, these data strongly suggest that honeybees do have a significant negative impact on the population biology of other social bees in Europe, and that this impact should be considered when deciding on placement of hives and on conservation strategies for native bee species.

DNA barcoding reveals the area of origin of the highly invasive horse chestnut leaf-miner *Cameraria ohridella*

Carlos Lopez-Vaamonde[1], Romain Valade[1], Ferenc Lakatos[2], Sylvie Augustin[1], Marc Kenis[3]

[1]INRA-Orléans, Zoologie Forestière, Olivet, France, [2]University of West-Hungary, Institute of Sylviculture and Forest Protection, Sopron, Hungary, [3]CABI Bioscience Switzerland Centre, Delémont, Switzerland

Introduction: Recent biological invasions usually start with a small number of founder individuals which are likely to be a small fraction of the total genetic diversity found in the original population from which they derive. The aim of our work is to genetically trace the geographical origin of the horse-chestnut leafminer, *Cameraria ohridella*, an invasive microlepidoptera, whose area of origin is unknown. Since its discovery in Macedonia twenty years ago, this insect has experienced an explosive westward range expansion progressively colonizing all central and Western Europe. Here we use DNA barcoding to assess the genetic variability of *C. ohridella* populations and to test the hypothesis that *C. ohridella* comes from the Balkans. The Balkans is the region where the moth was first found and from where the European horse-chestnut originates.

Methods: We use DNA barcoding to study the genetic variability of *C. ohridella*, across its known geographical distribution.

Results: Our results show a reduction in genetic diversity of *C. ohridella* populations sampled from natural stands of horse-chestnuts in the Balkan mountains to *C. ohridella* sampled in parks across Europe.

Conclusions: These findings suggest that European populations of *C. ohridella* may indeed derive from the Balkans.

Taking dengue control from the government to the people: Development of a 'Do it yourself' Lure and Kill technology for dengue control

Scott Ritchie[1], Luke Rapley[1], Brian Montgomery[2], Richard Russell[3]

[1]James Cook Univ., Cairns, Queensland, Australia, [2]Queensland Health, Cairns, Queensland, Australia, [3]Un. Sydney, Westmead, New South Wales, Australia

We have been engaged in a R&D program to develop a “lure and kill” approach (L & K) to control dengue in north Queensland Australia. The basic lethal ovitrap employed (Williams et al. Impact of a bifenthrin-treated lethal ovitrap on *Aedes aegypti* oviposition and mortality in north Queensland, Australia. J Med Entomol 44: 256-262) has proven successful in lab and field trials. Several interventions against dengue have also been successful. Indeed, we have been able to reduce our pesticide usage by at least 90%, and gain access to many more properties, using L & K rather than the previously employed Interior Residual Spraying (IRS). We are currently improving the methodology by using biodegradable lethal ovitraps that leak before they become a breeding site, and thus do not require retrieval by staff. Finally, we have conducted field trials demonstrating that metofluthrin emanaters readily kill *Ae aegypti* within rooms and provide nearly 100% protection from biting. We are developing a "do it yourself" dengue kit composed of LOs and, potentially, metofluthrin emanaters that would allow rapid community engagement for emergency dengue control on a broad scale.

Predator identity and the nature of trait-mediated indirect effects

Oswald Schmitz

Yale University, New Haven, Connecticut, United States

Introduction: Trait-mediated indirect effects propagated by herbivore anti-predator responses to their predators are widespread in ecological food webs. But, trait-mediated effects vary in their nature and strength. Predicting when and how trait-mediated effects arise is important for understanding the role of predators in communities. Such understanding might be derived by knowing predator hunting mode and the spatial domain of predator and prey habitat use.

Methods: A synthesis of literature on predator hunting mode and prey and predator habitat domain led to a framework for predicting the nature of trait-mediated indirect effects.

Results: The nature of trait-mediated indirect effects varied with predator hunting mode (e.g., sit-and-wait vs. active hunting) and habitat domain (narrow vs. broad). Trait-mediated effects arose whenever sit-and-wait predators have a narrow habitat domain and prey have a broad domain that allows habitat switching because the predators emit chronically strong cues of presence. Sit-and-wait predators cause chronic feeding activity reductions (as opposed to habitat sifts) when they face prey with narrow habitat domains. Alternatively, predators that actively hunt throughout the entire habitat (broad domain) will leave very diffuse cues of presence. Prey will thus only respond to imminent predation threat. Such predators tend to cause largely density-mediated indirect effects.

Conclusions: Predator hunting and predator and prey habitat domain provides a useful functional way of predicting the nature and strength of trait-mediated indirect effects.

Selection on the integrated phenotype: Responses in migratory traits of *Gryllus firmus*

Derek Roff, Daphne Fairbairn

University of California, Riverside, CA, United States

Introduction: We investigated the coevolution of the integrated suite of traits associated with migratory capability in insects by imposing selection on two core traits, ovary weight (an index of fecundity) and weight of the dorso-longitudinal flight muscles (DLM) in females of the wing dimorphic cricket, *Gryllus firmus.* Micropters lack significant DLM and have heavier ovaries than macropters. Within macropters, ovary weight is negatively correlated with DLM weight. Wing morphology, ovary weight and DLM weight are all inherited and genetically correlated. We selected for increased ovary or DLM weight, or an increased index (= product of ovary and DLM weight) and then compared the direct and correlated responses with those predicted by an individual-based quantitative genetic model constructed using parameters estimated from a previous half-sib breeding experiment.

Methods: We used 5 generations of family selection, taking the top 25 families out of an average of 60 families/generation, based on the mean of 5 females/family.

Results: All predictions were sustained. Selection for increased fecundity caused a correlated increase in ovary weight and proportion micropterous but decreased DLM weight. Selection for increased DLM weight produced the opposite responses. Selection on the index increased both ovary and DLM weight. In all three cases the intercept of the regression of fecundity on DLM weight increased.

Conclusions: Selection produced quantitatively predictable changes in both the focal traits and the suite of correlated traits, indicating that quantitative genetic parameters adequately capture the short term coevolutionary dynamics of this complex suite of integrated traits.

Introduction to the structure and function of termite mounds

Jo Darlington

University of Cambridge, Cambridge, United Kingdom

When termites build nests in the soil, they are exposed to soil predators. One response is to concentrate the nest into a single populous hive and so minimise soil contact. A side effect of this is that metabolic products (gases and heat) cannot easily disperse through the soil pores. The extreme case is in fungus-growing termites, where the biomass of the termites themselves is augmented by that of the fungus combs, so that overall nest metabolism is at least trebled. Improved ventilation is supplied by the structure of the hive, surrounding passages, and the soil mound above it. This is a passive ventilation system because the nest is built of soil, and so its structure is rigid. There are several different designs. The simplest and commonest type consists of open vertical shafts that link up underground. External wind draws ambient air through the shafts in response to the height and structure of their rims. A rare type of nest has a single tall chimney through which air vents directly from the nest. This is the only outflow, and enables us to make direct measurements of metabolic products from the nest. The most complex type consists of a structured passage system inside a closed mound, where gas exchange takes place through the outside wall. This has proved more difficult to interpret than the mounds with open ventilation systems, and new work from several sources will be presented in this section.

The air-conditioned termite nest revisited

Scott Turner

SUNY College of Environmental Science & Forestry, Syracuse, New York, United States

Termites of the genus *Macrotermes* are renowned for the building of spectacular mounds. In 1960, the Swiss entomologist Martin Lüscher proposed that these mounds provide "air-conditioning" (i.e. temperature and humidity control) for the metabolically effervescent nest. Lüscher's beautiful conception is, to this day, a textbook example of "superorganismal physiology." In recent years, however, Lüscher's conception has come under criticism: his proposed mechanism for the air-conditioning appears to be wrong; it is unclear precisely what property of the nest is being regulated, and it says little about how such a remarkable structure comes to be built in the first place. In my presentation, I will outline recent work on the mechanisms of nest ventilation, nest temperature and nest moisture of *Macrotermes michaelseni*, a species that is widespread through sub-Saharan Africa. I will argue that it is nest water balance, rather than regulation of nest gas exchange or temperature, that drives mound construction and repair, and that the mound's respiratory function is a secondary adaptation that has evolved on this foundation.

Community dynamics of *Ips typographus* - associated fungi in spruce stands following storm disturbance

Rimvydas Vasaitis[1], Bo Långström[2], Halvor Solheim[3], Ylva Persson[1], Katarina Ihrmark[1], Jan Stenlid[1]

[1]Department of Forest Mycology and Pathology, Swedish University of Agricultural Sciences, Uppsala, Sweden, [2]Department of Ecology, Swedish University of Agricultural Sciences, Uppsala, Sweden, [3]Norwegian Forest and Landscape Institute, Ås, Norway

Ips typographus is economically most important insect pest of mature spruce in Eurasia. Normally, it prefers to reproduce in dead and/or dying trees, but following large-scale storm disturbances, its outbreaks kill waste areas of living stands. One factor triggering such epidemics is a surplus of broken and uprooted trees with non-existent, or weak, defence. While infesting vigorous spruce, blue-stain fungi carried by *I. typographus*, play important role for success of beetle attack. In Europe, *I. typographus* is associated with about 30 fungal species, among which primary invaders *Ceratocystis polonica* and *Ophiostoma europhioides* are the most pathogenic: artificial inoculations with those fungi kill healthy spruce even in absence of the insect. During the rise of beetle outbreak, living trees are increasingly attacked and pathogenic primary invaders gain habitat in which they are more competitive than other fungi, e.g. due to ability to grow through resin-impregnated sapwood under oxygen deficient conditions. During non-outbreak periods, the beetles utilize dead wood, more accessible to saprotrophic fungi. Consequently, the dynamics of *I. typographus* outbreak might influence the incidence and frequency of the pathogens, which could play a major role in further development of the epidemics. We hypothesize that during non-outbreak periods pathogenic blue-stain fungi occur at low frequencies in overall fungal community, but their frequencies increase gradually when living trees are attacked, enhancing future dieback. In Sweden, the storm on January 2005 resulted in approximately 164 million of downed spruce. Here, we present preliminary results on community dynamics of blue-stain fungi during the subsequent outbreak of *I. typographus*.

To free or not to free: the New Zealand experience

Libby Harrison[1], Rachel Helson[1], Barbara I.P. Barratt[2]

[1]Environmental Risk Management Authority, New Zealand, Wellington, New Zealand, [2]AgResearch, Invermay, Mosgiel, New Zealand

New Zealand is a South Pacific archipelago with a classic island ecology. It was first settled by Polynesians – ancestors of today's Māori – less than 1000 years ago, followed by Europeans in the late 1700s. Most of its native fauna and flora are endemic and highly valued by New Zealanders. Agriculture makes an important contribution to the national economy, which means the agricultural landscape, too, is highly valued. In 1996, the Hazardous Substances and New Organisms Act (HSNO Act) was passed to prevent or manage adverse effects on the environment, and on the health and safety of people, from the introduction of either hazardous substances or new organisms. In the Act the principal definition of a new organism is a species not established in New Zealand before 1998, when the Act came into force. An important feature of the regulatory process is that when the decision to approve or decline the introduction of an organism is being made, the beneficial effects of the organism are weighed against the adverse effects. This presentation uses case histories of approved introductions of invertebrate biological-control agents to demonstrate how New Zealand evaluates beneficial and adverse effects across the board – on the environment, on the health and safety of people, on societies and communities, on the economy and on Māori culture.

Priming of inducible defenses by volatiles from neighboring plants and endophytic bacteria

Ted Turlings[1], Jurriaan Ton[2], Matthias Erb[1], Marco D'Alessandro[1]

[1]University of Neuchatel, Neuchatel, Switzerland, [2]Rothamsted Research, Harpenden, United Kingdom

Plants have evolved an elaborate arsenal of physical and chemical defenses that allow them to cope with their numerous attackers. An increasing number of studies suggest that, if properly understood, these natural plant defenses can be manipulated and exploited for the control of insect pests. We have been studying a form of indirect plant defense, whereby, in response to insect feeding, plants emit various volatile compounds that attract the natural enemies of their attackers. Using maize as our model plant, we recently found that such induced volatiles affect defense responses in neighboring plants. This effect is only evident when the exposed plants themselves are attacked, at which point defense genes show rapid and enhanced expression and direct, as well as indirect defense compounds are produced faster and in larger quantities. This so-called priming for defense has now been demonstrated in several plant species and is expected to primarily function in within plant communication. We have also found that endophytic bacteria contribute to a plant's volatile emissions and thereby enhance the resistance of the host plant to other pathogens. I will give an overview of our work in these areas with an emphasis on the possibility to manipulate volatile emissions in crop plants in order to enhance direct and indirect resistance against pests.

Outbreak dynamics of geometrid moths in climatic gradients in sub-arctic birch forest

Jane U. Jepsen[1], Snorre B. Hagen[1], Rolf A. Ims[1], Nigel G. Yoccoz[1], Helena Bylund[2]

[1]University of Tromsø, Tromsø, Norway, [2]Swedish University of Agricultural Sciences, Uppsala, Sweden

Periodic population outbreaks of geometrid moths constitute the most pronounced disturbance factor in sub-arctic birch forest in Fennoscandia. The most important insect herbivores in the system are winter moth, *Operophtera brumata* and autumnal moth, *Epirrita autumnata*, both of which experience cyclic outbreaks every 9-10 yrs, with severe impacts on the birch forest ecosystem. Historically outbreaks by winter moth have been restricted to low-altitude, coast-near forest in W-NW Norway, while outbreaks by autumnal moth have occurred throughout northern Fennoscandia with the exception of the coldest inland regions.
We present evidence that suggests that distinct, climate-change related shifts in geometrid outbreak ranges are now taking place in northern Fennoscandia. Coinciding with a period of increasingly earlier springs, winter moth has expanded its outbreak range to reach the altitudinal and latitudinal forest limit in NE Finnmark County. There the winter moth now overlaps with the normal outbreak range of the autumnal moth as to cause intense and long-lasting defoliation leading to extensive forest death. During the same period autumnal moth outbreaks have for the first time been recorded in the most continental regions. Furthermore, during the last 3 years, a novel geometrid for northern Norway, *Agriopis aurantiaria*, has rapidly become abundant as to inflict forest damage locally in the coastal birch forest in Troms County. *A. aurantiaria* is known as a forest pest species further south in Europe and it may thus represent a putative new pest in the sub-arctic birch forest.

Distribution, habitats, taxonomy and ecological niche models of malaria vectors, *Anopheles hyrcanus* group (Culicidae: Diptera), from Asia

Pollie L.M. Rueda[1], Desmond Foley[1], Richard Wilkerson[1], Terry Klein[2], Heung-Cheul Kim[2]

[1]Smithsonian Institution/WRAIR, Suitland, Maryland, United States, [2]18th MEDCOM, US Army, Seoul, Republic of Korea

Mosquito collections were carried out from1999-2007 from various parts of Asia including China, Japan and Korea. The distribution records of *Anopheles* Hyrcanus Group species in selected Asian countries were updated based on published records and original observations. In China, 21 out of about 30 known species of the Old World Hyrcanus Group (*Anopheles* subgenus *Anopheles*) are found in 24 provinces and 2 cities including *An. belenrae* Rueda. In Korea and Japan, about 6 species of the Hyrcanus Group were collected. *Anopheles sinensis* Wiedemann is the most widely distributed species in all countries surveyed. The habitats of known and potential malaria vectors (e.g. *An. lesteri* Baisas and Hu*, An. sinensis, An. kleini* Rueda*, An. pullus* Yamada*, An. kunmingensis* Dong and Wang*, An. hyrcanus* [Pallas]) included rice paddies, irrigation ditches, irrigated sugar cane and vegetable fields, ground pools, permanent ponds, and others. The taxonomy, including the status of the type specimens of some Hyrcanus Group species and their importance in disease transmission were also noted. Ecological niche models were constructed to predict the potential distribution of selected vector species in various parts of the Asian region.

Hazard assessment of fipronil and spinosad to aquatic organisms

John Stark[1], Roger Vargas[2]

[1]Washington State University, Puyallup, Washington, United States, [2]USDA, ARS PBARC, Hilo, Hawaii, United States

Introduction: Two of the newer insecticides being marketed for control of various pest species are spinosad, a natural product, and fipronil. Spinosad, in particular has been shown to be a selective insecticide which in general is more toxic to pest species than to their biological agents. Fipronil also is supposed to be less detrimental to the environment than the previous generation of insecticides.

Methods: In this study, spinosad was evaluated for toxicity to the Cladocerans, *Daphinia pulex*, *D. magna* and *Ceriodaphnia dubia* and Coho salmon, *Oncorhynchus kisutch*. Toxicity data for fipronil was developed for *D. pulex*. Hazard assessments were developed for both insecticides with the quotient method where the expected environmental concentration (EEC) for each product was divided by the acute LC50.

Results: The LC50 estimates for spinosad were: *C. dubia* - 1.8 µg/l, *D. pulex* - 129 µg/l, *D. magna* - 4.8 µg/l. No mortality was observed when the Coho salmon were exposed to spinosad concentrations as high as 500 mg/l. The LC50 estimate for *D. pulex* exposed to fipronil was 15.6 µg/l. USEPA EEC's for spinosad and Fipronil are 0.092 and 2 µg/l, respectively.

Conclusions: Hazard assessments based on EEC'c and LC50 estimates indicate that both spinosad and fipronil pose no hazard to Daphnids or Coho salmon.

Beyond Bt: alternative strategies for insect-resistant GM crops

Louise Malone[1], Angharad Gatehouse[2], Barbara Barratt[3]

[1]Horticulture and Food Research Institute of New Zealand Ltd, Auckland, New Zealand, [2]University of Newcastle, Newcastle, United Kingdom, [3]AgResearch, Invermay, New Zealand

Bacillus thuringiensis (Bt)-plants dominate today's commercial market for insect-resistant transgenic crops. However, not all pests are susceptible to Bt Cry toxins and there are concerns that even susceptible species may evolve to become resistant to these crops. The search for alternatives is well under way, with significant progress already made towards producing transgenic crops expressing insecticidal compounds from plants, such as protease inhibitors, lectins and alpha-amylase inhibitors. New types of proteins from *B. thuringiensis*, such as the vegetative insecticidal proteins, are also being exploited. At an earlier stage of development but attracting much research interest are other insecticidal compounds, such as chitinases, defensins, enhancins, biotin-binding proteins, proteases and toxins, sourced from bacteria, viruses, plants and arthropods. Fusion proteins, combining the features of different insecticidal proteins, have significant potential for extending the range of insect species which could be controlled via transgenic plants. In the future, metabolic engineering of plants could allow us to alter with great precision the ways in which plants and insects interact. The compatibility of these novel insect control strategies with biological control and integrated pest management is discussed.

Lessons from the development of Green Muscle® for the future of microbial insect control in Africa

Christiaan Kooyman

Fondation Agir pour l'Education et la Santé, Dakar, Senegal

Introduction: Like in most other parts of the world, insect pests are still mainly controlled by means of chemical insecticides in Africa. However, progress has been made over the last 20 years to develop alternative means of control. The case of Green Muscle®, a *Metarhizium*-based biopesticide for locust control, is presented to highlight some of the problems with biopesticide development and some of the lessons learnt.

Methods: The LUBILOSA program brought together a group of researchers with a wide diversity of expertise to be able to go through all the necessary steps for the development of an effective product, these being the search for isolates, bioassays to select the best ones, field testing, (eco)toxicological testing, mass production and storage studies, formulation, application and commercialisation. Licensing agreements were signed with two African producers that have registered the product under the name Green Muscle® in different parts of Africa.

Discussion: One of the main lessons learnt is that end users can often live with the delayed effects of a biopesticide but that it has to be supplied in an easy-to-use formulation. Another is that the requirement of separate registration in each African country will slow down the spread of biopesticides.

Conclusion: Green Muscle® is well on its way to become an established commercial product. Though the commercialisation of new microbial products remains difficult, the current demand for biological or residue-free food has created a much better climate.

Invasive alien species, Classical Biological Control and the Convention on Biological Diversity.

Fabian Haas, Bernhard Loehr

icipe, Nairobi, Kenya

The Convention on Biological Diversity (CBD) introduced Access and Benefit Sharing (ABS) to promote the concept of ownership to biodiversity and to ensure that owners receive benefits from biodiversity use. Basically, this approach assumes that biodiversity products are marketed by private businesses to generating continuous income and benefits to owners.

Also, Invasive Alien Species (IAS) pose a major threat to the well-being of millions of people. Classical Biological Control (CBC) combats IAS by the controlled release and establishment of natural enemies from the home of the IAS in the invaded regions. Thus, a public good is created with no income to a business but with benefits to all.

However, after the CBD entered into force ABS legislation was introduced that seriously impedes scientific studies including the search for natural enemies. The ABS regulations apply to CBC, despite the fact that CBC already successfully works along the lines of benefit sharing, capacity building and conservation, as requested by the CBD.

The workshop will bring together experts from organizations (such as FAO, IOBC, IUCN), regulating authorities, and practitioners to discuss these issues and to inform the policy makers on the special situation and value of CBC. A concluding statement of the workshop will be drafted and be presented to the CBD, to raise awareness of decision-makers at CBD's top level.

Do dietary constraints promote intraguild predation and antagonistic interactions among predators in complex-structured food webs?

Robert Denno[1], Rachel Goeriz[1], Masaya Matsumura[2], Deborah Finke[1]

[1]University of Maryland, College Park, Maryland, United States, [2]National Agricultural Research Center, Nishigoshi, Kumamoto, Japan

Introduction: Given the important consequences of intraguild predation for prey suppression and food-web dynamics, it becomes essential to identify factors that promote its occurrence. Here we contrast food resource stoichiometry (C:N) and prey behavior as potentially important food characteristics that influence predator performance.

Methods: We fed an intraguild predator (the spider *Pardosa littoralis*) and an omnivore (the katydid *Conocephalus spartinae*) diets from multiple trophic levels and measured their performance and nitrogen intake.

Results: Weight gain and nitrogen intake in *Pardosa* were highly correlated with the biomass of prey consumed. However, there was little evidence that the C:N stoichiometry of specific prey items contributed to *Pardosa* growth. For *Pardosa*, behavioral characteristics of prey played a significant role in prey capture and predator performance. However, *Pardosa* performed best when fed a mixture of herbivores and intraguild prey suggesting that dietary supplementation with N-rich prey may be a foraging compromise between satisfying high-nitrogen demands and reducing the risk of counter attack. Likewise, the consumption of prey from higher trophic levels enhanced the growth and survival of *Conocephalus*.

Conclusions: Dietary constraints associated with nitrogen limitation may contribute to the strategy of diet mixing and promote the frequent occurrence of omnivory and intraguild predation in complex-structured food webs.

Changing landscapes, predator subsidies, and altered biodiversity at higher trophic levels: Consequences for plant-herbivore interactions

Robert Denno[1], Deborah Finke[2], Danny Lewis[1]

[1]University of Maryland, College Park, Maryland, United States, [2]University of Missouri, Columbia, Missouri, United States

Introduction: Climate change and anthropogenic disturbance are contributing to fragmented habitats, altered species distributions and the increased exchange of species across habitat boundaries. In particular, the composition of the predator complex (proportion of intraguild predators) at higher trophic levels is highly subject to habitat change. Thus, it becomes imperative to assess how compositional changes in the predator complex influence herbivore suppression and food-web dynamics. Here we investigate how the spatial subsidy of an intraguild predator (*Pardosa* wolf spiders) from neighboring habitats interfaces with the composition of the resident predator complex to influence the suppression of herbivorous insects.

Methods: After documenting the occurrence of an extensive incursion of an intraguild predator, we employ a factorial experiment to explore the consequences of increasing the proportion of intraguild predators in the natural-enemy complex on prey suppression.

Results: We found that increasing the proportion of intraguild predators in the natural-enemy complex results in reduced herbivore suppression.

Conclusions: In fragmented landscapes, the exchange of consumers across habitat boundaries can have drastic consequences for resident herbivores. In particular, the incursion of intraguild predators, the composition and diversity of the resident predator complex, and habitat structure interact to affect the strength of top-down control on herbivores.

Population dynamics and biological control

H Charles J Godfray

Dept. Zoology; University of Oxford, Oxford OX1 3PS, United Kingdom

Introduction: Biological control is applied population dynamics, an attempt to change artificially the abundance of a detrimental organism. Biological control can be improved by a better understanding of population dynamics, while fundamental population biology can be informed by an analysis of successful and failed biological control attempts. My talk will explore the exchange of ideas between biological control and population dynamics, concentrating on host-parasitoid interactions.

Content: The study of host-parasitoid interactions is one of the most highly-developed branches of population dynamics. It was initially spurred by the need to understand biological control, though subsequently parasitoids became in their own right a model system for exploring general issues in population biology. I will first explore how the interplay of applied and fundamental questions have moulded the development of the field, and then look in more detail at a series of questions of interest to both ecologists and pest managers. First, what is the evidence that the density of natural populations of insect herbivores is determined by natural enemies in general and by parasitoids in particular, and the degree to which information from agricultural systems may be useful in studying more complex natural systems. Second, what are the biological processes responsible for damping the intrinsic propensity of host-parasitoid systems to oscillate unstably. Third, the complexities that arise in host-parasitoid interactions with overlapping generations. Fourth, the question whether ecological theory can help practitioners decide which and how many natural enemies it is best to release.

Resource partitioning and the relationship between natural-enemy diversity and the strength of prey suppression

Deborah Finke[2], William Snyder[1]

[1]Washington State University, Pullman, Washington, United States, [2]University of Missouri, Columbia, Missouri, United States

Introduction: Resource partitioning is often implicated as a mechanism leading to greater resource consumption with increasing consumer biodiversity, but empirical studies explicitly examining its importance have proven difficult.

Methods: We conducted this study using a community of parasitoids (*Aphidius colemani, Aphidius matricariae,* and *Diaeretiella rapae*) which attacks three aphid species (*Brevicoryne brassicae, Lipaphis erysimi,* and *Myzus persicae*) on radishes (*Raphanus sativus*). To isolate the impact of resource partitioning among natural enemies on the strength of herbivore suppression, we factorially manipulated parasitoid species diversity (1 versus 3 species) and resource-use differentiation (complete overlap in resource use versus complementarity in resource use among parasitoid species) while controlling for parasitoid species identity. To manipulate the breadth of resources used by a single parasitoid species, and thus resource-use differentiation among species, we took advantage of the host fidelity expressed by parasitoids. Parasitoids were reared on single versus multiple aphid hosts to create populations of wasps within a single species that exhibited narrow (1 aphid species attacked) or broad (3 aphid species attacked) resource-use breadth.

Results: We found that the relationship between enemy species diversity and herbivore suppression is mediated by differentiation in resource use among consumers, with the benefit of diversity only occurring when there is complementarity among consumers in resources exploited.

Conclusions: Resource partitioning among natural enemies is an important mechanism which can lead to enhanced herbivore suppression with greater enemy diversity.

Tracing the origins of the invasive maritime pine bast scale *Matsucoccus feytaudi* in Corsica and Italy: use of mitochondrial and microsatellite markers

Carole Kerdelhué, Christian Burban

INRA UMR1202 BIOGECO, Cestas, France

Introduction: The bast scale *Matsucoccus feytaudi* (Hemiptera: Coccoidea: Margarodidae) is a specific pest of the maritime pine (*Pinus pinaster*). It is naturally present in the western part of the Mediterranean basin, i.e. in the Iberian Peninsula, Morocco and Southwestern France, where its impact on the host tree is neglictable. On the contrary, the scale is supposed to have been introduced in southeastern France where it caused severe outbreaks responsible for the decline of 120 000 ha of maritime pine in the 1960s. It reached Italy in the late 1970s and is still expanding southwards there. Moreover, *M. feytaudi* was detected in Corsica in 1994 where its range is continuously growing, causing heavy tree mortality.

Methods: Males were caught from pheromone trapping in the natural range of the species as well as in Southeastern France, Italy and Corsica. 30 individuals per population were genotyped using 8 microsatellite markers. Data were compared to phylogeographic data obtained by PCR-RFLP and SSCP for part of the mitochondrial COI-COII and cytochrome b genes.

Results and discussion: Mitochondrial data showed that the populations are highly structured in space, with intra-population variability in the natural range of the species. However, the invasive populations were all monomorphic for the chosen marker and bear the most frequent haplotype. Microsatellite markers were useful to trace the most plausible invasion events and expansion pathways, as the successive bottlenecks did not lead to complete allelic fixation.

Allochronic differentiation of a phenologically atypical population of the pine processionary moth *Thaumetopoea pityocampa* (Lepidoptera: Notodontidae)

Carole Kerdelhué[1], Helena Santos[2], Jérôme Rousselet[3], Maria-Rosa Paiva[4], Manuela Branco[2]

[1]INRA UMR1202 BIOGECO, F-33612 Cestas, France, [2]ISA/DEF, Universidade Técnica de Lisboa, Tapada da Ajuda, 1349-17, Lisboa, Portugal, [3]INRA, URZF, F-45166 Olivet cedex, France, [4]DCEA/FCT, Universidade Nova de Lisboa, 2829-516 Campus de Caparica, Portugal

Introduction: Allochronic speciation refers to a mode of sympatric speciation in which the differentiation of populations is primarily due to a phenological shift without habitat or host change. *Thaumetopoea pityocampa* is a Mediterranean insect with winter larval development. A phenologically atypical population with early adult activity and summer larval development was detected ten years ago in Leiria, Portugal (hereafter summer population). We used neutral genetic markers to test the hypothesis of allochronic differentiation and we measured several ecological parameters to determine the ecological impacts of the phenological shift.

Methods: Larvae were sampled from the summer population of Leiria as well as from surrounding winter populations. We used mitochondrial and nuclear sequences as well as microsatellite markers to test the divergence of the summer population and to compare the allelic richness. For both populations, male flight was monitored by pheromone trapping and egg mortality and parasitism rates compared.

Results: Sequences strongly suggest that 'summer' individuals are closely related to the sympatric winter population, while microsatellite data show a reduction in allelic richness, a distortion of allelic frequencies and significant genetic differentiation. Monitoring of adult flight suggests that reproductive activity does not overlap. Furthermore, significantly different egg mortality and parasitism rates were observed between populations.

Discussion: The summer population probably appeared after a sudden phenological shift of some individuals, leading to a founder effect and complete reproductive isolation. Given that the individuals showing this new phenology are subjected to different selection pressures, the observed allochronic differentiation may rapidly lead to deeper divergence.

Cross-effects between below- and aboveground tritrophic interactions in maize

Ted Turlings[1], Sergio Rasmann[2], Matthias Erb[1]

[1]University of Neuchatel, Neuchatel, Switzerland, [2]Cornell University, Ithaca, United States

Plants under attack by arthropod herbivores have been shown to employ a strategy of indirect defense by attracting natural enemies of the herbivores. Such interactions have been intensively investigated for aboveground tritrophic systems, whereby leaf-feeding insects induce the emissions of specific volatiles that attract predatory and parasitic arthropods. Recently it was found that similar interactions also occur belowground when insects-damaged roots release compounds that attract entomophatogenic nematodes. We have investigated such root signals for maize plants under attack by larvae of *Diabrotica virgifera virgifera*, a ferocious pest on maize. It was found that *D.v.virgifera*-damaged roots produce large quantities of the (E)-β-caryophyllene and that this sesquiterpene is highly attractive to the entomophatogenic nematode *Heterorhabditis megidis***.** Using a setup of interconnected above- and belowground olfactometers we have studied how root feeding may affect aboveground signaling and the attraction of parasitoids, and *vice versa* how leaf feeding affects the belowground signal and the attraction of nematodes. Such double infestation renders maize plants less attractive to both types of natural enemies. Measurements of volatile emissions showed that the principal root attractant was indeed reduced due to double infestation, but this was not evident for the leaf volatiles. The parasitoid showed an ability to learn the differences in odour emissions and increased its response to the odour of a doubly infested plant after experiencing this odour during an encounter with hosts. Investigations into the molecular mechanisms into the cross-effects between above- and belowground signaling are underway.

Share the resources or displace the natives: different strategies in invasive *Megastigmus* seed insects

Marie-Anne Auger-Rozenberg, Alain Roques

INRA, Orléans, France

Introduction: Because of the rapidly- increasing, and often unregulated, seed trade, exotic seed chalcids in the genus *Megastigmus* invaded Europe where they presently represent 9 out of the 21 species recorded from tree seeds. We investigated their impact on both the native chalcid entomofauna exploiting seed resources and the potential of natural regeneration of trees.

Methods: Using a standardized procedure, seeds of firs (*Abies* spp.), true cedars (*Cedrus* spp.) and wild roses (*Rosa* spp.) were sampled all over Europe in order to assess the relative importance of the native and invasive species, and their specific impact on tree seed yield. Experimental trials consisted in offering enbagged cones to the attack of *Megastigmus* spp. using various ratios of invasive/ native species. Using X-rays and rearings of infested seeds, we analyzed the spatial distribution of the different species in the cones with and without competition for seed resource

Results: In firs, the exotic *M. rafni* became over the last 10 years the dominant species in most stands, replacing the native species rather than sharing the seed resources within the cone. The decrease in seed yield thus remained equivalent when only one exotic species was present instead of the native species or together with the native. However, seed yield significantly decreased as soon as 2 or more exotic species were present. In this case, all the zones of the cone were attacked. The cone resources were similarly shared in cedars and wild roses when 2 exotic species were present with large consequences on the potential of natural regeneration of the trees.

Conclusions: Research has now to focus on the biological traits susceptible to be involved in the competitive superiority of the exotic seed chalcids with regard to the native ones.

Population genetics of the larch budmoth *Zeiraphera diniana* (Lepidoptera: Tortricidae)

Sophie Delamaire, Alain Roques

INRA, Orleans, France

Introduction: Population densities of larch budmoth, *Zeiraphera diniana* (LBM), exhibit cyclical outbreaks in the Alps. Outbreaks usually occur at 8-10 year intervals, larval populations increasing by ca. 10^5 times during the 3-4 years following a short latency phase. In addition, outbreaks are subject to travelling waves across the Alps. We hypothesized that there is a link between changes in the genetic structure of the populations and the outbreak development.

Methods: LBM adults and larvae were sampled for 3 consecutive years at several sites of France, Switzerland and Italy showing delayed outbreak patterns.
We use mitochondrial and nuclear molecular markers (mtDNA sequences and AFLPs) to study the spatial and temporal changes in the genetic structure of LBM populations, and try to relate it to the demography.

Results: mtDNA sequencing results suggested that the demographical explosion at the onset of an outbreak is associated with an increase in populations genetic diversity. Spatial comparisons also showed that outbreaking populations present a higher genetic diversity than populations in latency. The star-like shape of the haplotype network obtained by mitochondrial sequences is congruent with the sudden demographic expansion.

Conclusions: This study is a first step towards the understanding of its population dynamic via genetic tools. Additional data will be supplied during the presentation. Nuclear data are expected to confirm this trend, and temporal data that are in process should give more information on the underlying phenomena of this particular cyclic outbreak pattern.

Newest quick scan and comprehensive evaluation methods of environmental risks for exotic natural enemies

Joop C. van Lenteren, Antoon J.M. Loomans

[1]Laboratory of Entomology, Wageningen, Netherlands, [2]Section Entomology Plant Protection Service, Wageningen, Netherlands

First, we summarize the international situation concerning environmental risk assessment for biological control agents. Next, we illustrate a new, comprehensive risk evaluation method consisting of a stepwise procedure, which can be used for all types of biological control agents used in augmentative and classical biological control programmes, and for native and exotic natural enemies. The new comprehensive method solves weaknesses that we encountered when using the previous assessment methods: decision criteria are more clear and the decision to advise a release is taken at relevant steps in the process, thus preventing unnecessary research.

We applied the new procedure to about 100 species of natural enemies used in Europe. The elimination of obviously risky species early in the process, and the acceptance of other species that previously wrongly scored a high index, clearly show improvements of the new procedure.

For those natural enemies that have been in use for many years in certain ecoregions of the world, we propose that environmental risks are evaluated by using a quick scan method, based on available information only. We have applied this method to all 150 species of natural enemies that are currently commercially available in Northwest Europe and concluded that 80% of the species were expected to cause no problems, while about 5 % of the species (all exotic) were considered too risky for release in this region. Information was not sufficient for another 15% of the species, but the necessary information to make a final decision could usually be obtained easily.

Cheating honey bee workers produce royal offspring

Lyndon A Jordan[3], Michael H Allsopp[1], Theresa C Wossler[2], Benjamin P Oldroyd[3], Madeleine Beekman[3]

[1]Honey bee Research Section, ARC-Plant Protection Research Institute, Stellenbosch, South Africa, [2]University of Stellenbosch, Stellenbosch, South Africa, [3]University of Sydney, Sydney, Australia

The Cape bee (*Apis mellifera capensis*) is unique among honey bees in that workers can lay eggs that instead of developing into males develop into females via thelytokous parthenogenesis. We show that this ability allows workers to compete directly with the queen over the production of new queens. Genetic analyses using microsatellites revealed that 23 of 39 new queens produced by seven colonies were offspring of workers and not the resident queen. Of these, eight were laid by resident workers, but the majority were offspring of parasitic workers from other colonies. The parasites were derived from several clonal lineages that entered the colonies and successfully targeted queen cells for parasitism. Hence, these parasitic workers had the potential to become genetically reincarnated as queens. Of the daughter-queens laid by the resident queen, three were produced asexually, suggesting that queens can 'choose' to produce daughter-queens clonally and thus have the potential for genetic immortality.

What has the 'selected anarchist' line told us about reproductive parasitism in honey bees?

Benjamin Oldroyd

University of Sydney, Sydney, NSW, Australia

The 'selected anarchist' (SA) line of honey bees maintained at Sydney University has been developed by 10 years of recurrent selection for worker reproduction. In the SA line about one third of 10-day-old workers have activated ovaries and lay eggs that produce males. This is in stark contrast to wild-type (WT) workers in which almost no workers are reproductive. The SA line offers the opportunity to investigate the pheromonal and genetic mechanisms that regulate worker sterility in WT honey bees.

Pheromonal studies have shown that SA queens have similar mandibular pheromones to wild-type queens, but that ovary activation in SA workers is less inhibited by exposure to queen mandibular pheromones. Similarly, SA workers are less inhibited by brood pheromones than WT workers, but the brood of SA queens is less inhibitory than the brood of WT queens.

Microarray studies have revealed a number of genes that are differentially expressed between young, age-matched WT and AN workers. These include key regulatory proteins including Major Royal Jelly proteins and vitellogenin.

Backcrosses between WT and SA lines reveal that there are several genes of both small and large effect that control expression of worker sterility. Our goal is to elucidate the molecular genetic mechanisms that regulate worker sterility in honey bees, and to show how reproductive parasitism by individual workers is controlled.

The SA line can also be used as an independent test of the 'reproductive ground plan hypothesis' (RGPH) for the regulation of reproductive potential in honey bee workers. The RGPH suggests that workers with higher than normal reproductive potential are likely to forage early in their life and to focus on pollen foraging (Amdam et al *Nature* 439: 76). Our studies of the SA line show that in contrast to the predictions of the RGPH, SA workers are significantly older than WT workers when they commence foraging, and the proportion of pollen foragers does not differ significantly from the proportion of pollen foragers among WT workers.

‘Wallacea’ – The origin of diversity for butterflies (Lepidoptera) in the Indo-Pacific? Biogeographic patterns across three co-occurring tropical genera

Chris Muller, Luciano Beheregaray

Macquarie University, Sydney, Australia

Introduction: This work is a comparative molecular phylogenetic and biogeographic analysis of separate co-occurring genera in the Indo-Pacific. The subjects studied included all known species of the butterfly genera *Cethosia* (48 taxa) and non-African *Charaxes* (51 taxa) (both Nymphalidae) and representatives from all recognized species groups within the genus *Delias* (72 taxa) (Pieridae). The focus was to determine the biogeographical importance of ‘Wallacea’, in central Indonesia, a biological hotspot which is poorly understood.

Methods: Sequence data from three genes (mtDNA: 650 base pairs COI, 410 bp ND5; nuclear DNA: 430 bp wingless gene) were used to reconstruct the molecular phylogenies for each genus. Phylogenetic analysis included Maximum Parsimony, Maximum Likelihood and Bayesian Inference methods.

Results: Several clades within each genus were consistently resolved and showed strong concordance between phylogenetic relationships and morphology. Morphologically divergent species had longer branch lengths between taxa and formed basal clades, whereas more recently derived species displayed similar phenotype. For each of the three genera the tree topology indicated that basal clades consisted of species largely confined to Wallacea.

Conclusions: The biogeographical histories of the three genera are consistent with the interpreted geological evolution of the region. Long term isolation and hence higher genetic diversity of taxa within Wallacea likely parallels the independent formation and drifting of microplates during the Tertiary. Repeated connection/isolation of land masses and mountain ranges during Pleistocene inter glacial periods in Sundaland and New Guinea, respectively, resulted in the recent evolution of numerous taxa with lesser genetic divergence.

Using population modelling to assess the risk of pesticides to non-target arthropods with different life history strategies

John Stark

Washington State University, Puyallup, Washington, United States

Introduction: Traditionally, estimation of the ecological impacts of chemical toxicants has been done by comparing individual-level endpoints of toxicity to an expected, or range of expected environmental concentrations. However, the ability of this approach to protect nontarget species has been questioned. The use of population modeling has been suggested as a more feasible means to ascertain the fate of populations under stress. In this talk I will discuss the use of matrix models to estimate the effects of pesticides on non-target arthropods.

Methods: The advantages and disadvantages of matrix models will be discussed. Results from Hazard Ratios (ratio of expected environmental concentration and LC50), a commonly used approach used to determine the hazard of a pesticide to nontarget organisms will be compared to modeling results using examples with tephritid fruit flies and *Daphnia*. Lethal and sublethal effects will be modeled.

Results: Matrix models can be used to make better assessments of pesticide effects on populations compared to the Hazard Ratio method.

Conclusions: Hazard assessments based on expected environmental concentrations and the LC50 can provide estimates of risk but are limited because they do not take into account multiple effects of pesticide and differences in life history traits.

Post-release evaluation of risks of a biocontrol agent: a New Zealand case study

Barbara Barratt[1], John Kean[2]

[1]AgResearch, Mosgiel, New Zealand, [2]AgResearch, Lincoln, New Zealand

Introduction: The parasitoid *Microctonus aethiopoides* Loan (Hymenoptera: Braconidae) was introduced into New Zealand in 1982 to control the lucerne pest, *Sitona discoideus* Gyllenhal (Coleoptera: Curculionidae). Previous studies have shown that a number of non-target weevil species are attacked in the field by this parasitoid. A field study was carried out over a seven-year period to investigate non-target parasitism by *M. aethiopoides* in native grassland.

Methods: Sampling was carried out at three locations in Otago. Parasitism of *S. discoideus* in lucerne growing in the valley floor was assessed, and at progressively higher altitude grassland sites, weevils were sampled monthly and dissected to determine parasitism levels. Simple population models were used to estimate the likely impacts of the observed parasitism rates on non-target population densities.

Results: Of the 36 species of weevils identified, eight were found to be parasitized, including *S. discoideus* which was found at all sites. Parasitism of the target pest in lucerne ranged from 17-78% and for non-target species was 2% overall but this varied with location, site, and season. Substantial nontarget parasitism was found at only one location, with up to 24% parasitism of a native weevil, *Nicaeana fraudator* Broun recorded. Modelling suggested that impacts of non-target parasitism are likely to vary between species and sites.

Conclusions: The target host has the potential to transport parasitoids to native grassland areas. There was no apparent relationship between nontarget parasitism by *M. aethiopoides* and weevil density or between altitude or distance from lucerne. Post-release studies can be of value to regulatory agencies for future decision support.

Terrors from beyond space: Alien arthropods in the movies

Richard Leskosky

University of Illinois at Urbana-Champaign, Urbana, Illinois, United States

Most science fiction films with arthropod menaces (Insect Fear Films) have earthly settings and terrestrial arthropod antagonists, but many of them feature extraterrestrial arthropods of one sort or another. In fact, from its very beginnings, the cinema has relied on arthropods as models for alien creatures because of both their intrinsic otherness with respect to humans and the social behavior exhibited by various species. Such alien arthropods belong to three major categories: arthropods encountered in extraterrestrial settings, extraterrestrial arthropods invading the Earth, and earth-based arthropods turned into menaces by extraterrestrial forces. This presentation will trace the history of alien arthropods in Insect Fear Films, examine the reasons for their popularity with filmmakers, and relate their appearances in films to their depictions in other popular media.

Too hot to handle: Ecophysiological responses of the southern green stink bug *Nezara viridula* (Heteroptera: Pentatomidae) to climate warming

Dmitry I. Musolin, Daisuke Tougou, Kenji Fujisaki

Lab. of Insect Ecology, Grad. School of Agriculture, Kyoto University, Kyoto, Japan

Introduction: The climate warming promotes northward expansion of *N. viridula*'s range by providing favourable overwintering conditions close to the species' range limit. We present results of an experiment in which this species responds to the simulated climate warming.

Methods: Adults collected in Kochi (33.6ºN, 133.6ºE) were transferred to Kyoto (35.0ºN, 135.8ºE), close to the current species' north range limit. The progeny was divided into two groups and reared over a year under outdoor conditions and in a specially constructed transparent incubator which simulated climate warming by adding in real time 2ºC to the outdoor temperature.

Results: The moderate temperature increase (2ºC) affected many life history traits. In summer, nymphs suffered higher mortality, their development was significantly more retarded and emerged adults were significantly smaller under simulated warming conditions than outdoors. In late autumn, on the contrary, warming resulted in a shorter nymphal period and, thus, earlier emergence of adults. These adults successfully changed colour, entered diapause and survived winter, while their siblings failed to change colour and suffered high winter mortality outdoors. Simulated warming affected overwintering mortality directly (by increasing survival) and indirectly (by advancing adult emergence). It also advanced the beginning of reproduction in spring.

Conclusions: The effect of even moderate warming is complex. In summer, it might affect performance even at the northern limit of the species' range, likely because of the deleterious effects of daily maximum temperatures. In other seasons, warming might advance phenology and enhance survival, thus promoting range expansion and establishing in newly colonized areas.

Biological control of *Chromolaena odorata* in Africa: some progress made but much more is needed

Costas Zachariades

Agricultural Research Council, KwaZulu-Natal, South Africa

The two biotypes of *Chromolaena odorata* invading Africa continue to spread. The Asian/West African biotype is spreading into East Africa, while the southern African biotype is spreading north. Although research into the biological control of chromolaena was initiated by Nigeria in the 1960s, and several species of biocontrol agents were released in West Africa in the 1970s, the first establishment in Africa only occurred in the 1990s. To date, agents have been established on chromolaena in two countries: *Pareuchaetes pseudoinsulata* (Lepidoptera: Arctiidae) in Ghana, and *P. insulata* and *Calycomyza eupatorivora* (Diptera: Agromyzidae) in South Africa. These agents are effecting a degree of control but more agents are needed. The introduction of the host-specific, damaging stem-galler *Cecidochares connexa* (Diptera: Tephritidae) into one or more countries where the Asian/West African biotype is present, is recommended. Because this fly cannot develop on the southern African *C. odorata* biotype, other potential agents are under consideration, with a particular emphasis on those adapted to the severe dry season typical of much of the invasive range of this biotype. The conflict of interest in West Africa concerning the useful versus harmful attributes of *C. odorata* has not yet been resolved and still acts as a block to international funding for chromolaena biocontrol there. The South African programme on *C. odorata* biocontrol is the only one world-wide investigating new agents, and hopes to supply these not only to African countries but also to the drier parts of South-East Asia where *C. connexa* has not performed well.

Immunogen-induced anorexia in locusts

Graham Goldsworthy, Khadijo Osman, Mary Lightfoot, Ilona Wenzel

Birkbeck College, London, United Kingdom

Illness-induced anorexia is a widespread phenomenon in animals, and infection is known to inhibit feeding activity in locusts. Anorexia can be induced by injecting immunogens such as bacterial LPS or the ∃ 1,3-glucan, laminarin. After a 2 h period of food deprivation, Ringer-injected locusts feed with latency of 1-2 min and continue to eat for *c.* 4 min. During a test period of 1 h, they may take up to three meals. The effect of injecting immunogens on feeding behaviour of adult and nymphal *Locusta* is apparent immediately: adult locusts injected with >10 µg of laminarin, or nymphs injected with >1 ug, do not eat at all during a 1 h test period starting 10 min after treatment with the immunogen. They perch on the wheat seedlings provided, but do not palpate the leaf surface and do not attempt to eat. Sub-optimal doses of laminarin allow some locusts to feed, but with an increased latency and normal first meal duration.

The anorectic effect of laminarin or LPS is modulated by injection with a serotonin antagonist such as Mianserin, or by injection of adult locusts with Adipokinetic Hormone (AKH-I) 2h before the immune challenge: latency to feed increases relative to that in controls, while meal duration is unaffected. Injection of AKH-I into nymphs does not block the anorectic response to laminarin, suggesting that increased lipid mobilisation, which occurs in adults but not nymphs in response to AKH, is implicated in modulation of the anorectic response to this immunogen. Experiments in which serotonin or octopamine is injected suggest strongly that serotonin receptors are involved in the mechanism of sickness-induced anorexia in locusts.

A locust model can be used to study virulence determinants of *Escherichia coli* K1

Graham Goldsworthy, Behzad Mokri-Moayyed, Naveed Khan

Birkbeck College, London, United Kingdom

E. coli K1 meningitis involves invasion of the CNS by the bacterium *Escherichia coli*, and results in 50,000 human deaths per year worldwide. Understanding of the pathogenesis of this disease has, until now, relied on vertebrate models, but parallels between the innate immune responses of mammals and insects, and the fact that *E. coli* K1 meningitis occurs mostly in neonates, suggest that insects could be useful models for studying the pathogenesis of *E. coli* K1. The physiology of *Locusta migratoria*, the African migratory locust, has been studied extensively in our laboratories, and was chosen as a model to study *E. coli* K1 pathogenesis *in vivo*. The aim of this study is to determine how well *E. coli* infection can be modelled by testing in the locust some of the virulence factors known currently to be required for *E. coli* K1 pathogenesis in mammals.

The *E. coli* K12 strain HB101, which is non-pathogenic in mammals, has also very low pathogenicity to locusts and does not invade the locust CNS, whereas the *E. coli* K1 strain RS218 (O18:K1:H7; isolated from a meningitis patient) kills almost 100% of locusts within 72 h, and invades the brain. After injection of *E. coli* K1 into adult male locusts, both mortality and invasion of the locust brain require at least two of the known virulence determinants shown for mammals. Deletion mutants that lack OmpA (Outer membrane protein A) or CNF1 (cytotoxic necrotizing factor 1) have reduced abilities to kill locusts and to invade the locust brain compared with the parent *E. coli* K1. The locust model can be used to examine the dynamics of invasion of the brain and to test the virulence in locusts of *E. coli* K1 mutants in which known pathogenicity islands in the K1 genome have been deleted. In this way, as yet unknown virulence determinants may be identified.

Insect conservation in practice: lessons in the real world

Michael Samways[1], Timothy New[2]

[1]Stellenbosch University, Matieland, South Africa, [2]La Trobe University, Melbourne, Australia

Insect conservation comprises both theoretical and practical exercises, the latter drawing on the accumulated wisdom of both these facets. With massive current and future threats (ranging from habitat and resource loss, influences of invasive species, and effects of climate change) to insects, the practice of insect conservation is increasingly important. In this symposium, we emphasize practice, and examine a variety of cases and scales through which practical conservation is contributing to insect well-being, and how the mutual lessons from theory and practice are being tested and will apply in the future.

Assessing freshwater health using macroinvertebrate surrogates, especially adult dragonflies

Rembu Magoba[1], Michael Samways[2], John Simaika[1]

[1]Stellenbosch University, Matieland, South Africa, [2]Stellenbosch University, Matieland, South Africa

In many countries, benthic macroinvertebrates are being used to assess the quality of freshwater ecosystems. This is also the case in South Africa, where, in addition, adult dragonfly assemblages are being matched to them, with excellent concordance. However, adult dragonflies, as surrogates for biodiversity, have the distinct advantage that they can be used at the more sensitive, species level, rather than at the more general higher taxonomic level, as in the case of macroinvertebrates. Thus, dragonflies can be used at both fine spatial scales and for measuring compositional biodiversity i.e. ecological integrity, as well as freshwater health. Furthermore, adult dragonflies are much easier and more practical to sample than benthic macroinvertebrates, and therefore are an excellent practical tool for conservation managers. A scoring system for adult dragonflies has been developed which will enable national implementation of dragonfly surrogates for various uses, including measuring the success of the national clearing of invasive alien riparian trees.

Implementing ecological networks using grasshoppers as indicators

Corinna Bazelet, Michael Samways

Stellenbosch University, Matieland, South Africa

The forestry industry in South Africa has implemented a very large scale mitigation measure for the conservation of biodiversity. This involves setting aside about a third of forestry land, a total of 500,000 hectares, in the form of interconnected corridors and nodes of remnant habitat, together called an ecological network (EN). Most of these ENs are grasslands, at various elevations and often following the hydrological landscape. Previous research has shown that an EN can fulfill a habitat function for a range of taxa, if large enough. Since the majority of the ENs fall below this size threshold, guidelines must be developed to optimize the structure and management of the ENs. Surrogates are also necessary to measure the mitigation success of the EN and to use as a monitoring tool for adaptive management. Possible surrogates include landscape, vegetation and management variables, and bioindicators. Of the potential bioindicators, grasshoppers may prove to be a prime practical tool for quantifying the conservation success of the ENs.

Shading by agricultural and natural plants affects growth and development of malaria mosquito larvae in Western Kenya

Susan Imbahale, Richard Mukabana, Willem Takken

[1]Kenya Medical Research Institute, Kisumu, Kenya, [2]University of Nairobi, Nairobi, Kenya, [3]Wageningen University and Research Centre, Wageningen, Netherlands

Malaria in tropical Africa is a major cause of illness and death, and its control depends on drugs and vector control. The latter is accomplished by reducing populations of malaria mosquitoes. We have investigated the effect of crop plants on larval growth and development in a peri- urban environment, using locally available plants. Larval habitats were created in agricultural fields in Kisumu, western Kenya. The fields are used for irrigated rice production and vegetable production. Small plots of 1 x 1m were dug and filled with water naturally by seepage and rainfall. 5, 1 by 1 m plots were provided with canopy cover from the following plants, Napier grass (*Pennisetum purpureum*), rice (*Oryza sativa*), yams (*Dioscorea batatas*), papyrus reeds (*cyperus papyrus*) and one open plot which acted as a control. Larval sampling was done once on weekly basis from the 7th week to 25th week of 2007.

The results show that plots provided with Napier grass had the lowest larval densities, followed by rice, yams, and papyrus reeds and finally the open/ control plots had highest anopheline larval densities

Biological control as a component of IPM for cowpea

Manuele Tamo[1], Cyriaque Agboton[1], David Arodokoun[2]

[1]International Institute of Tropical Agriculture (IITA), Cotonou, Benin, [2]Institut des Recherches Agricoles au Benin (INRAB), Cotonou, Benin

For many years, biological control has been considered of marginal importance to IPM of cowpea pests. This fact was based on the assumption that, cowpea being an indigenous crop to Africa, all pests were also native to Africa, and hence less amenable to be targets for biological control. Critical issues in developing biological control for cowpea can be summarized as 1) the complexity of the cropping system, with multiple pests attacking different stages of the plant, and sharing a wide range of alternative host plants; 2) the evidence that each pest would need at custom-tailored solution; and 3) interactions with other IPM interventions including pesticides.

Using three case studies involving three major cowpea pests, the flower thrips *Megalurothrips sjostedti*, the pod borer *Maruca vitrata*, and the aphid *Aphis craccivora*, various aspects of the above issues are presented. All these key pests have naturally-occurring alternative host plant, which, in many areas, are far more important for their population dynamics than cowpea, the cultivated host. On-going investigations have revealed that the introduced thrips parasitoid *Ceranisus femoratus* was able to establish on shrubs such as *Tephrosia candida*, and leguminous trees such as *Pterocarpus santalinoides* in the three countries it was released, Benin, Ghana and Nigeria. On the latter host plant, preliminary observations indicate that it was able to reduce the thrips population by up to 43%. Similar studies are being carried out for the exotic parasitoid *Apanteles taragamae* attacking *M. vitrata*, and *Aphidius colemani* attacking *A. craccivora*.

Effect of temperature on the viability and toxicity of *B. bassiana* and *M. anisopliae* on *P. rapae*

Cipriano Garcia-Gutierrez[1], Hiram Medrano-Roldan[2], Isaias Chairez-Hernandez[1]

[1]CIIDIR COFAA IPN, Sinaloa, Mexico, [2]ITD, Durango, Mexico

Introduction: The temperature, humidity and sunlight have influence on the growth of *Beauveria bassiana* and *Metharhizium anisopliea*; the cabbage worm *Pieris rapae* (L.) is controlled with native strains of fungus applications on cauliflower *Brassicae oleraceae* (L.) in in many sites with different ranges of temperature and altitude.

Methods: A contamination leaf bioassay was used to calculate the CL_{50} for 10 isolates, then these spore concentrations were used to study the effect of different temperature conditions (25,30,35, and 40^0C) in the spore viability and strain´s toxicity on 1-3 old-day *P.rapae* larvae, using a factorial design 10x4x3.

Results: The LC_{50} to *B.bassiana* and *M. anisopliae* ranged from 10^{7-6} conidia/ml, respectively. There were significant statistical differences between mean larvae mortality of all strains (F= 34.45, p = 0.001), but not between the same strains (MSD=2.3). The highest larval mortality was present in the isolate code *B.b*4 ($1.2x10^9$ spores/ml) at 30ºC, while the lowest mortality was to Mtz3 ($2.3x10^7$) at 25ºC; the better spore viability percentage was obtained by the isolate Bb1(98±0.6 $_{C.V\ 0.3}$) at 30 ºC, and the lowest to Mtz2 (76±2.1 $_{C.V\ 0.6}$) at 40 ^{0}C. In all *B.b* strains the highest viability spores were observed, as well as the better toxicity values at temperatures between 30-35ºC, while for *Mtz* these same results were obtained at 25-30 ºC; the strain origin, altitude and temperature, were also important.

Conclusions: The results showed that *B. bassiana* strains had better tolerance to high temperatures than *M. anisopliae*, preserving the spore viability and toxicity, this characteristic allows a selective choice of *B.bassiana* strains as first candidates to use it in cabbage worm control in sites with maximum temperatures around 30^0C in Mexico.

Functional roles of short neuropeptide F in the brain of Drosophila

Dick R. Nassel, Lina E. Enell, Elisabeth Gustafsson, Helena A. D. Johard

Department of Zoology, Stockholm University, Stockholm, Sweden

The expression of the gene *snpf* and its neuropeptide products (short neuropeptide Fs; sNPFs) is widespread in the CNS of larval and adult *Drosophila.* We studied the distribution by means of in situ hybridization and antisera against sequences of the precursor and two of the encoded peptides (Johard et al., J Comp Neurol, in press). sNPF expression is seen in Kenyon cells of the mushroom bodies and in various chemosensory neurons, as well as interneurons and neruosecretory cells of different types. A previous report has shown that *snpf* plays a role in feeding in larvae and adults of Drosophila (Lee et al., J Biol Chem 279:50781, 2004). This was shown by global (pan-neuronal) interference with *snpf* expression. Here we analyze the role of different subpopulations of sNPF expressing neurons in feeding and locomotor activity. This is done by neuron-specific interference with sNPF expression using the binary Gal4-UAS system to drive RNA interference, followed by behavioral tests.

Expansion of pine processionary moth in Europe: patterns and predictive model

Christelle Robinet[1], Alain Roques[1], Jérôme Rousselet[1], Andrea Battisti[2]

[1]INRA Forest Zoology, Olivet, France, [2]University of Padova, Legnaro, Italy

Introduction: Many species are already affected by the warming up of climate. Their distribution is expanding or retracting depending on climatic tolerance, dispersal capabilities and response to environmental changes. During the last decades, the pine processionary moth, *Thaumetopoea pityocampa*, has expanded northwards and upwards in Europe. We investigated the role of climate warming in this expansion and developed a predictive model with regard to climatic scenarios for the future.

Methods: Experimental studies have been carried out to determine the effects of low temperatures on the survival of larvae during the cold period, and climatic thresholds for development. A reaction- diffusion model relying on these thresholds has been developed. The effects of climatic anomalies have also been considered.

Results: We found close relationships between the increase in winter temperatures and feeding activity and survival of larvae. By including these relationships into a diffusion model, we successfully reconstructed the range expansion in the southern Paris Basin since the early 1990s. Under moderate hypotheses for average winter warming during the next 50 years (+3°C), model predictions suggest a colonization of downtown Paris by 2025. However, climatic anomalies such as the heat wave which occurred in August 2003 in Western Europe are likely to modulate such expansions because of contrasting effects: extremely high temperatures in the Italian Alps enhanced the range expansion in higher elevations whereas processionary populations collapsed at the same time in the Paris Basin.

Conclusions: In the future, the impact of climatic anomalies should be explored and included in predictive models. Because of its northwards expansion, this forest insect is likely to become an urban pest, causing serious troubles to public health due to its urticating properties.

Termites and Namibian fairy circles: No connection

Walter R. Tschinkel

Florida State University, Tallahassee, FL, United States

The sandy plains of the Pro-Namib Desert are punctuated by thousands of bare areas 3 to 15 m in diameter edged by a circle of taller grasses. The cause of these “fairy circles” is unknown, although several hypotheses have been advanced. We tested the hypothesis that the circles are caused by the termite *Baucaliotermes hainsei*, a harvesting termite endemic to southern Namibia. Excavation of 10 fairy circles to a depth of 1.5 to 2 m revealed no evidence of termites. We then exposed the underground foraging tunnel systems of two nests using a soft brush and a petrol-powered lawn blower. Areas containing nests of this termite are underlain by complex, interconnecting underground highway systems with risers to the surface at regular intervals. The tunnels themselves are not simple tubes, but consist of a raised central portion serving as a runway, and lateral pockets and grooves in which foragers deposit cut grass pieces for eventual transport to the nest. The extent and complexity of this foraging/transport system is extreme. We also censused a nest of this species, finding it to be occupied by about 40,000 individuals, including all castes and stages.

Pest management: An emergent property of biodiversity

Mark Brown

USDA, ARS, Appalachian Fruit Res. Sta., Kearneysville, WV, United States

A number of studies have demonstrated that increasing the diversity of agricultural ecosystems can allow for a reduction in insecticide applications without an increase in insect damage to the crop. However, it has been very difficult to demonstrate the specific mechanism involved in producing the pest management benefit: interspecific competition, biological control, plant resistance, etc. Several examples of habitat diversification studies in apple ecosystems will be used that demonstrate a reduction in pest damage but no identification of specific mechanisms responsible for pest control. Pest management is an emergent property of the ecosystem, an ecosystem service, resulting from the interactions among all the components in the system. Diversification of the ecosystem affects each trophic level making it difficult to isolate one specific mechanism. Traditional agricultural research experiments are good at detecting treatment effects but are not the best method for explaining emergent properties that are a result of system-level interactions. An appropriate analysis should include a combination of resource limitation, landscape and food web analyses. Before landscape analysis is performed, basic biology of the pests and natural enemies is needed to identify what resources, if any, are limiting. Then the spatial range of key pests and natural enemies must be known to evaluate the availability of limited resources. Landscape analysis can then be applied to evaluate how and where limiting resources can be supplemented. Food web analysis is needed to evaluate the resulting interactions when selected species are provided resources in preference of other species. Such complex analyses are needed to provide sufficient data for predicting the result of ecosystem modifications, whether for pest management or any other objective.

Novel resistance response of a perennial vine crop (kiwifruit) to armoured scale insect (Diaspididae) feeding

Garry Hill, Nicola Mauchline, Midori Jones, Paul Sutherland

Horticulture and Food Research Institute of New Zealand, Auckland, New Zealand

Introduction: The polyphagous sibling diaspidid species, latania scale (*Hemiberlesia lataniae*) and greedy scale (*H. rapax*), shown major differences in survival and growth on kiwifruit (*Actinidia* spp.) genotypes. The responses of petiole, bark and fruit from 'resistant' kiwifruit genotypes to feeding by both species is described.

Methods: Crawlers of both scale species were settled onto petiole, bark (1 year-old canes) and fruit of 5 kiwifruit genotypes in an experimental orchard in New Zealand. Insect growth and survival were monitored and samples of challenged plant material taken at weekly intervals over a 5-week period. The histological responses of the plant to insect feeding were characterised using light microscopy.

Results: On bark and fruit, the vines responded to latania scale by developing, over a 5-week period, a bowl-shaped neoplasm in the collenchyma, 200-400 µm from the settled insect, caused by massive cell proliferation (hyperplasy). Cell growth (hypertrophy) and the deposition of lignin on cell walls occurred within this hyperplasic bowl, isolating the insect's stylet from unmodified collenchyma and parenchyma cells beneath, leading to stunted growth and death of the insect within 1-2 weeks. Fruit from one genotype responded to latania scale with cell death (hypersensitive response) occurring directly beneath the insect. Greedy scale initiated no plant response and developed normally. Petiole tissue showed no response to either species.

Conclusions: Selected kiwifruit germplasm shows strong and unique resistance responses to latania scale but not to its equally polyphagous sibling species, greedy scale. The latania-kiwifruit interaction appears to fit the gene-for-gene model of plant defence.

Comparative toxicity of neem seed powder with three local leaf powders to *Sitophilus zeamais* and the influence of drying regime and particle size on insecticidal efficacy

Elias Nukenine[1], Florence Chouka[1], Cornel Adler[2], Christoph Reichmuth[2]

[1]University of Ngaoundere, Ngaoundere, Cameroon, [2]Federal Biological Research Centre for Agriculture and Forestry, Berlin, Germany

Introduction: *Sitophilus zeamais* is a serious pest of maize in the tropics. Peasant farmers in Cameroon can not afford chemical insecticides. The toxicity of neem seed powder and leaf powders from *Plectranthus glandulosus*, *Steganotaenia araliacea* and *Annona senegalensis* to adult *S. zeamais* was determined in the laboratory. The influence of drying regime and particle size on the insecticidal efficacy of *P. glandulosus* and *S. araliacea* was also assessed.

Methods: The seeds and leaves were harvested in northern Cameroon, dried under shade or sunlight, pulverized until they passed through a 1 mm or 0.2 mm sieve. Maize grains were admixed with the powders at four rates (5, 10, 20 and 40 g/kg) for the assessment of mortality over a 14-day or 30-day period, as well as for population increase and damage.

Results: *S. zeamais* mortality increased with ascending contents for all the powders. Within two weeks exposure, *P. glandulosus* powder caused the highest weevil mortality followed by *A. indica* (powder. Neem seed powder was by far more efficacious in reducing grain damage and population increase compared with all the leaf powders within three months of storage. The leaves dried under shade compared with those dried under sunlight and the larger compared with the smaller particle size powders, caused higher mortality of the weevil.

Conclusions: Neem seed powder and powdered leaves of *P. glandulosus* could be of value in the protection of maize against weevil attack in the subsistence storage systems of northern Cameroon.

Managing a mountain in a biodiversity hotspot for maximizing arthropod diversity

James Pryke, Michael Samways

Stellenbosch University, Matieland, South Africa

Table Mountain, Cape Town, South Africa, is a very significant mountain in terms of biodiversity, being a hotspot within a global biodiversity hotspot (Cape Floristic Region). Recent research on the mountain, and the Cape Peninsula in general, has identified some management procedures which are feasible and should be implemented. The arthropod fauna is very sensitive to various environmental variables, including aspect, elevation, fynbos type and presence versus absence of alien trees such as pines and of the Argentine ant. General concern that accidental fires on the mountain are too frequent is borne out by new, quantitative data. Evidence is accumulating that in the future, one mitigation measure would be well-planned patch burning. Removal of the alien trees, which is currently taking place, is clearly very beneficial for indigenous plant and arthropod diversity. A management priority for the future is to give particular attention to the lower elevations on the mountain which are under extreme anthropogenic pressure.

Integration of new insecticides into apple pest management programs in Washington

Jay F. Brunner

Washington State University, Wenatchee, WA, United States

The US-EPA has determined a phase-out schedule for the use of azinphosmethyl in apple by 2012. This insecticide has historically been the key chemical control for codling moth, *Cydia pomonella* (L.). Several new insecticides have been registered as organophosphate (OP) replacements; some classified as reduced risk. The number of new products, differing modes of action, and target stage brings added complexity to pest control decisions. Concentration response and field-aged bioassays coupled with replicated field trials were used to assess the inherent toxicity, residue longevity, and efficacious rates and timings of different insecticides. Base-line data provided by concentration response bioassays have been used to assess the potential of OP-mediated cross-resistance or resistance development after new insecticides have been in use for a period of time. There are nine insecticides that are OP alternatives for codling moth control, eight for leafroller control and five that will control both pests. Efficacies of insecticides against codling moth and leafrollers differ but combining them into a seasonal program can provide acceptable control. A new on-line Decision Aids System has been developed to help practitioners make the best possible decisions on when to use new insecticides. Resistance to some insecticides has been detected after only 6 years use in the field. OP mediated cross-resistance may be an issue for some new insecticides limiting their efficacy and useful life before they are introduced. A resistance management program is being stressed in educational programs to help delay the development of resistance to new insecticides.

GrubPlan: A greyback canegrub monitoring program in Australian sugarcane fields

Mohamed Sallam, Peter Samson

BSES Limited, Queensland, Australia

Introduction: The GrubPlan program was developed to encourage proactive management of the greyback canegrub (*Dermolepida albohirtum*) and advise growers on best management strategies.

Methods: The program relies on large scale pest monitoring in selected areas of North and Central Queensland. Monitoring involves counting grub numbers in these fields, assessing crop damage before harvest and monitoring adult beetle densities on the regional scale.

Results: Results from Far North Queensland over 5 years showed that pesticide use was an effective means of combating grub damage, however, growers' attitude tends to be reactionary, where rates of pesticide application drop considerably when grub damage declines, and this causes damage to start rising again which in turn leads to a rise in pesticide application. The GrubPlan program is designed to "fine tune" this process, where, based on thorough monitoring, growers can strategically treat their most vulnerable crops and on the same time be prepared to increase their treatment levels if grub populations start to surge. Monitoring results are shared with growers to keep them informed of the pest's population levels and this enables them to maintain sustainable grub management on the local and the regional level.

Conclusion: Queensland canegrowers can improve their grub management and reduce reliance on chemical treatment by committing to a thorough, long-term monitoring program.

Enhancing sugarcane biosecurity measures in Australia

Mohamed Sallam, Peter Allsopp

BSES Limited, Queensland, Australia

Introduction: Invasive pest and disease species pose an ongoing threat to agricultural industries world wide. In Australia, a sugarcane biosecurity scheme has been initiated, whereby Incursion Management Plans are developed for major exotic pests and diseases such as species of moth borers and sugarcane smut.

Methods: The plans detail steps to be taken following an incursion of a sugarcane pest or a disease into Australia, with specific information on the pest's biology, identification, geographical distribution, economic impact and control strategies. All plans are continuously updated in light of new information on changing pest status and recent expansions. The plans also provide information on the "pest risk category", which places the pest into one of four categories depending on its economic status in its area of distribution, with predicted levels of damage that might be incurred in Australia in case of incursion. These categories assist in deciding on sharing eradication and compensation costs between the state government and the industry(s) concerned.

Results: Our preparedness has been tested when an unknown moth borer was found on Thursday island north of the Australian mainland. The moth species was found to be *Chilo crypsimetalla*, which is not a pest of sugarcane and unlikely to cause any economic damage.

Conclusion: Our detection, quick diagnosis and response confirms our good level of preparedness for any possible exotic pest or disease introduction.

Belowground mycorrhizal endosymbiosis and aboveground insects: can multilevel interactions be exploited for a sustainable control of pests?

Emilio Guerrieri[1], Maria Cristina Digilio[2]

[1]Institute for Plant Protection, National Research Council of Italy, Portici, Naples, Italy, [2]Department of Agricultural Entomology and Zoology, University of Naples, Portici, Naples, Italy

More than 20 years have passed from the first report of a multilevel interaction between an arbuscular mycorrhizal fungus and an aboveground insect herbivore. Since then, this intriguing topic has been developed by including other partners, such as the natural enemies of insect pests and by considering top-down interactions, i.e. the effect of insect herbivory on mycorrhizal development. As for bottom-up interactions, it appears that their final outcome mainly depends on the species-specificity of the effects induced by AM fungi on plant responses. In other words, through AM symbiosis more nutrients are transferred to the plant, but whether this leads to an improvement (e.g. tolerance) or a reduction (e.g. better performance of herbivore) of plant resistance depends on the partners involved. Moreover, the alteration of plant volatiles induced by AM symbiosis can play a role in the attractiveness towards the natural enemies of insect pests (indirect defence). However, many aspects of these interactions remain to be elucidated before considering AMF-insects interaction as a new tool to be exploited for the sustainable control of agricultural pests. In this view, the use of modern techniques could be of great help in unravelling the inner mechanisms regulating the interaction between AM symbiosis and aboveground insects. This ambitious result can only be achieved by following a multidisciplinary approach that involves plant physiologists, geneticists, microbiologists, chemists, mycologist, entomologists and ecologists.

Male morph predicts investment in larval immune function in the dung beetle, *Onthophagus taurus*

Sheena Cotter[1], Leigh Simmons[3], Sheena Cotter[2]

[1]University of Cambridge, Cambridge, United Kingdom, [2]CSIRO Entomology, Perth, WA, Australia, [3]The University of Western Australia, Perth, WA, Australia

Investment in immunity is costly, so that resource-based trade-offs between immunity and sexually-selected ornaments might be expected. The amount of resources that an individual can invest in each trait will be limited by the total resources available to them. It would therefore be informative to investigate how investment in immune function changes during growth or production of the sexual trait as resources are diverted to it. Using the dung beetle, *Onthophagus taurus*, which displays both sexual and male dimorphism in horn size, we examined changes in one measure of immune function, phenoloxidase activity, in the haemolymph of larvae prior to, and during horn growth. We found that phenoloxidase levels differed between small and large horned males throughout the final instar prior to the point where investment in horn growth was taking place. PO levels in females were intermediate to the two male morphs. These differences could not be accounted for by differences in condition, measured as haemolymph protein levels and weight. We suggest that the observed differences might be associated with sex and morph specific variation in juvenile hormone levels.

The role of chemical cues on host selection by female sunflower moth, *Homoeosoma electellum* (Hulst) (Lepidoptera: Pyralidae), and banded sunflower moth, *Cochylis hospes* Walsingham (Lepidoptera: Tortricidae).

Maboko Mphosi, Stephen Foster

Agricultural Research Council, Potchefstroom, South Africa

The sunflower moth, *Homoeosoma electellum* (Hulst), and banded sunflower moth, *Cochylis hospes* Walsingham are important economic pests of cultivated sunflower, *Helianthus annuus* L., in North America. The role of chemical cues on female sunflower moth and banded sunflower moth host selection was investigated. *H. electellum* females used volatile chemical differences in order to distinguish between two different stages of sunflower heads. In contrast, *C. hospes* females do not appear to distinguish between the odours of the different head stages, but rather do so when in contact with the head. The presence of conspecific larvae on a head influenced oviposition by females, with females of both species laying fewer eggs on heads infested by conspecific larvae, than on uninfested heads. Larvae of both species also showed preferences for material from different stage sunflower heads, corresponding to the head stage they would normally feed on. *H. electellum* neonate larvae preferred florets from R5 heads over bracts from R2 heads, while *C. hospes* neonate larvae preferred bracts from R2 heads over florets from R5 heads. This study demonstrated that chemicals produced by different stages of sunflower are likely important for the selection of appropriate head stage by both adult females and larvae of both *H. electellum* and *C. hospes.*

Influence of biodiversity in the bio-control of African rice gall midge, *Orseolia oryzivora* H & G (Diptera: Cecidomyiidae)

E. O. Ogah, J. A. Odebiyi, F. E. Nwilene

Ebonyi State University, University of Ibadan, Africa Rice Centre (WARDA), IITA, Abakaliki, Ebonyi state, Ibadan Oyo State, Ibadan, Oyo State, Nigeria

Introduction: The bio-control of African rice gall midge (AfRGM) in the tropical rice over the past 30 years using *Platygaster diplosisae,* an indigenous endoparasitoid*,* has not given the desired results, despite high level of parasitism recorded. This has been attributed to late arrival of this parasitoid in the field. The current management efforts are directed at integrating biodiversity with bio-control agents.

Methods: We tested the hypothesis that diversifying the rice ecology will conserve *P. diplosisae* in alternative host, *Orseolia bonzii* in *Paspalum scrobiculatum* weeds, in the management of AfRGM. The strategy adopted in the study was to plant raised seedlings of *P. scrobiculatum* on a strip of land at the border of each plot one metre around it early in the season and allowed to be fully established before planting of the rice plants inside each plot. The control experimental plots were planted with only rice seedlings leaving the border empty without any weed. All infestations were natural. The responses of *P. diplosisae* to AfRGM infestations were monitored in two ecologies. The host transfer experiment to ensure that *P. diplosisae* can transfer from the alternative host to rice midge was conducted in a screen house.

Results: The results of the statistical analysis indicated that field diversification was the most important sources of early season peak of alternative host insects, which provided a highly consistent, abundant and well dispersed food sources for *P. diplosisae*. This allows parasitoid population to develop early in advance of rice pest population, thereby consistently keeping pests well below economically damaging levels. The host transfer experiment confirmed this result followed by the significant positive correlation recorded, which justifies its economic usefulness.

Conclusions: The results of the study therefore demonstrate the role of biodiversity in the management of AfRGM, and provide a mechanistic understanding of the important contribution of conservation in the bio-control of AfRGM.

Foraging behaviour of the African honey bee (*Apis mellifera adansonii*) on *Combretum nigricans, Erythrina sigmoidea, Lannea kerstingii* and *Vernonia amygdalina* flowers

Fohouo Fernand-Nestor Tchuenguem[1], Jean Messi [2], Dorothea Bruckner[3]

[1]*University of Ngaoundéré, Ngaoundéré, Cameroon,* [2]*University of Yaoundé I, Yaoundé, Cameroon,* [3]*University of Bremen, Bremen, Germany*

Introduction: In Cameroon, demand for hive products is growing. Honey and pollen yields are low in this country, partly because of the poor knowledge of the apicultural value of the flora. In orther to determine the apicultural value of *Combretum nigricans, Erythrina sigmoidea, Lannea kerstingii* and *Vernonia amygdalina*, a study of the activity of the African honey bee, *Apis mellifera adansonii*, were carried out on the flowers of these plant species, from December 2001 to May 2002, then from December 2002 to May 2003.

Methods: Flowers of each plant species were prospected at least four days per month, between 7 am and 6 pm, for the registration of the nectar and/ or pollen foraging behaviour of *A. m. adansonii* workers.

Results: *A. m. adansonii* harvested nectar of each plant species. In addition, *L. kestingii* and *V. amygdalina* were visited for pollen. The greatest number of workers foraging on a plant at the same time varied from 26 in *E. sigmoidea* to 4200 in *V. amygdalina*. *A. m. adansonii* workers were faithful to the flowers of each plant species. During foraging, *A. m. adansonii* increased the pollination possibilities of visited flowers.

Conclusions: Each of the studied plant species could be cultivated and protected to increase honey production. *L. kestingii* and *V. amygdalina* could enable beekeepers to increase their pollen production.

Sustainable management of pests of vegetable crops in Ghana with neem insecticides

Daniel Obeng-Ofori

University of Ghana, Legon, Accra, Greater-Accra, Ghana

Introduction: The production of vegetables is a major all-year-round agricultural activity of small and medium-scale farmers in Ghana and has a great potential to increase the income level and standard of living of growers. However, vegetable production is constrained by attack by insects, diseases, nematodes and the declining soil fertility, necessitating the use of high rates of pesticides and artificial fertilizers. Currently, the main method of controlling pests and diseases of vegetable crops is the use of synthetic pesticides. This sole dependency on pesticides to control pests is posing serious environmental and health problems. There is, therefore, the need to develop a sustainable and environmentally sound alternative pest management strategy to combat insect pests and diseases of vegetable crops in Ghana. Native to India and Burma, the neem tree, *Azadirachata indica* A. Juss was introduced to Africa earlier this century and is now well established in at least 30 countries, including Ghana where it has become an important source of fuel, lumber and biopesticide. Calneem oil is cold pressed, double filtered, pure and natural oil derived from high quality neem seeds, produced and marketed in Ghana by AQUA AGRIC Community Projects (AACP), Accra. It contains about 0.3% azadirachtin as its major active ingredient. It is a broad spectrum insecticide which is effective against several pests of vegetables, food crops, fruit and other tree crops.

Methods: The efficacy of different concentrations of Calneem oil and 'home made' neem seed extract against major pests of okra, cabbage, pepper, garden egg and cucumber were carried out in different locations in Ghana namely: Weja Irrigation Site, Ashman Irrigation Site and the University Farm, Legon.

Results: Both Calneem oil and 'home made' neem seed extract were effective in controlling the major pests of okra, cabbage, pepper, garden egg and cucumber. The major target species included the diamondback moth, fruit files, mealy bugs, aphids, pod borers, bud borers, bud worms, leafhoppers, plant bugs, beetles, grasshoppers and other defoliators. The neem products were also less harmful to some beneficial organisms such as certain ant species, lady bird beetles and dragon flies.

Conclusion: The practical utilization of neem insecticides for sustainable protection of vegetables against pest infestation in Ghana has been demonstrated in the field.

Herbivore-induced bottom-up trophic cascade

Takayuki Ohgushi, Shunsuke Utsumi

Center for Ecological Research, Kyoto University, Otsu, Shiga, Japan

Introduction: In ecological communities prey-predator interactions are potentially affected by the phenotypic plasticity of plants. If plant traits influence community structure of herbivores and predators, then the bottom-up effects would alter the outcomes of multiple prey-predator interactions. Insect herbivores induce a diversity of trait changes in plants, which, in turn, greatly affects the abundance and species richness of insect herbivores. These bottom-up effects produced by insect herbivores through changes in plant traits will extend upward to the third trophic level, altering the abundance and species richness of natural enemies.

Methods: we experimentally examined how the secondary regrowth of willows in response to the swift moth boring and artificial herbivory affects the abundance and species richness of higher tropic levels on three willow species.

Results: The swift moth boring and artificial cutting induced the rapid regrowth of lateral shoots followed by increased new leaves with high nutritious status. In response to the secondary regrowth, species richness and relative abundance increased not only in herbivorous insects but also in predators. Note that specialist herbivores increased in response to the secondary regrowth but generalists did not. Also, the numerical response of predators largely depended on predator taxa, such as ants and spiders.

Conclusions: We revealed the herbivore-induced bottom-up trophic cascade induced by swift moth boring and artificial herbivory. Feeding mode of herbivores and predator taxa are important in determining the community consequences of the herbivore-induced bottom-up trophic cascade.

What can chemical neuroanatomy tell us about signalling in the lamina of the *Drosophila* visual system?

Dick Nassel, Agata Kolodziejczyk

Stockholm University, Stockholm, Sweden

Synaptic connections of neurons in the *Drosophila* lamina, the most peripheral synaptic region of the visual system, have been comprehensively described. Thus the lamina is not only an excellent model for the development and plasticity of synaptic connections, but also a neuropil in which functional circuits can be analyzed with particular clarity. To unravel neurotransmitter circuits in the lamina of *Drosophila* we combined Gal4 driven green fluorescent protein in specific lamina neurons with antisera to g-aminobutyric acid (GABA), glutamic acid decarboxylase, a $GABA_B$ type of receptor, a vesicular glutamate transporter (vGluT), ionotropic and metabotropic glutamate receptors, choline acetyltransferase and a vesicular acetylcholine transporter. We furthermore analyzed distribution of serotonin and two of its receptors in the lamina. Whereas acetylcholine, GABA and glutamate appear to act within synaptic circuits of the lamina neuropil (classical short-range synaptic transmission), serotonin seems to signal non-synaptically by volume transmission. Surprisingly the two types of serotonin receptors were detected on glial cells in the lamina, not on neurons. The neuron-specific expression patterns of neurotransmitters and receptors will be discussed in the light of known synaptic connections and proposed visual processing elements.

Population structure and the conservation of bumblebees in western Europe

David Goulson, Gillian Lye, Ben Darvill

University of Stirling, Stirling, United Kingdom

Bumblebees (*Bombus* spp.) are among the most important pollinators in western Europe, but have undergone major declines in the last 60 years. We review causes of these declines, which can largely be attributed to changes in agricultural practices. However, populations of bumblebees continue to go extinct in protected areas which have not been directly affected by agricultural change. Recent molecular studies have revealed much about the population structure of declining bumblebee populations. These data suggest that many surviving populations may be doomed to extinction through breakdown of metapopulation structure and the effects of inbreeding, the latter exacerbated by the social nature of bumblebees which renders their effective population size low (most bees are sterile workers). It has become clear that effective conservation of bumblebees requires concerted action at a landscape-scale, and that most existing nature reserves are too small to conserve viable populations of bumblebees in the long term. Strategies for the conservation of bumblebees in Europe are discussed.

A fixed spray system for applying pesticides to high-density apple plantings

Arthur Agnello, Andrew Landers

Cornell University, Geneva, New York, United States

Introduction: Pesticide application to tree fruits using airblast sprayers can be inefficient and inaccurate, resulting in spray drift, off-target contamination, and ineffective pest control. A spray system fixed into the tree canopy was used to apply all seasonal pesticide sprays to a commercial planting and compared with results using a conventional sprayer.

Methods: A high-density Gala apple planting received all its pesticide and thinning sprays through a system of microsprinkler nozzles attached to polyethylene tubing running through the row middles and supplied by a central tank and pumping station. Insect and disease control, thinning results, and spray deposition data were compared with those taken in a section of the orchard treated using a tractor pulling an airblast sprayer.

Results: Sprays were applied quickly and efficiently, each taking only a few minutes to completely cover all the trees in the fixed-spray section of orchard. In-season sampling sessions revealed identical zero-damage levels in both spray treatments from leaf- or fruit-infesting insects. The fruit harvest evaluation showed comparable levels of clean fruit (96-97%) in the two halves of the block, with the fixed-spray half receiving slightly more late leafroller damage, and the grower's comparison showing more apple maggot and plum curculio damage. Spray deposition in different canopy sectors, as measured by a dye tracer, was comparable using the fixed-spray or airblast application methods.

Conclusions: A fixed nozzle plus tubing arrangement could offer benefits in pesticide application efficiency and accuracy while maintaining crop protection efficacy and production quality in modern apple plantings.

Functional and phylogenetic implications of the sting apparatus of solitary wasps

Silke Mosel, Michael Ohl

Museum of Natural History, Department of Research, Berlin, Germany

The sting apparatus of solitary wasps is one of the most prominent apomorphic characters of the Aculeates. It is of importance for an understanding of phylogenetic and evolutionary processes of the aculeate Hymenoptera. Derived from the ovipositor it serves as a tool for prey paralysis in addition to its defense function. It can be presumed that the sting apparatus has evolved in close functional association to its specific biological meaning, for example in adjustment to reproduction strategies. Apoid wasps exhibit a great diversity of foraging and parental behaviours as well as a great variation of morphological characters. Modifications of the sting apparatus may be expected to result from variation in the prey utilized and the precision of the stinging action. These modifications are particularly pronounced in the shape and structure of the stylet and lancets and may reflect a correlation with the mobility and physical strength of the prey. The presence of barbs on the distal parts of the lancets can be correlated with a less sclerotized body wall of the prey. This morphological diversity can be found on all systematic levels and is of great significance for the phylogeny of solitary wasps. A representative set of morphological characters taken from the sting apparatus has been examined. A comprehensive cladistic analysis based on these characters was performed in order to investigate the relationships among apoid wasps. The results combined with the different behavioural strategies will give rise to a scenario of the evolution of the sting apparatus of solitary wasps.

Vibrational communication in the new insect order Mantophasmatodea

Monika J. B. Eberhard[1], Mike D. Picker[2], Guenther Pass[1]

[1]Department of Evolutionary Biology, Faculty of Life Sciences, University of Vienna, Vienna, Austria, [2]Zoology Department, University of Cape Town, Rondebosch 7700, Cape Town, South Africa

Introduction: In Mantophasmatodea, both sexes produce vibrational communication signals. Two sympatric species, *Karoophasma biedouwensis* and an undescribed species, were used to determine the role of communication in a) species identity and b) potential mate location.

Methods: Vibrational signals were recorded from laboratory-reared adults drumming directly onto the membrane of a loudspeaker. The digitized signals were analyzed using Sound Forge Software and were used in one-sided stimulation playback experiments. The responses of males and females to different calls were monitored on a Y-shaped apparatus.

Results: Each sex produced a distinctive call. The female call consisted of repeated single pulses, whereas the more complex male call comprised repeated pulse trains. The calls of males and females of the two species were of similar general structure, but differed in most temporal characters such as pulse and pulse train repetition time. Females reacted to the call of conspecific males by calling and becoming less active, but did not react to the call of heterospecific males. Males exhibited abdominal rubbing, high tapping rates, increased activity and characteristic searching behaviour at the fork of the Y apparatus when presented with the call of a conspecific female. These responses were significantly depressed when males were stimulated with the call of a heterospecific female, or of a conspecific male.

Conclusions: Temporal features of the vibrational signals used by duetting male and female Mantophasmatodea convey cues for both mate location and species recognition.

Coexistence of *Aphidius* species: Does interspecific competition structure the parasitoid community?

Joan van Baaren, Cécile Le Lann, Pauline Le Guigo, Liliane Krespi, Yannick Outreman, Jean-Sébastien Pierre, Jacques van Alphen

[1]*University of Rennes 1, Rennes, France,* [2]*Agrocampus Rennes, Rennes, France*

Introduction: Three species of *Aphidius* parasitoids exploit the wheat aphid *Sitobion avenae* in western Europe. *Aphidius rhopalosiphi* is a habitat specialist and the only species present in wheat fields in winter. It is the commonest species throughout spring. Two generalists, *A. avenae* and *A. ervi,* invade wheat fields by the end of spring. Wheat aphids defence themselves actively when attacked by parasitoids and emit alarm pheromone when attacked.

Methods: Behavioural analyses of interspecific host discrimination, competition, patch exploitation were realized.

Results: *A. rhopalosiphi* is sensitive to host defensive behaviour, and exploits host patches only partially. *Aphidius avenae* displays a particular behaviour, with wing fluttering before attacking a host, which results in suppression of defensive behaviour. This allows them to exploit patches with alerted aphids abandoned by *A. rhopalosiphi*. *Aphidius ervi* has a fecundity twice that of *A. rhopalosiphi*, is less sensitive to the host defence behaviour and is a better competitor than *A. rhopalosiphi* in multi-parasitized hosts. Interactions between *A. avenae* and *A. ervi* are limited due to the low densities of these species. When females of the three species encounter each other in a host patch they display no aggressive behaviour to each other.

Conclusions: We showed that the three species can coexist with little overlap in host use, because they have different phenologies and densities, different host exploitation strategies and different life histories.

Spatial co-occurrence networks couple with DNA analysis to reveal the dynamics and feeding histories of polyphagous predators

James R. Bell, R. Andrew King, David A. Bohan, William O.C. Symondson

[1]Rothamsted Research, Harpenden, Hertfordshire, AL5 2JQ, United Kingdom, [2]Cardiff School of Biosciences, Cardiff University, Biomedical Sciences Building, Museum Avenue, Cardiff CF10 3US, United Kingdom

Explaining the relationships between complex polyphagous feeding histories and pest suppression is essential for sustainability in those agricultural systems that rely heavily on the role of beneficial invertebrates for pest control. For some time it has been argued that univariate predator-prey relationships may be an abstract and simplistic model of polyphagous predator behaviour. Selection may therefore have led to the evolution of patterns of behaviour or prey detection systems that require multivariate approaches. In this presentation we demonstrate the utility of a spatially explicit, ecological-network model that uses spatial co-occurrence to link above-ground and below-ground species in winter wheat. In addition, we include extra layers for within-field environmental gradients. Spatial co-occurrences were computed for all pairwise relationships between polyphagous beetles and spiders and key pests, which included orange blossom wheat midge, slugs and aphids and a range of alternative prey that have either beneficial (e.g. worms) or negligible (e.g. springtails) effects on crop production. From these spatial co-occurrences we infer important interactions between species groups and effects on winter wheat productivity, with support from DNA analysis of the gut contents of selected predators.

Unraveling a chalcidoid wasp complex associated with galls in the seed capsules of *Eucalyptus camaldulensis* in South Africa

Hildegard Klein[1], Stefan Neser[1], Ottilie Neser[1], John Hoffmann[2]

[1]*Agricultural Research Council, Plant Protection Research Institute, Pretoria, South Africa,* [2]*University of Cape Town, Cape Town, South Africa*

Introduction: Five chalcidoid species were reared from galls in the flower buds and seed capsules of river red gum (*Eucalyptus camaldulensis*) in South Africa: *Megastigmus zebrinus* (Torymidae: Megastigminae); *Quadrastichodella nova*, *Aprostocetus* sp., and two species belonging to different, undescribed genera (all Eulophidae: Tetrastichinae). All five species are probably inadvertent introductions from Australia. Both *M. zebrinus* and *Q. nova* were previously described as gall inducers elsewhere. We aimed to determine the roles of each of the five species (gall inducer, parasitoid or inquiline) and the impact of galling on seed numbers.

Methods: Hymenopterans found as juveniles during dissection of, or reared from, flowerbuds and seed capsules of *E. camaldulensis*, were recorded, and correlated with the development stage of tagged flower buds and capsules. Gene sequencing was used to match juveniles with adults. The oviposition behaviour of wasps was observed in the laboratory. The insects were also sleeved on reproductive shoots on the trees, and the ensuing capsules examined for galling. Viable seed numbers were plotted against gall numbers per seed capsule.

Results: Two of the chalcidoid species had distinct emergence peaks, and the others emerged throughout the year. Some species diapaused for a year or longer. The biological role of some of the insect species could be deduced. Capsules containing more than one gall produced hardly any viable seeds.

Conclusions: Present indications are that only *Q. nova* initiates galls, which originate in the placenta. No indication of endoparasitism was found, and at least one of the species is entomo-phytophagous.

Application of statistical models for efficient monitoring of invasive insects

Gudeta Sileshi, Gerson I. Nyadzi

[1]World Agroforestry Centre (ICRAF), Lilongwe, Malawi, [2]UN Millennium Villages Project, Tabora, United Republic of Tanzania

Introduction: Rapid and accurate estimation of abundance patch occupancy is critical to understanding the spatial and temporal dynamics of invasive insects and their management. An inherent problem associated with monitoring small and often abundant species is the time and resources required to collect a sufficient number of sampling units to obtain a reliable estimate of abundance or patch occupancy (occurrence probability).

Methods: This paper describes a synthetic method for estimation of abundance and occupancy of invasive insects. The method uses nonlinear mixed modelling (NLMM) approach for estimating parameters of abundance and occupancy as functions of environmental covariates. It also applies conventional and non-standard occupancy–abundance models to estimate abundance from presence-absence data.

Results: The proposed approach allows rigorous testing of adequacy of habitat models and more realistic predictions of abundance from records of presence-abundance for zero-inflated, time-series and clustered data. Parameter estimation and statistical inference are demonstrated using field data on the invasive species *Heteropsylla cubana* collected in Zambia and Tanzania. Potential applications of the approach in large-scale monitoring of site colonization and establishment by alien invasive species are also discussed.

The genetic basis of a plant–insect coevolutionary key innovation

Heiko Vogel[1], Hanna Fischer[1], Cristopher Wheat[2]

[1]Max Planck Institute for Chemical Ecology, Jena, Thuringia, Germany, [2]Pennsylvania State University, PA, United States

The unresolved central tenet of Ehrlich and Raven's theory is that evolution of plant chemical defenses is followed closely by biochemical adaptation in insect herbivores, and that newly evolved detoxification mechanisms result in adaptive radiation of herbivore lineages. Using one of their original butterfly-host plant systems, the Pieridae, we identify a pierid glucosinolate detoxification mechanism, nitrile-specifier protein (NSP), as a key innovation. This unique host adaptation system, not based on universal detoxifying enzymes (eg P450), offers the opportunity to serve as a model system to study molecular evolution events leading to the gain of new traits. Butterfly NSP activity matches the distribution of glucosinolates in host plants across Pieridae. Moreover, by using five different temporal estimates, NSP seems to have evolved shortly after the evolution of the host plant group (Brassicales) (10 Myr). An adaptive radiation of these glucosinolate-feeding Pierinae followed, resulting in significantly elevated species numbers compared with related clades. Mechanistic understanding in its proper historical context documents more ancient and dynamic plant–insect interactions than previously envisioned. Moreover, these mechanistic insights provide the tools for detailed molecular studies of coevolution from both the plant and insect perspectives.

Natural repellents from human hosts against biting insects

James Logan[1], Michael Birkett[1], Gregor Devine[4], Ahmed Hassanali[3], A. Jennifer Mordue[2], Elvira Perea[5], John Pickett[1]

[1]Rothamsted Research, Biological Chemistry Department, Harpenden, Hertfordshire, United Kingdom, [2]Aberdeen University, Aberdeen, United Kingdom, [3]International Centre of Insect Physiology and Ecology, Nairobi, Kenya, [4]Naval Medical Research Center Detachment, Trujillo, Iquitos, Peru, [5]Laborotorio Referencial, Direccion de Salud, Iquitos, Peru

Introduction: Haematophagous insects show differential behavioural responses to odours from individual human hosts with some hosts being much less attractive than others. Such hosts are known to produce compounds that attract haematophagous insects as well as compounds that can interfere with host attraction. In a previous study, we identified behaviourally-active compounds that are associated with low human attractiveness to mosquitoes and midges. These compounds significantly affect host location behaviour and cause a reduction in flight activity of host-seeking female mosquitoes in behavioural studies.

Methods: Recently, we have tested several putative human-derived repellents in laboratory and field trials, as topically applied repellents, against several species of biting flies, including *Anopheles*/*Aedes/Culex* spp. mosquitoes and *Culicoides* spp. midges. Single compounds and mixtures (including different combinations and specific ratios) were tested in dose response assays. Additionally, we have investigated the potential of using the compounds as spatial repellents in a chemical dispenser, which maintains ratio integrity of the active compounds upon release.

Results: Two of the human-derived compounds, released in the correct ratio, show effective topical and spatial repellency against mosquitoes and midges. Despite the high volatility of the active compounds, some persistence over time has been achieved.

Conclusions: This study provides an insight into how biting insects respond to naturally produced human-derived repellent compounds, and how such compounds could be exploited as new, topically applied or spatial repellents.

On the frontier of risk management: Potential nontarget effects of classical biocontrol agents stimulate innovation by entomologists in the U.S.A.

Keith Douglass Warner, Waide Hicks

Santa Clara University, Santa Clara, California, United States

Introduction: Biological control practitioners worldwide now encounter difficulties obtaining permits to import exotic control agents due to nontarget concerns. Practitioners in the U.S.A. have devised strategies, individual and collective, to address risk concerns.

Methods: Bibliometric analyses and semi-structured interviews with U.S. practitioners, critics and regulators provided data describing how entomologists have responded to concerns regarding potential nontarget effects.

Results: Entomologists report developing: new molecular analytical tools to identify sub-species of candidate control agents, new rearing methods which make more natural enemies available as classical biocontrol agents, new partnerships with international scientists to conduct nontarget studies of agents in their countries of origin, and new modeling strategies to understand probable specificity of action on hosts. Practitioners repeatedly referred to the international code of conduct for weed biocontrol, and arthropod biological control practitioners are considering one. Many individual practitioners are increasing public outreach about their work and responding to public interest in proposed agent introductions.

Conclusion: Concern about risks associated with nontarget impacts of introduced control agents has prompted changes in practice by individuals, their laboratory groups, and research-sponsoring organizations. These have generally been voluntary in character, but some policy development is occurring as well. Entomologists also report conducting public outreach efforts. Nontarget concerns have been acute in the U.S.A. and will likely become more so in other countries. The innovations developed here may be applicable to other entomologists confronting concerns about the risks of nontarget effects.

Potential leafhopper vectors associated with potatoes in Alaska

Alberto Pantoja[1], Aaron M. Hagerty[1], Susan Y. Emmert[1], Joseph Munyaneza[2]

[1]United States Department of Agriculture, Agricultural Research Service, Fairbanks, Alaska, United States, [2]United States Department of Agriculture, Agricultural Research Service, Wapato Washington, United States

Leafhopper transmitted phytoplasma diseases are an emerging problem for potato and vegetable producers in the conterminous United States of America (USA)**.** Due to its geographical isolation and climatic constrains, Alaska is considered relatively free of diseases and insect pests. Potato growers in the state are exploring the potential of producing seed potato for export. However, the biology of agricultural insect pests in the circumpolar region is lacking or poorly understood. Research conducted from 2004 to 2006 in the main potato (*Solanum tuberosum* L.) production areas of Alaska resulted in the identification of 33 leafhopper species associated with agricultural settings. Fourteen species were associated with potato. Two species, *Macrosteles facifrons* (Stål) and *Davisonia snowi* (Dorst) made up approximately 60% of the total number of individuals collected. Four of the species collected are known vectors of phytoplasma diseases of potatoes and other agricultural crops or have the potential to cause mechanical damage to potatoes. Data on vectoring capacity, population dynamics, and geographic distribution will be presented.

Resistance and physiological differences among three species of stored product beetle pests exposed to diatomaceous earth

Charles Adarkwah, Paul. G Fields, Christoph Reichmuth, Carmen Buttner, Daniel Obeng-Ofori

Humboldt University of Berlin, Berlin, Germany

Dosages of diatomaceous earths (DE) killed approximately 70% of the beetle populations. DE-susceptible and DE-tolerant adult insects were compared for: water loss, speed of movement and progeny production. For all the tests, the diatomaceous earth Protect-It™ was used at the following dosages and exposed for 7 days**:** red flour beetle *Tribolium castaneum,* 0.6 g/kg wheat; rice weevil *Sitophilus oryzae,* 0.3 g/kg wheat and rust-red grain beetle *Cryptolestes-ferrugineus*, 0.15 g/kg, wheat respectively. The use of different dosages reflected the different susceptibilities of the three species towards the DE.

Tolerant strains lost significantly less water when exposed to DE-treated grain; they moved more quickly through grain and two tested insect species, *Tribolium castaneum* and *Sitophilus oryzae* produced less progeny. Tests with measurements of the movement and activity in Petri dishes were similar to the movement through grain for *T. castaneum*, but not for the other two species. If this level of increased tolerance towards exposure to DE was present in insect populations found in commercial stores, it would probably cause control failures. However, if tolerant species produced fewer offspring, as in these strains, tolerant strains would probably diminish with time.

Insects in western art

Marcel Dicke

Wageningen University - Laboratory of Entomology, Wageningen, Netherlands

Insects have been a source of inspiration to artists throughout the centuries. From the 13th century until present artists have depicted insects in two-dimensional and three-dimensional works. Insects have often been used as symbols for the brevity of life, for the transcendence of the soul, but also because of the beauty of their forms and colours. Some artists paint or sculpt with insects themselves, either dead or still alive.

Over the past seven years I have visited 180 art museums and recorded the representation of insects in the works on display. As a result I have gained an entomological view of the history of art. This has provided insight both in the history of art itself as well as in the role of insects in its development.

At present I have seen more than 3,700 works of art in which insects are represented. The majority occur in the Netherlandish still-lifes of the 17th and 18th centuries, in surrealistic works and in art nouveau works. Some artists have depicted only a single insect while others have represented over 100 insects in a single work of art. Of some artists I know only a single work with insects, while of others more than 100 works are known.

The value of omics to community ecology

Marcel Dicke

Wageningen University - Laboratory of Entomology, Wageningen, Netherlands

Insects comprise the most diverse group of organisms that attack plants and plants have evolved a diverse array of induced defenses against insects, including direct and indirect defenses. These defenses can be investigated at various levels of biological organization and integrating such approaches from genes to community ecology is an exciting challenge to biologists. Recent developments have shown a rapid expansion of mechanistic knowledge of plant-insect interactions in terms of induced resistance and induced attraction of carnivorous enemies of herbivorous insects. In the laboratory the effects of certain genes on individual plant-insect interactions can be investigated. An exciting development is that plants that have been altered in the expression of specific genes involved in induced defenses are exposed to their natural ecological community. By integrating approaches aimed at understanding subcellular mechanisms with those on addressing ecological functions in a natural environment the field of molecular ecology of insect-plant interactions is rapidly expanding our understanding of the intricate phenotypic plasticity that plants exhibit in their contest with the large number of herbivorous insect species. In this presentation the added value of integrating transcriptomics, metabolomics, phenomics and community ecology will be highlighted.

Using GM to enhance bodyguard attraction in crops

Marcel Dicke

Wageningen University - Laboratory of Entomology, Wageningen, Netherlands

Almost half of all insect species are carnivorous and attack herbivorous insects. Thus, plants are surrounded by a multitude of potential bodyguards. In crop protection two main strategies are employed, i.e. (i) host plant resistance aimed at making plants that are toxic or repellent to herbivorous insects and (ii) biological control aimed at releasing the best natural enemy of an insect pest. Plants generally respond to herbivory with the production of volatiles that attract carnivorous insects such as parasitoids or predators as bodyguards. This allows for plant breeders to select for plants with an enhanced attraction of bodyguards through classic methods. Moreover, now that genes underlying the biosynthesis of bodyguard attractants are being uncovered (e.g. Kappers et al. 2005, Science 309: 2070-2072; Schnee et al. 2006, PNAS 103: 1129-113), also genetic modification may be used to produce crops with enhanced bodyguard attraction. In this presentation I will highlight the potentials and the questions related to this new development.

The biological significance of the shape of magnetic termite mounds

Judith Korb[1], Peter Jacklyn[2], Anna Schmidt[1]

[1]University of Regensburg, Regensburg, Germany, [2]Charles Darwin University, Darwin, Australia

The “Magnetic Termite” *Amitermes meridionalis* is restricted to a small part of northern Australia where it occurs in seasonally flooded areas and builds famous wedge-shaped mounds with an elongated axis that is orientated in a striking north-south direction. This shape is unique among all other termite mounds which are always more or less radially symmetrical and many hypotheses have been advanced to explain the remarkable shape and orientation. Most of these investigations focus on the orientation, but the biological significance of the shape is rarely explored. The currently accepted hypothesis considers shape and orientation as adaptation to maintain a thermo-stable eastern face. We tested the importance of seasonal flooding to explain the unique shape of these mounds. We hypothesized that elongated mounds with a large surface area and thin walls offer more favourable conditions (a) to dry the grass storage, on which the termites depend during the floods, (b) to increase mound stability by drying the mounds quickly after heavy rainfalls, and (c) to facilitate respiratory gas exchange when dampness decreases the porosity of the walls. These hypotheses were tested by manipulating mound shape and ambient temperature conditions to test their influence on the termite colonies. The results of this still ongoing project will be presented.

Spatial and temporal patterns in the abundance of beech bark disease-associated organisms in North America: evidence for negative feedback within the subcontinental landscape

Jeff Garnas[1], Celia Evans[2], Mark Twery[3], David Houston[4], Matthew Ayres[1]

[1]Dartmouth College, Hanover, NH, United States, [2]Paul Smiths College, Paul Smiths, NY, United States, [3]USDA Forest Service, Burlington, VT, United States, [4]USDA Forest Service, retired, Danville, VT, United States

Beech bark disease (BBD) in North America is a cankering disease complex of American beech (*Fagus grandifolia* Ehrh.) arising from the association of an introduced scale insect (*Cryptococcus fagisuga* Lind.) and one of several species of ascomycete fungi of the genus *Neonectria*. To test alternative hypotheses regarding the epidemiology of beech bark disease, we evaluated spatial patterning in populations of the insect and fungus at three different spatial scales: (1) trees within stands, (2) stands within forests, (3) forests within the subcontinental landscape. We found no evidence for spatial autocorrelation at either of the two smallest spatial scales; trees and stands that were close together were no more likely to harbor similar population densities of scale insects or fungi than those farther apart. Across the landscape however, disease agent populations were significantly related to the estimated time since local introduction of BBD organisms to a stand. Scale insect densities peak soon after infection and decline thereafter, whereas fungal densities are highest in long-infected stands and forests. This indicates that disease ontogeny follows a predictable trajectory and suggests the existence of negative feedback among the associated organisms at a broad spatiotemporal scale. This finding contradicts the conventional wisdom that BBD associates function as mutualists. Instead, it raises the possibility that the fungal symbiont is actually an antagonist at the scale of the landscape and may therefore mitigate the long-term effects of the disease on North American forests.

Mapping *Drosophila* color-vision circuits

Chi-Hon Lee, Shuying Gao, Chun-Yuan Ting

NIH, Bethesda, MD, United States

Introduction: *Drosophila* color vision is mediated by three types of photoreceptor neurons, each of which has a distinct spectral response. Visual information gathered by all three types of R-cells converges to the medulla ganglion. The post-receptoral mechanism by which color information is processed in the medulla is not known.

Methods: By combining molecular genetic, histological, and behavioral approaches, we determined (a) the connection patterns of the first-order interneurons in the medulla, (b) their dendritic and axonal compartments, and (c) their expression of neurotransmitters and receptors, and (d) their requirement for discriminating different wavelengths of lights.

Results: We analyzed five types of the first-order interneurons, including one distal medulla cell type (DM5) and four types of transmedullar neurons (projection neurons). The projection neurons extend dendritic arbors in specific medulla layers and project axons to the lobula neuropil to form a topographic map. The projection neurons, including TM5 and TM20, appear to receive inputs from two color-channels, suggesting that they might function as color-opponent or summation neurons. The DM5 neurons, which receive direct inputs from multiple R7s, are required for ultraviolet phototaxis behavior.

Conclusions: The flies' innate preference to ultraviolet light is driven by a single subset of neurons. True color vision might be mediated separately by the color-opponent/summation neurons, which directly output to the higher visual center lobula.

Surfactants, but not fatty acid amides contribute to caterpillar defence against predators

Michael Rostás[1], Katrin Blassmann[2]

[1]University of Würzburg, Würzburg, Germany, [2]University of Basel, Basel, Switzerland

Introduction: Plants respond to insect attack by releasing volatile organic compounds that attract the herbivores' natural enemies. Fatty acid amides are potent elicitors of such plant volatiles and have been isolated from the oral secretions of caterpillars. The question why herbivores produce these elicitors, despite the negative selection pressure, remains obscure. We assessed the role of fatty acid amides as potential defence compounds against predators because regurgitation of oral secretion is a widespread mode of self-protection in many caterpillars. Commonly, the effectiveness of herbivore oral secretion has been ascribed to the presence of deterrent secondary metabolites sequestered from the host plant. However, this notion also implies that generalists are particularly vulnerable on plants with low levels of chemical defences. A defensive function of ubiquitous primary compounds such as fatty acid amides could resolve this dilemma.

Methods: A combination of contact angle measurements to assess the physicochemical properties of oral secretion and behavioural assays using caterpillars of *Spodoptera exigua* were applied to test the hypothesis that amphiphilic fatty acid amides in the oral secretion provide protection by wetting the hydrophobic cuticle of predatory ants and forcing the attacker to engage in intensive cleansing.

Results: Our data confirm that surfactants alone can sufficiently explain the defensive character of oral secretion and we speculate that this novel mechanism may be widespread among caterpillars. However, proteins rather than fatty acid amides caused the wetting effects.

Conclusons: Detergency can provide a base level of protection which may or may not be further enhanced by plant-derived secondary metabolites.

Managing harvester termites: the ecosystem approach

Jannette Mitchell

ARC-PPRI, Pretoria, South Africa

The harvester termite, *Hodotermes mossambicus*, is an important component of semi-arid grassland ecosystems of southern and eastern Africa where it occupies a central position in the food chain. It has a wide range of natural enemies, many of them highly specialised. Harvesting is most intense during winter months when little other prey is available. When predators are present in sufficient numbers their impact on the foraging worker population is potentially enormous. Termite populations fluctuate depending on rainfall. Populations are low (± 9,000 workers/ha/yr) following seasons of above average rainfall, while following dry summers numbers can be as high as ± 0.26 x 10^6/ha/yr. Eruptive population growth with consequent high off-take of grass during seasons of low primary productivity brings termites into competition with large herbivores (domestic stock and game). High termite populations also remove all litter, exposing the soil surface and leading to compaction, low infiltration, erosion and loss of nutrients. Ignorance of ecosystem functioning has resulted in mismanagement of these grasslands. Declining predator numbers were also noted as early as the 1930's. These factors favour the development of large residual populations in degraded areas.

Evidence suggests that seasonally appropriate management of herbivore numbers, adequate grassland restoration and conservation measures, and even reintroduction of a suite of predators suited to the area may prove beneficial tools for the management of termite infestations in rangeland. The use of poison bait in areas of high residual population at appropriate times may need to be part of a successful management strategy.

SPLAT formulations: Optimization of semiochemical IPM tools

Agenor Mafra-Neto, Reginald Coler

ISCA Technologies, Inc, Riverside, California, United States

Introduction: SPLAT is a semiochemical technology that has spawned a series of new insect control agents that have been marketed or are going to be marketed in the near future, with the promise of being highly efficacious, compatible with biological control agents, and exhibiting low environmental impact thus making them excellent candidates for integrated pest management programs. We will introduce to the public several of the current SPLAT formulations and describe their modes of application and resulting modes of action. The novel SPLAT formulations their uses in integrated pest management programs will be discussed.

Results: SPLAT is a monolithic and long lasting formulation, but it is amorphous and flowable, allowing for easy mechanization of its application. SPLAT is rainfast and biodegradable. SPLAT has been formulated with different active ingredients, including insecticides and semiochemicals, and successfully biologically and chemically tested both in the laboratory and in the field. Mechanization allows the application of the same mass of SPLAT in either a few large point sources that last for a very long time in the field, or in a multitude of very small point sources allowing management of high density populations. It is possible, therefore, to use SPLAT applications to achieve the density of point sources necessary to control insect pest populations at the density that they are found in the field. This plasticity has allowed SPLAT to be successfully used as a mating disruption agent as well as an attract and kill agent in field trials around the world, which in turn has resulted in a host of successful commercial products.

Conclusions: SPLAT is a long lasting, flowable formulation that allows for easy mechanical application, thus increasing the utility and commercial feasibility of semiochemical pest control formulations.

Amalgamative action of phytoextract and synthetic insecticide against the larvae of the filaria vector, *Culex quinquefasciatus*

Lalit Mohan, Preeti Sharma, C. N. Srivastava

Dayalbagh Educational Institute (Deemed University), Dayalbagh, Agra, Agra, India

Mosquitoes are referred as “Public Enemy Number One”, by WHO, 1996, due to the most common and nuisance-creating dipteran-vector responsible for transmitting various dreadful diseases. It continues to pose the major public health problems in India as well as in other countries with resurgence of chiefly malaria, encephalitis and dengue fever.

Chemical insecticides used in mosquito management, though are quite effective but have some drawbacks like environmental pollution, toxic to non-target organisms and emergence of resistant vector varieties. This deleterious effect caused by the insecticidal applications encouraged the scientific professionals towards the development and advancement of novel, ecofriendly and non-hazardous insecticides of plant origin. Plant products are successfully tested for various biological control activities of different insect pests but the availability and development of bio-pesticides are so far limited. For the effective field applications of phyto-pesticides, plant materials are required in huge quantity to get sufficient amount of the phyto-pesticides. In recent years, the scientists related to pest management have, therefore, diverted their approach from the application of either pure synthetic pesticides or pure phyto-pesticide towards the combined application of both for more effective vector management. In the present correspondence, it is a step forward in the direction of combined application of *Solanum xanthocarpum* and Temephos for the control of *Culex quinuefasciatus* larvae.

Effect of temperature on toxicity and persistence of *Artemisia annua* against *Anopheles stephensi* larvae

Preeti Sharma Rawat, Lalit Mohan, C. N. Srivastava

Dayalbagh Educational Institute, Agra, Uttar Pradesh, India

Synthetic insecticides, on account of their efficiency and fast action, have been constantly used all over the world for more than five decades. It has led to the series of problems of precipitation of resistance in the vector population jeopardizing all important insect control programmes worldwide. In addition, the danger of environmental contamination related with persistence and high toxicity of these insecticides has necessitated the search for newer methodologies in various insect control programmes. The alternative advances in this direction are towards the selection of ecofriendly and cost effective pesticides and propagating the idea of using effective biodegradable chemicals of plant origin. Botanical pesticides in general, possess low mammalian toxicity and thus constitute least health hazards and environmental pollution and there is practically no risk of developing pest resistance to these products, when used in natural forms. Further, these cause less hazards to non-target organisms and insect resurgence has not been reported except synthetic pyrethrins. In view of these facts, under the present study, an attempt has been made to study the larvicidal activity of certain botanical extracts against the vector for urban malaria in India.

Further, the effect of temperature, a very important physical parameter affecting the activity of chemical and botanical insecticide, has been investigated for *Artemisia annua*, one of a potent extract, against the anopheline larvae. The extract was found to be stable within the temperature range of 15-30 ^{0}C. However, above 30 its efficacy was reduced depicting biodegradable the effect of temperature on this botanical insecticide.

Multiple origins of social parasitism in the bee subgenus *Dialictus* (Halictidae: *Lasioglossum*) identified using morphology and DNA barcodes

Jason Gibbs, Laurence Packer

York University, Toronto, Ontario, Canada

Introduction: The sweat bee subgenus *Dialictus* displays an incredible array of social systems and is an ideal group for studying the evolution of social behaviour. Solitary, communal, primitively eusocial and socially parasitic behaviours have been identified. We take advantage of the large numbers of DNA barcodes currently being generated for alternate purposes to examine the evolution of social parasitism in these bees using a phylogenetic approach.

Methods: DNA barcode and morphological data were analysed in isolation and in combination using TNT to generate most parsimonious phylogenetic trees of North American *Dialictus* species. Character mapping was used to examine the origin of social parasitism in this group.

Results: Phylogenetic analyses of morphology and DNA barcodes used with character mapping suggest that social parasitism has arisen multiple times in the subgenus *Dialictus.* The origins of parasitism in *Dialictus* follow the loose form of Emery's rule (ie. parasites are not sister taxa to their hosts). DNA barcode data provides superior resolution of the phylogeny to morphology alone.

Conclusions: Current DNA barcoding efforts are generating a pool of data that may be utilized to aid in phylogenetic inference and improve the density of taxonomic sampling. Since DNA barcoding is in many ways external to mainstream systematics, these data might be used to improve phylogenies at essentially no cost. The discovery that *Dialictus* species have evolved a parasitic lifestyle multiple times may generate new avenues of research into the evolution of social systems in the sweat bees.

Estimating the economic injury level and the economic threshold for the use of α-cypermethrin against the sugarcane borer, *Eldana saccharina* Walker (Lepidoptera: Pyralidae.)

Graeme Leslie

South African Sugarcane Research Institute, Mt Edgecombe, Kwa Zulu - Natal, South Africa

Introduction: The sugarcane borer *Eldana saccharina* Walker (Lepidoptera: Pyralidae) is the most serious pest of sugarcane in South Africa. Approaches to control comprise several practices including insecticide use. To enable more effective management of insecticide use, estimates the Economic Injury Level (EIL) and the Economic Threshold (ET) were developed.

Methods: Five years of results from field–scale insecticide trials assessing the value of α–cypermethrin (Fastac®) against this pest, were used to estimate the EIL and ET. The analysis was based on estimates of borer damage (percent internodes bored) and larval numbers, and the impact of these on crop yield, as estimated by percentage recoverable sugar (ERC%) and tons ERC /ha.

Results: The estimated EIL, based on percent internodes bored and ERC%, was more reliable than estimates based on larval numbers and ERC% and was calculated to be 6.3%IB (± 1.00) or 7.9% IB (± 1.24), depending on the level of treatment efficacy selected (50% and 40% respectively). Where tons ERC/ha was used, estimated EIL was 8.3% IB (± 1.51) or 10.5% IB (± 1.88) for efficacy levels of 50% and 40% respectively. Least reliable were estimates based on larval numbers. Using estimates of damage accumulation over time, the ET, based on %IB and ERC%, was estimated to be 3% IB, assuming a 40% treatment efficacy.

Conclusions: The EIL and ET were estimated to be 7%IB and 3%IB respectively, derived from data on crop damage. Such estimates provide measures that can aid in deciding whether or not the use of an insecticide is justified.

Plant-mediated interactions between rhizobacteria, herbivorous insects and parasitoids

Si-Jun Zheng[1], Jeroen P. van Dijk[2], Anna Costa[1], Marcel Dicke[1]

[1]Laboratory of Entomology, Wageningen University, Wageningen, Netherlands, [2]RIKILT-Institute of Food Safety, Wageningen University and Research Centre, Wageningen, Netherlands

Plants are members of complex communities. Yet, most studies of plant defences against herbivorous insects are made in simple systems usually consisting of the plant and the herbivorous insect and one of its natural enemies. It is well-known that non-pathogenic rhizobacteria can influence aboveground anti-pathogen defences. To understand whether and how anti-insect defence is affected by rhizosphere microorganisms, a multitrophic system consisting of microorganism-plant-herbivore-parasitoid interactions was established. The system consists of two caterpillar species, i.e. the specialist *Pieris rapae* and the generalist *Mamestra brassicae*; the parasitoids *Cotesia glomerata* and *Diadegma semiclausum* and the non-pathogenic rhizobacteria *Pseudomonas fluorescens.* We investigated *P. fluorescens*-mediated plant-insect multitrophic interactions and *P. fluorescens*-mediated gene expressions in cabbage plants through transcriptomics, behavioural ecology and life history analysis. The results indicate that *P. fluorescens* inoculation affects herbivore-induced gene expression and plant-insect interacdtions. This is the first finding that *P. fluorescens* mediates microorganism-plant-herbivore-parasitoid multitrophic interactions. These results may provide novel insights for biological control of insect pests in the future.

Benefits and fitness costs of learning in insects

Frederic Mery

CNRS, Gif sur Yvette, France

Learning and memory play a crucial role in the development of an animal's behavior within its lifespan and are important for its survival and reproductive success. They are products of evolution and the degree to which information is learned and maintained in the brain varies among species and among different types of behavior. Recently these differences in learning ability and memory capacities among species and populations began to be studied in the context of their natural environment and analyzed in terms of fitness benefits and costs. While fitness benefits of learning are relatively well understood, we know little about fitness costs of learning ability, constraints on its evolution, and the nature of heritable variation on which natural selection can act. As with any fitness-related trait, knowledge of these aspects is essential to understanding why, how, and when learning ability evolves under natural selection. Some authors have proposed that learning and memory may trade off with other fitness related traits. In the evolutionary context it is important to distinguish between the costs of inducing memory and the costs of memory capacities.

Studies on Drosophila have greatly advanced our understanding of learning and memory, especially in the context of associative classical (Pavlovian) conditioning and represent an interesting model for the study of the evolutionary biology of learning and memory. From different experiments on this model I will present some evidence of fitness costs and benefits of learning and memory.

Diversity of Agromyzidae and associated parasitoid species in the Afrotropical region

Robert Musundire[1], Benhard Lohr[1], Kerstin Kruger[2]

[1]icipe, Nairobi, Kenya, [2]University of Pretoria, Pretoria, South Africa

Introduction: The Agromyzidae (mining flies) are a diverse dipteran family of exclusively phytophagous species. A number of species are of economic importance, especially those feeding on Fabaceae and some horticultural plants. The economic challenges posed by these species have brought about the need for them to be managed through sustainable methods of which biological control by parasitoids is a key aspect. In the Afrotropical region, there is a need to provide harmonised information about agromyzid and parasitoid diversity to aid in the implementation of biological control.

Methods: The existing knowledge from published information and museum records on species diversity and distribution of agromyzids and associated parasitoid species within the Afrotropical region was reviewed. Information on agromyzid species, origin, associated host plants, parasitoids, and species distribution was captured. An analysis was undertaken to examine the diversity and distribution patterns of agromyzids and how they may have affected parasitoid assemblage size within this region.

Results: Approximately 265 species of agromyzids have been recorded in the Afrotropical region, representing only 10 percent of the world diversity. A total of 42 parasitoid species including introduced species are associated with agromyzids in this region.

Conclusions: Intensive regional collaborative effort on the biodiversity of agromyzids and associated parasitoid species in the Afrotropical region is needed to ascertain whether the apparent paucity of the Afrotropical agromyzids and associated parasitoid species is real or an artefact caused by a lack of sampling effort.

Bemisia tabaci biotype B manipulates its host to suppress effective defenses

Linda Walling, Sonia Zarate, Louisa Kempema

University of California, Riverside, CA, United States

Introduction: The basal defense mechanisms that deter phloem-feeding insect performance are largely unknown. The genetic and genomics resources from *Arabidopsis thaliana* were used to identify the defense pathway that controls basal resistance to *Bemisia tabaci* biotype B.

Methods: Affymetrix ATH-1 GeneChips were used to determine the RNA profiles changed after *B. tabaci* feeding. Defense gene RNAs that controlled by salicylic acid (SA), jasmonic acid (JA) and ethylene (ET) were monitored by RT-PCR or qPCR after adult or nymph feeding. The percentage of nymphs in each instar was measured after 24 d of infestation in wild-type and six defense mutants (*cim10, NahG, npr1, coi1, cev1, pad4* and *ein2*).

Results: There were differences in RNA profiles after *Bemisia tabaci*, aphid and caterpillar feeding. The changes in defense RNAs to *B. tabaci* were biphasic. Responses to adult feeding were distinct from nymph feeding. After nymph feeding, SA-responsive gene transcripts accumulated locally and systemically and SA levels increased. In contrast, JA- and ET-dependent RNAs were repressed or not modulated by *B. tabaci*. Nymph development was accelerated on *cim10* and *coi1* and delayed on *cev1*, *npr1,* and NahG plants. *npr1* plants treated with MeJA displayed a dramatic delay in nymph development. Unlike *Myzus persicae*, *B. tabaci* performance on wild-type, *ein2* and *pad4* mutants were similar.

Conclusions: *B. tabaci* nymphs suppress JA-regulated defense genes. Nymphs develop most rapidly when JA-defenses are impaired. Collectively, these data indicate the *B. tabaci* avoids or suppresses effectual JA defenses.

Circadian and circannual oscillators share the same mode in phase resetting

Hideharu Numata[1], Yosuke Miyazaki[1], Tomoyosi Nisimura[2]

[1]Osaka City University, Osaka, Japan, [2]The University of Shiga Prefecture, Hikone, Japan

Introduction: In circadian rhythms, the shape of the phase response curves (PRCs) depends on the strength of the resetting stimulus. Weak stimuli produce Type 1 PRCs with small phase shifts and a continuous transition between phase delays and advances, whereas strong stimuli produce Type 0 PRCs with large phase shifts and a distinct break point at the transition between delays and advances. A stimulus of an intermediate strength applied close to the break point in a Type 0 PRC sometimes produces arrhythmicity. In the circannual pupation rhythm of the varied carpet beetle *Anthrenus verbasci*, we constructed PRCs to long-day pulses on a background of constant short days, and examined the relationship between phase resetting of the circannual rhythm and the strength of long-day stimuli.

Methods: Larvae of *A. verbasci* kept under LD 12:12 were exposed to LD 16:8 for 2 or 4 weeks (long-day pulse) at various phases of the rhythm at 20ºC.

Results: The PRC to 4-week long-day pulses was similar to circadian PRCs of Type 0. However, the PRC to 2-week long-day pulses was Type 1, and a 4-week long-day pulse administered close to the PRC's break point induced arrhythmicity in pupation.

Conclusions: The phase response of the circannual rhythm in *A. verbasci* closely resembles circadian phase responses reported in various organisms.

Honeybee learning of complex scents: from behaviour to odorant receptors

Judith Reinhard, Charles Claudianos, Michael Sinclair, Julie Lim, Mandyam Srinivasan

The Queensland Brain Institute, St Lucia, QLD, Australia

Introduction: Honeybees (*Apis mellifera* L.) are exposed to countless floral scents in their natural foraging environment, most of which are complex chemical mixtures. While processing of single odorants has been well studied in honeybees, it is still unclear how bees learn and process scent mixtures.

Methods: Using the well-known Proboscis-Extension-Reflex Assay (PER), we investigated olfactory learning of floral scent mixtures. We also examined learning preferences of individual floral scent components, and determined expression patterns of olfactory receptor proteins (OR) potentially involved in floral scent processing using qRT-PCR and microarrays.

Results and Conclusions: (1) Honeybees use one of two strategies to learn a scent mixture, depending on the type of mixture. They either learn key compounds as representative of the entire mixture, or they learn the mixture as a unit. The first strategy keeps scent recognition flexible, while the second strategy enables bees to discriminate even between subtly different scents. We will discuss under which circumstances bees might employ which strategy, and propose a hypothesis of the neural mechanisms underlying complex scent processing. (2) Honeybees learn certain floral odorants better than others, however the preferences are in no correlation to the molecular structure or physico-chemical properties of the tested odorants. Behavioural data and OR expression patterns indicate that sensory exposure in the foraging environment may cause olfactory preferences, suggesting that honeybee olfaction is not entirely hard-wired, but subject to experience-based modulation at the molecular level.

Funded by CSIRO Food Futures Flagship.

Sensory driven synaptic remodelling in the honeybee brain

Charles Claudianos[1], Sunita Biswas[2], Judith Reinhard[1], John Oakeshott[3], Robyn Russell[3], Alexandre Dos Santos Cristino[4], Mandyam Srinivasan[1]

[1]The Queensland Brain Institute, St Lucia, QLD, Australia, [2]The Australian National University, Canberra, ACT, Australia, [3]CSIRO Entomology, Canberra, ACT, Australia, [4]The University of Sao Paulo, Sao Paulo, Ribeiro Preto, Brazil

Introduction: Precise cell-to-cell contact is fundamental to proficient synapse connectivity. Several vertebrate studies highlight the post-synaptic neuroligins and pre-synaptic neurexins (cell adhesion binding partners) as critical to proper synapse development and function. Aberrations to the neuroligin/neurexin complex have been associated with a number of neuro-psychiatric disorders such as autism, Aspergers and schizophrenia. Our honeybee study represents the first comprehensive study of these molecules in invertebrates.

Methods: Isolation and characterisation of five neuroligins and one neurological neurexin provided the basis for examining localisation and developmental expression of these molecules in the honeybee. To investigate the role of *neuroligins* and *neurexin I* in the adult honeybee brain, we conducted a quantitative expression analysis using three different experimental paradigms: environmental deprivation, associative learning, and unilateral or bilateral amputation of the antennae.

Results and conclusion: *Neuroligins* and *neurexin I* were found to be highly expressed throughout the adult honeybee brain including the higher order processing centre, the mushroom bodies. This suggests that the neuroligin/neurexin system has a broadly similar role in synaptogenesis in insects as in vertebrates, with the scope to generate substantial functional diversity through alternative splicing. Experiments using environmental deprivation, associative learning, and antennal amputation all showed that *neuroligin 1* expression was highly correlated with sensory input, suggesting a critical role in synapse development associated to sensory processing, learning and memory. This study is one of the first to investigate a role for these molecules at an organismal level.

Plant-mediated interactions between gall-formers and leaf-chewers

Lilach Zexer[1], Efraim Lewinsohn[2], Einat Bar[2], Moshe Inbar[1]

[1]University of Haifa, Haifa, Israel, [2]Newe Ya'ar Research Center, Ramat Yishay, Israel

Introduction: Indirect, plant-mediated interactions (negative or positive) between herbivores might be common and important. We investigated such interactions between a leaf-galling aphid, *Smynthurodes betae* (Fordinae), and the folivorus moth (*Thaumetopoea solitaria*) both feeding exclusively on *Pistacia atlantica* trees. The aphids induced leaf galls in early spring in which they reproduce until the fall. In the spring the moth caterpillars feed on the same leaves; occasionally, leavening the plant totally defoliated. It is expected therefore, that both insects will be engaged with complex interactions.

Methods & Results: In Field and laboratory experiments we found that: 1. The caterpillars repeatedly avoid the galls while consuming the leaves creating intact "trimmed galls". 2. The galls are protected physically, but primarily chemically from the moth. 3. In GC-MS analysis we found higher levels of mono- and sesquiterpenes in the galls that may contribute to such defence. 3. In the field, gall density on defoliated shoots increased (X 4) comparing to caterpillar-free shoots, due to compensatory tree growth which extended the availability of young leaves. 4. Trimmed galls maintained strong sink for nutrients from alternative sources as reflected by the unaffected reproduction of the aphids in these galls.

Conclusions: Plant-mediated effects between the caterpillars and the aphids are complex and involve various mechanisms. The aphids manipulate the host plant (gall tissue) to avoid gall consumption and draw assimilates from alternative sources. The aphids also utilize plant response to defoliation to their own benefit.

Megachile unbripennis Smith: Leaf cutting behaviour on rose leaves (*Rosa*)

Dita Nurtjahya

SMAN 1 Senior High School, Sungailiat, Bangka Belitung, Indonesia

The research was carried out based on being unsatisfied with the previous research results. The objective was to identify the leafcutter bee species that cuts the leaves of roses (*Rosa* sp.) that grow in Sungailiat, Bangka Island; secondly it was to study its leaf cutting behaviour. The information might be useful to uncover the role of leaf-cutter bees in ecology. Identification was carried out at Entomology Laboratory, LIPI (Indonesian Science Research Institute) in Cibinong. By observing the *Megachile* spp. collection, doing some morphological research especially on the fourth tooth of the mandibles, and by examining the position of its cutting edge, the 1.0 – 1.5 cm the bee belongs to *Megachile unbripennis* Smith. This species prefers to cut the young healthy reddish leaf (97.1%). The average time for selecting the leaf is 19.3 seconds, cutting the leaf is 14.8 seconds, and perching after cutting is 97.2 seconds. The bee prefers to cut at 12:00 – 13:00, but its cutting time is from around 07:00 – 17:30 and they avoid rainy days. The average number of cuts in every leaflet is 1.1, the average of the cut area is 98.2 mm^2, the cut position away from the main leaf vein is 57.3%, and only 6.1% through the main vein. The number of leaflets which is unsuccessfully cut is 3.8%. The nest is in the form of hole.

Macadamia IPM: A Southern African perspective

Schalk Schoeman

Agricultural Research Council, Nelspruit/Mpumalanga, South Africa

Introduction: Macadamia production is currently centred in Southern Africa, Hawaii and Australia. These areas account for more than 90% of the global production and pest complexes generally consist of nut borers (Tortricidae) and stinkbugs (Pentatomidae & Coreidae). The Southern African tortricid complex consists of, *Thaumatotibia leucotreta*, *Thaumatotibia batrachopa* and *Cryptophlebia peltastica* (Meyrick) while the stinkbug complex consist of *Nezara viridula* as well as ± 45 indigenous species. Currently the tortricid complex is of relative minor importance, but the stinkbug complex was responsible for a monetary loss of ± R20 million (US$ 3 million) during the previous production season. The pentatomid *Bathycoelia natalicola* is particularly troublesome because its relative long mouthparts (12mm) enable it to feed on the kernel at any time during the development of the nut.

Methods: Damage profiles of both pest complexes were studied in relation to phenological development of macadamias. This study was conducted over three years on 10 farms in the Mpumalanga province of South Africa

Results and conclusion: Field trials successfully demonstrated that withholding commonly applied “clean up sprays” immediately before and after flowering had no effect on kernel yield or quality at harvest. This reduced the spray frequency of disruptive foliar applied synthetic pyrethroids from ± 6 – 4/season. Although tortricids are not generally economically important, the availability of suitable host plants can induce severe localised outbreaks. A large component of immature kernels was linked to late season infestation of the fruit. Spray timing is critical and depends on the main oviposition period. Larvae normally feed inside the nuts effectively out of reach of contact insecticides. The main oviposition period of the moths was determined and was subsequently linked to possible physiological changes in the plant at the end of premature nut drop. Uptake of research is normally a slow process therefore the second phase of this project currently focuses on extension. Methods used to assist all sectors of South African agriculture are briefly discussed.

Trait-mediated indirect effects on the structure of insect communities through herbivore-induced changes in plants

Takayuki Ohgushi

Center for Ecological Research, Kyoto Univesity, Otsu, Shiga, Japan

One of the most fundamental problems in ecology is determining the causal mechanisms that shape the structure of ecological communities. Ecologists have long focused on constructing traditional food webs that have less appreciated the potential importance of nontrophic, indirect, and facilitative interactions in structuring communities. Recently, there is a growing appreciation that trait-mediated indirect effects have important community consequences. Thus, we need to start combining these effects with trophic effects to create indirect interaction webs as an alternative to traditional food webs. In terrestrial systems there is a strong contrast between the effects of herbivory and predation: predators kill prey, but instead of killing mature plants herbivores usually alter a wide variety of plant traits such as secondary substances, growth, physiology, morphology, and phenology. There is rapidly increasing evidence that such herbivore-induced responses of plants are common and widespread in nature. Plant responses following herbivory substantially influence the structure of arthropod communities by creating indirect connections among herbivore species. These herbivore-induced plant responses act as mediators of interactions among species by linking multiple plant-insect interactions. As a result, they can increase not only abundance and species richness, but also the number of direct, indirect, and facilitative interactions involved in higher trophic levels. Consequently, plant-centered insect communities are largely organized by nontrophic, trait-mediated indirect, and facilitative interactions that have been little underscored in insect community ecology.

Functional studies of ORN populations on the antennae and maxillary palps of *Anopheles gambiae*

Yu Tong Qiu, Joop J.A. van Loon, Larry Zwiebel, Willem Takken

[1]Wageningen University, Wageningen, Netherlands, [2]Vanderbilt University, Nashville, TN, United States

Introduction: The malaria mosquito *Anopheles gambiae* is a highly human-specific blood feeding mosquito. Host seeking and oviposition site location behaviour are mainly odour-mediated and 79 putative olfactory receptor genes have been identified in this mosquito. Understanding the function of the olfactory receptor neurons is essential for developing strategies to disrupt odour-mediated behaviour with the aim to diminish malaria transmission.

Methods: We mapped functional groups of olfactory receptor neurons (ORNs) on the antennae and maxillary palps of female *A. gambiae*. Single sensillum recording was used to study the function of trichoid and grooved peg sensilla on the antennae and capitate peg sensilla on the maxillary palps.

Results: Based on the responses of ORNs to 44 human- or oviposition site-related odours, two functional types were found for E-type trichoid sensilla, three types for type C trichoid sensilla and five types for grooved peg sensilla. After a blood meal, a new functional type was found for E trichoid sensilla, which was highly responsive to indole and 3-methylindole, known as mosquito oviposition stimuli. All the tested capitate peg sensilla on the maxillary palps house three neurons belonging to three functional types based on their responses to 97 odours; and all of these sensilla are innervated with neurons highly sensitive to the known mosquito kairomone CO_2 and 1-octen-3-ol.

The influence of the parasitoids on the development of their aphid hosts

Amalia Kati, Jim Hardie

Imperial College London, Silwood Park, Ascot, Berks, United Kingdom

Changes in wing formation and development of the black bean aphid *Aphis fabae* (Scopoli) (Homoptera: Aphididae) are examined after parasitisation by *Aphidius colemani* (Viereck) (Hymenoptera: Aphidiidae) along with an investigation of the mechanisms of how changes are effected.

Parasitisation of nymphs of presumptive winged gynoparae of *A. fabae* induced by short days show that wing development is inhibited and the earlier parasitism takes place, the stronger the effect. Consideration of the timing of events indicates that the active component(s) is most likely injected along with the egg during oviposition and is not related to the parasitoid larva.

When saline extracts of female parasitoids or venom glands are injected into late-second stadium aphids they develop to fourth-stadium nymphs with rudimentary wingbuds, show developmental arrest and die usually in an attempt to moult to the adult stage. Injections in later stadia gave similar results. Injected late-fourth stadium insects develop normally.

Experiments with long-day winged virginoparae reveal similar results in regard to developmental arrest but injections into long-day wingless aphids, which develop more rapidly, had this effect only when treated during the early-third stadium. There seems to be a correlation between the time remaining to the final moult and the effect of the injected extract on preventing adult development.

The results indicate that there is an active factor(s) in the parasitoid's venom that disrupts wingbud development and/or inhibits moulting; the loss of activity after heat or protease treatment makes it likely that it is a protein.

In search of monophyly: the Ctenopelmatinae (Hymenoptera: Ichneumonidae) and its included tribes

Jacques Dubois[1], Matt Yoder[2], Debra Murray[3], Aubrey Colvin[4], Mika Cameron[4], Robert Wharton[4]

[1]Department of Invertebrate Zoology, American Museum of Natural History, New York, New York, United States, [2]Department of Entomology, Ohio State University, Columbus, Ohio, United States, [3]Department of Entomology, North Carolina State University, Raleigh, North Carolina, United States, [4]Department of Entomology, Texas A&M University, College Station, Texas, United States

Introduction: Ichneumonidae is the most speciose family of Hymenoptera with over 23,000 valid species assigned to approximately 40 subfamilies. Members of the subfamily Ctenopelmatinae are primarily parasitoids of sawflies and are characterized by an apical tooth on the fore tibia. This feature is also present in members of at least three other subfamilies, leading to concerns about characterization of the subfamily and support for its monophyly.

Methods: Ctenopelmatines and various out-group taxa were extracted from Malaise trap samples, and hind legs were removed for DNA analysis. Specimens were then pinned, labelled, databased, and their identification confirmed. DNA was extracted from exemplar taxa, amplified, and sequenced for three gene regions: 28S D2-D5, CAD, and RNA Polymerase II (POL). Data were analyzed using cladistics and Bayesian methods.

Results: Sequence data were obtained for over 100 in-group (ctenopelmatine) and out-group (other subfamilies) taxa. Although 28S has been used in prior assessments of ichneumonoid relationships, this gene was insufficient for resolving issues of monophyly at the subfamily and tribal levels, despite dense sampling. Not surprisingly, both better resolution and stronger support were obtained when all three gene regions were employed. Mesoleiini, perhaps the most poorly defined tribe morphologically, was consistently resolved as monophyletic, with strong support, in our analyses.

Conclusions: For Ichneumonoidea, a superfamily with approximately 40,000 species, the use of molecular data for resolving higher order relationships is still in its infancy.

Nocturnal oviposition in forensically important flies (Diptera: Calliphoridae, Sarcophagidae): laboratory and field studies

Kirstin Williams[1], Martin Villet[2], Nkosinati Mazungula[2]

[1]Durban Natural Science Museum, Durban, South Africa, [2]Rhodes University, Grahamstown, South Africa

Introduction: Nocturnal oviposition by blowflies is a debated factor that can affect the precision of forensic estimates of a post mortem interval (PMI) by more than 14 hours, depending on latitude and season.

Methods: Field and laboratory experiments involving forensically important African flies were conducted using rat carcasses and pieces of rotting meat to determine if these flies were able to lay eggs at night.

Results: It was found that *Lucilia sericata* could lay at night in the field, and that *L. sericata*, *Chrysomya chloropyga, C. albiceps* and *C. putoria* could do so in the laboratory, especially at temperatures above 22°C. This brings the number of species that have been found to be able to lay at night to thirteen species in three subfamilies. Thus, the forensic issue is not whether nocturnal oviposition occurs, but rather whether the environmental conditions of a particular case are more or less conducive to it.

Conclusions: The circadian rhythms and physiological thresholds (e.g. minimum temperature for flight and laying, and minimum humidity for laying) of each species of fly involved in a case are likely to need simultaneous consideration. The significance for experimental design of carcass size, freezing of carcasses, handling of carcasses and comprehensive quantification is discussed, and recommendations are made for future experiments. When estimating a PMI, it is recommended that the likelihood of nocturnal oviposition is considered probabilistically, and even empirically, for each forensic case, rather than on the basis of a categorical generalization.

Neuropeptides, receptors and innate behaviors in the silkmoth *Bombyx mori*

Dusan Zitnan, Ladislav Roller, Ivana Daubnerová, Inka Zitnanová, Young-Joon Kim, Michael E. Adams

[1]Institute of Zoology, SAV, Bratislava, Slovakia, [2]Institute of Medical Chemistry and Biochemistry, Comenius University, Bratislava, Slovakia, [3]Institute of Molecular Pathology, Vienna, Austria, [4]Depts of Entomology & Neuroscience, University of California, Riverside, United States

Introduction: The *Bombyx* model is becoming attractive with availability of its genome, the growing utility of gene transformation and suitability for physiological and behavioural studies, including ecdysis. The moth ecdysis sequence is composed of different movements (pre-ecdysis, ecdysis and post-ecdysis) necessary for shedding of the old cuticle. It is controlled by ecdysis triggering hormones (ETH) from endocrine Inka cells and multiple neuropeptides from neurons expressing ETH receptor in the central nervous system (CNS).

Methods: We cloned two subtypes of ETH receptor (ETHR-A and ETHR-B) and detected their expression in peptidergic neurons by in situ hybridization and immunohistochemistry. We used electrophysiology techniques, various bioassays and molecular approaches to determine functions of neuropeptides expressed in specific ETHR neurons.

Results: Our data showed that each behavioural phase during ecdysis sequence is under control of a specific set of neuropeptides. Central release of these neuropeptides from identified neurons results in initiation of pre-ecdysis, switch from pre-ecdysis to ecdysis, and activation and termination of ecdysis. Peripheral actions of the same neuropeptides involve regulation of water balance and contractions of skeletal muscles and hindgut. Electrophysiological analysis of the CNS from pharate pupae and pharate adults indicates considerable functional shift of neuronal networks and neuropeptides during metamorphosis.

Conclusions: Our data provide evidence that the ecdysis sequence is a very complex process controlled by multiple neuropeptides centrally and peripherally released from the CNS upon ETH action on specific neurons expressing ETHRs. Each neuropeptide may control different functions depending on timing of their release and site of action.

This work was supported by a grant from the National Institute of Health, USA (GM 67310), and Slovak grant agencies, Agentúra na podporu výskumu a vývoja (APVV-51-039105) and Vedecká grantová agentúra (VEGA 2-6090-26).

GM crops and biological control: What are the concerns and how to address them.

Nick Birch

SCRI, Dundee, United Kingdom

The presentation will focus on GM pest-resistant crops to discuss the development, testing and use of environment- and scale-sensitive biosafety testing procedures. An overview will be given of the potential risks and benefits (direct and indirect) for using GM pest-resistant crops in Integrated Pest and Disease (IPDM) crop protection systems. The risk:benefit approach will be discussed in relation to hypothesis-driven, functional ecology based methodologies for GM trait and crop assessment. These methods are designed to address the main concerns surrounding the compatible use of GM crop technologies with biocontrol agents, as part of IPDM frameworks in varying geographic regions. The GM biosafety methods are developed and tested at different scales (laboratory, glasshouse / mesocosm, field) in the EU and several developing countries. They assess impacts of GM crops on above- and below-ground agro-ecosystems, in relation to existing crop protection options. The effectiveness of biosafety testing methods to measure GM crop impacts on non-target biocontrol agents and on other components of biodiversity which provide valuable 'ecological services' will be discussed in terms of predictability and 'ecological context setting'.

Community response of phytophagous and transient non-target canopy insects associated with eastern hemlock, *Tsuga canadensis* (L.) Carrière, to imidacloprid and horticultural oil applications

Carla Dilling[1], Paris Lambdin[1], Jerome Grant[1], Rusty Rhea[2]

[1]University of Tennessee, Knoxville, Tennessee, United States, [2]USDA Forest Service, Forest Health Protection, Ashville, North Carolina, United States

Introduction: Hemlock woolly adelgid, *Adelges tsugae* Annand, is an invasive species reducing populations of eastern hemlock, *Tsuga canadensis* (L.) Carrière, throughout the eastern United States. While systemic imidacloprid and horticultural oils are the primary chemicals used to control infestations of this pest, their impact on non-target canopy insects is unknown. A study was initiated in November 2005 to assess the effects of imidacloprid soil drench, soil injection, and tree injection applications, and horticultural oil applications on multiple levels of organization within the phytophagous and transient insect community.

Methods: Eastern hemlocks were arranged in a split plot 2 x 5 factorial complete randomized block design consisting of three blocks of ten trees each. Treatments were made in the fall and spring with monthly sampling methods consisting of: canopy malaise traps, beat sheet, direct observation, and branch sampling.

Results and Conclusions: Analysis of similarity of Bray-Curtis distances infer significant differences between community composition and treatments. Mean species richness and abundance were significantly reduced by one or more application methods. Species richness was significantly reduced among detritivore and phytophaga guilds by soil drench applications. Species abundance was significantly lower across all guilds when compared with the control trees, with the exception of the haematophaga guild. From 293 species evaluated, 35 were found to be directly effected by one or more of the chemical treatments. Of the 35 species, 27 were lepidopterans that directly consume needles of eastern hemlock. The remaining eight species were psocopterans that feed on micro-fungi found on the needles.

The relevance of economic thresholds in transgenic corn: Does IPM affect IRM?

Michael Gray, David Crowder, David Onstad

[1]University of Illinois, Urbana, Illinois, United States, [2]University of Arizona, Tucson, Arizona, United States, [3]University of Illinois, Urbana, Illinois, United States

Introduction: The use of transgenic crops is increasing rapidly worldwide, particularly in the midwest of the United States. Questions have arisen regarding the necessity of economic thresholds used in conjunction with transgenic crops such as Bt maize. We conducted a simulation model to determine the benefits of scouting and economic thresholds in improving resistance management programs.

Methods: A population model for the western corn rootworm, *Diabrotica virgifera virgifera* LeConte, was used to elucidate resistance development to transgenic maize and crop rotation. A diploid genetic system with the following assumptions was utilized: autosomal inheritance, two-locus, and two-alleles per locus. The simulated model landscape was comprised of 100 hectares with a maximum of four crop rotation schemes and six fields.

Results: Unless transgenic maize was planted each season without a refuge, along with a simulated high dose, durability of transgenic maize was greater than 15 years (assuming allele for resistance to transgenic Bt maize is recessive). If the allele for resistance is partially recessive or dominant, the time for resistance development was generally well below 15 years, particularly at the medium and lose dose simulations across each of the four management strategies. Using economic thresholds only slightly delayed the onset of resistance to transgenic maize by corn rootworms.

Conclusions: Due to the effectiveness of transgenic maize and favorable economic returns, escalating use of Bt hybrids is anticipated in the United States. Concurrent with this trend, producers may be increasingly inclined to use transgenic maize each year without the use of traditional IPM tactics such as scouting and economic thresholds.

Differences between thermal requirements of native and exotic insect species

Vojtech Jarosik, Marc Kenis, Alois Honek

[1]Department of Ecology, Faculty of Science, Charles University, Vinicna 7, 128 44 Prague 2, Czech Republic, [2]CABI Europe - Switzerland, Rue des Grillons 1, CH-2800 Delemont, Switzerland, [3]Research Institute of Crop Production, Drnovská 507, 161 06 Prague 6-Ruzyne, Czech Republic

Introduction: Temperature determines the rate of development and survival of insects, and thus enables predictions of the effects of climate change on the distribution of insects, and on the spread of invasive species. We ask whether two basic thermal requirements for insect development, the lower developmental thresholds (LDTs), i.e. temperatures at which development ceases, and sums of effective temperatures (SETs), i.e. numbers of day degrees above the lower developmental thresholds necessary for a completion of the total pre-imaginal development, differ among European native and invasive species.

Methods: Because the thermal requirements are similar for related taxa, pairs of closely related species, native vs. exotic in Europe, were compared for their LDTs and SETs by paired t-tests, using a database of thermal requirements, systematically gathered from original studies by Alois Honek.

Results: LDTs were higher for exotic comparing to native species, but only if exotic store product pests were included. SETs were systematically less for exotic than native species, meaning that closely related exotic species develop faster than their native congeners.

Conclusions: As LDTs systematically change with latitude, which in turn changes with temperature, similar LDTs for closely related exotic and native species suggest a good climatic match of introduced species with their new environments. That the exotic species develop faster than their related native congeners correspond to the results in other invasive taxa, in which fast development also belongs to characteristic traits of successful invaders.

Managing *Helicoverpa* spp. and *Creontiades dilutus* on cotton crops: Role of entomopathogenic fungus, semiochemicals and trap crops

Robert Mensah, Leah Austin

Australian Cotton Research Institute, NSW Department of Primary Industries, Narrabri, NSW, Australia

Introduction: *Helicoverpa* spp. is a major pest in cotton in Australia, but, with the introduction of transgenic (Bollgard II®) cotton crops *Creontiades dilutus* (green mirid), populations have increased to economically important levels resulting in an increase in insecticide use against green mirids. Consequently, there is the need to reduce insecticide use to minimise the risk of insecticide resistance to green mirids. The goal of this study was to search for and develop IPM compatible tools to minimise synthetic insecticide use against *Helicoverpa* spp. and green mirids.

Method: Studies were conducted in commercial Bollgard II® cotton surrounded by conventional cotton crops. The study assessed (1) different rates of entomopathogenic (fungal) insecticides (Beauveria and Metarhizium spp.) (2) trap cropping with lucerne crop to control green mirids on cotton crops and (3) attract and kill technique using attracticide applied to transgenic cotton crops to reduce *Helicoverpa* spp. population on the surrounding conventional cotton crops.

Result: The study showed that application of entomopathogenic (fungal) insecticides controlled green mirids on cotton crops. In addition, interplanting lucerne crop in cotton reduced green mirid numbers on the cotton crops. Application of attracticide onto transgenic cotton crops reduced Helicoverpa moth population on the adjacent conventional cotton crops by 91.5 per cent resulting in insecticide savings of $11.40 per ha on the conventional cotton crops.

Conclusion: The programme that involves the use of entomopathogenic fungi, semiochemicals and trap cropping can be used to manage cotton pests, reduced synthetic insecticide use and increase crop yield and profitability.

Unexpected relicts – Eocene insects indicate former widespread distribution of various insect groups

Sonja Wedmann

Senckenberg Research Institute, Research Station Grube Messel, Messel, Germany

Various insect groups presently restricted to certain biogeographic regions were once much more widely distributed. This is documented by a wide range of fossils, which are found in areas distant from where their extant relatives occur. Recent fossil evidence from the 47-million-year-old Eocene deposit of Messel in Germany shows that this list continues to grow.

For instance, the extant austral group of genera closely related to *Comptosia* (Diptera: Bombyliidae) has long been regarded as Gondwanan disjuncts. *Comptosia* fossils recently discovered in Messel and in the Eocene North American fossil site Florissant show that their present distribution is relictual rather than disjunct. The first fossil record of a leaf insect from Messel shows that their former geographical range was distinctly larger. Currently, all species of leaf insects (Phasmatodea: Phylliinae) are distributed primarily in south-east Asia and adjacent regions. Another record from Messel is a fossil belonging to a subgroup of mantidflies (Neuroptera: Mantispidae: Symphrasinae) which today occur only in South America, Central America and southern North America.

In the Eocene, the geographical range of many insect groups was substantially more encompassing than it is today. This is most likely connected with the warm and equable climate in the Eocene. The fossil insects from Messel indicate a high diversity of taxa comparable to the present tropical level of biodiversity. Seemingly, many insect groups retreated south as the Northern Hemisphere began to cool and their habitats began to recede. They became extinct in their former geographical ranges and now have a relict distribution.

Determining the efficacy curve of thiametoxam (Actara™ 240SC) with regards to the intensity and duration of oviposition of the mango seed weevil, *Sternochetus mangiferae* F. (Coleoptera: Curculionidae)

Cornelia Estelle Louw

Bavaria Fruit Estates / Westfalia, Hoedspruit, Limpopo, South Africa

Introduction: The mango seed weevil (MSW), *Sternochetus mangiferae*, is a serious phytosanitary pest, restricting South African export to certain foreign markets. Thiamethoxam, a neo-nicotinoid with a long residual activity, is effective in controlling MSW. However, since varying opinions exist regarding the onset and length of oviposition, the efficacy curve of thiamethoxam, applied at different times in the mango season, were investigated and compared to MSW oviposition and larval development.

Methods: Oviposition was ensured by enclosing bags containing adult weevils around fruit. Efficacy was expressed as the percentage MSW free fruit, out of the total number of fruit with induced egg-laying, compared to the chemically untreated fruit. This data was plotted over time to determine the efficacy curve. At the end of the season infestation levels due to natural seed weevil oviposition, as well as infestation levels of mango scale (*Aulacaspis tubercularis*) and mealybugs (*Planococcus citri* & *Pseudococcus longispinus*) were determined.

Results: Induced weevil infestation levels in fruit from trees treated during mid August or mid September were comparative and remained low throughout the trial period. Infestation levels in fruit treated in mid October were comparative to the other treatments 3 weeks after application. With natural oviposition, significantly fewer MSW were found in treated fruit, with no significant differences between treatments (time of application), although a time response did show earlier applications to be slightly more effective. Thiamethoxam had, contrary to registration data, no noticeable effect on mango scale, but mealybug numbers were significantly reduced, with a time response showing slightly better control with later applications.

Investigating mango seed weevil (*Sternochetus mangiferae* F. (Coleoptera: Curculionidae)) development in order to determine the most appropriate time for control measures

Cornelia Estelle Louw

Bavaria Fruit Estates / Westfalia, Hoedspruit, Limpopo, South Africa

Introduction: In order to control any insect pest, it is imperative to understand its biology. For the mango seed weevil (MSW), *Sternochetus mangiferae*, varying opinions exist regarding oviposition and development. It is therefore important to know the onset and duration of oviposition, as well as the duration of each developmental stage, to determine the most appropriate time for intervention. In order to ensure effective chemical control, it is important to determine the time elapsed from oviposition to the eggs hatching, and the time it takes for the larvae to penetrate the fruit and reach the safety of the seed.

Methods: Weevil oviposition on 'Keitt' fruit was artificially induced by enclosing adult weevils with bags around the fruit. Oviposition was induced during October, November and again in December. Exposed fruit were sampled at weekly intervals after oviposition to determine the developmental stage(s) present at subsequent time intervals. Every egg present on the fruit skin was inspected and counted and resultant developmental stages, where eggs had hatched, were noted. Further larval development stages were also recorded.

Results: During the October induction all the eggs were intact after 7 days, with a very small percentage (<1%) still intact after 14 days. Fourteen days after egg-laying 38% of the hatched larvae had already penetrated the seed. For the November induction, development appeared somewhat faster. One week after oviposition 9% of eggs had hatched, while 45% of hatched larvae had reached the seed by week 2. For the December induction 64% of the eggs, on average, did not develop. Initial hatching was comparative to the October induction, but no larvae were noted up to 5 weeks after oviposition.

Biotypic diversity and distribution of Russian wheat aphid *Diuraphis noxia* (Hemiptera: Aphididae) in the eastern and central Free State

Astrid Jankielsohn

ARC-Small Grain Institute, Bethlehem, South Africa

Introduction: Since the release of the first RWA resistant cultivar in 1992 wheat farmers in the eastern and central Free State relied on wheat cultivars with resistant genes to manage Russian wheat aphid (RWA). In 2005 a new biotype RWASA2 was described based on its ability to damage wheat with the resistant genes *Dn*-1 and *Dn*-2. To effectively manage RWA in the future it is important to know the biotype composition in the major wheat producing areas.

Methods: Russian wheat aphid was collected from 12 different localities in the central and eastern Free State. Between one and four samples were collected at each locality, depending on infestation level and size of the collection area. Russian wheat aphid clone colonies were made from these samples. Clones were screened against Betta (susceptible), Elands (*Dn*-1 resistance gene), Halt (*Dn*-4 resistance gene) and PAN 3144 (*Dn*-5 resistance gene). If the clones were able to damage the wheat with resistance gene *Dn*-1 but not wheat with resistance gene *Dn*-4 and *Dn*-5 they were considered to be RWASA2.

Results: RWASA2 was the dominant biotype across all the collection sites.

Conclusion: Based on the predominance of RWASA2 in the eastern and central Free State wheat with the *Dn*-1 resistance gene will have little value in controlling RWA in these areas.

Root-feeding insects as agents of change in agroecology

Scott Johnson, Carolyn Mitchell

Scottish Crop Research Institute, Dundee, United Kingdom

Introduction: Necessary reductions in pesticide usage have resulted in some crops being challenged by multiple pests, both above- and below the soil surface. It has been known for some time that root and foliar-feeding insects can interact via changes to their shared host plant, but comparatively less is known about how these interactions vary with genetic resistance and crop phenology. We investigated the interactions between root- and foliar-feeding insects in an annual (barley, *Hordeum vulgare*) and a perennial crop (raspberry, *Rubus idaeus*).

Methods: In laboratory and glasshouse experiments, we investigated how root-feeding vine weevils (*Otiorhynchus sulcatus*) affected genetic resistance in raspberry and how this in turn affected the large raspberry aphid (*Amphorophora idaei*). We measured changes to plant chemistry, most notably epicuticular waxes. We also measured how wireworms (*Agriotes* spp) changed the nutrient profile of barley at different time points and assessed how this affected the bird-cherry oat aphid (*Rhopalosiphum padi*).

Results: There was no interaction between vine weevils and aphids in raspberry cultivars containing single A10 gene resistance, but root herbivory by vine weevils promoted aphid populations in cultivars with multigenic resistance. Wireworms and aphids caused specific changes in P, K, Ca, S and soluble amino acids. At one time point, aphid populations were promoted by wireworm herbivory.

Conclusions: Root and foliar-feeding insects interact in both an annual and a perennial crop. Genetic resistance aboveground can be compromised by belowground herbivory in raspberry. In barley, temporal shifts in mineral and amino acid nutrients underpinned interactions between the two herbivores.

Plant mediation of intraspecific interactions and population dynamics

Timothy Craig

University of Minnesota Duluth, Duluth, Minnesota, United States

A central theme of the study of ecological interaction has been the role of competition for resources in determining the evolution and ecology of species. For herbivorous insects host plants are not just a fixed quantity of food that is competed for until it is exhausted, instead they are a dynamic resource that is continuously altered by herbivory. Modification of plant resources can have a positive or negative impact on subsequent generations of conspecifics. Herbivore damage can have a positive effect if it induces the plant to re-grow tissues where herbivore performance is high. For example, on the willow, *Salix lasiolepis*, the damage by the gall-inducing sawfly *Euura lasiolepis*, induces the growth juvenile tissue where sawfly performance is high. As a result sawfly population densities are continuously maintained at high densities on some plants. In contrast the lacebug, *Corythuca marmorata,* has a more complex intergenerational interaction mediated by the host plant within a growing season. These lacebugs are group feeders on rapidly senescing tissue. Initially, ovipositing females are attracted to plants where previous feeding has induced leaf senescence. However, at high population densities plant damage is so high that resources deteriorate in quality and females avoid ovipositing on them. When these plants are released from attack they can resume growth and become preferred host plants again. Thus there is a complex interaction of the oviposition preference, feeding damage, and host plant quality that determines the distribution and population dynamics of the lacebug.

A change for the better: Resurgence in biocontrol agents associated with the adoption of Integrated Fruit Production (IFP) in New Zealand apple orchards

Peter W. Shaw[1], Roger D. Wallis[2], James T.S. Walker[3]

[1]HortResearch, Old Mill Road, RD3 Motueka, New Zealand, [2]HortResearch, Old Mill Road, RD3 Motueka, New Zealand, [3]HortResearch, PO Box 1401, Havelock North, New Zealand

Introduction: Biological control of orchard arthropod pests has become a key component of the Integrated Fruit Production (IFP) system developed by the NZ apple industry in the 1990's to reduce reliance on agrichemicals and demonstrate environmental responsibility.

Methods: Yellow sticky traps and trays to collect insects knocked from branches were used to record the relative abundance of bio-control agents in apple blocks treated with either organophosphate (OP) or IFP based insecticide programmes.

Results: Apple blocks in Nelson, New Zealand, during 1995-1996, sprayed with a calendar programme of organophosphate (OP) insecticides, typical of production practice at the time, had very little arthropod fauna. Some beneficial arthropods were recorded in transitional IFP blocks treated with selective Insect Growth Regulator (IGR) insecticides during the same season. By comparison, the same monitoring methods revealed that by 2006-2007, bio-control agents were more varied and numerous in established IFP apple blocks using selective insecticides in a threshold-based pest management programme.

Conclusions: The change by the NZ apple industry from a calendar-based broad spectrum OP insecticide programme to an IFP system based on targeted use of selective insecticides has resulted in an associated increase in the diversity and abundance of arthropod bio-control agents in apple orchards. This has resulted in a marked decrease of some previously important pests while maintaining similar levels of control of key pests.

Molecular evidence of a rapid radiation and divergence times in carabid beetles

Karen Ober, Thomas Heider

College of the Holy Cross, Worcester, Massachusetts, United States

Evolutionary radiations are often considered to have been times of rapid origination of major clades as represented by their sudden appearance in the fossil record. Explosive evolution can, in principle, be tested by molecular estimates of divergence times. The fossil record indicates a rapid tempo of cladogenesis of major lineages early in the evolutionary history of beetles in the carabid subfamily Harpalinae. Lack of resolution in the molecular phylogeny at the base of Harpalinae may be evidence for rapid radiation in this clade. The beetle subfamily Harpalinae is the largest subfamily in Carabidae with approximately 19,000 species, most of carabid diversity. Its sister group, Brachininae, has about 655 species. Molecular clock estimates of divergence dates of major harpaline lineages were estimated. Temporal variations in estimated diversification rates in harpalines and it sister group were analyzed. Preliminary results suggest a rapid increase in evolutionary diversification in the subfamily Harpalinae compared to other related carabid beetle clades.

Disasters by design: Why pests outbreak in the urban forest

Michael Raupp, Adrianna Szczepaneic, Scott Creary

Department of Entomology, University of Maryland, College Park, MD, United States

The purpose of this presentation is to provide a synthesis of our knowledge of the many mechanisms underlying pest outbreaks in managed urban landscapes. We will provide evidence that several factors, either individually or in concert, act to uncouple trophic relationships in managed landscape systems, thereby altering ecosystem function. These factors include a critical lack of plant diversity and complexity in our cities and residential landscapes, failure to consider evolutionary relationships between plants and their pests in the selection of plant material, management practices such as elevated levels of fertilization that predispose plants to increased frequency and intensity of attack by pests, application of pesticides that uncouple natural enemies from their prey and hosts, thereby enabling pest outbreaks. These factors underlie a majority of arthropod outbreaks in managed landscapes ranging from residential gardens to large public parks and urban forests. In some cases the solutions will be very expensive and require paradigm shifts in the way urban forests are designed and planted. Other problems can be resolved through reductions in chemical inputs including fertilizers and insecticides. It is our hope that this synthesis will act as a catalyst for entomologists to work with urban planners, landscape managers, and the general public to create more sustainable landscapes. Our goal is to reduce dependence on inputs such as fertilizer and pesticides while providing enhanced levels of services including beauty, recreation, biodiversity, biological remediation, and ecosystem function in urban settings.

Neurohormonal control of diuresis in *Rhodnius prolixus* (the vector of Chagas' disease)

Ian Orchard, Jean-Paul Paluzzi, Juan Ianowski, Victoria Te Brugge

University of Toronto Mississauga, Mississauga, ON, Canada

Introduction: Diuresis in *Rhodnius prolixus* is under the neurohormonal control of neuropeptides and serotonin. These neurohormones act on the crop and Malpighian tubules to stimulate salt and water transport. These, and other factors, are also involved in a range of feeding-related physiological events, including cuticle plasticization, contraction of muscles of the digestive system, salivation, and increases in rate of heart-beat. The cessation of diuresis has been less studied, but is an essential phenomenon that prevents excessive loss of water and salts. It has been suggested that an anti-diuretic hormone, with properties similar to *Manduca sexta* cardioacceleratory peptide 2b (Manse CAP2b; pELYAFPRVa), might be present in *R. prolixus*.

Methods and Results: Using molecular biology in combination with MALDI-TOF/TOF tandem mass spectrometry, we have determined the sequence of the CAP2b/CAPA-related peptides in *R. prolixus*. Rhopr CAP2b is indeed an anti-diuretic factor, inhibiting serotonin-stimulated secretion from crop and Malpighian tubules. In addition, we have characterized the expression of mRNA encoding these peptides in various developmental stages and have also examined the tissue-specific distribution in fifth instars.

Conclusions: The overall control of events associated with gorging on a blood meal is complex, involving a range of neuropeptide families and serotonin that act upon a variety of tissues to bias them towards a new physiological state. The parasite causing Chagas' disease is transmitted during diuresis / excretion, and therefore neuropeptides and serotonin control the timing of transmission of this disease. Understanding these processes might lead to strategies for preventing the transmission of Chagas' disease.

Central neurons expressing multiple chemical factors are involved in the neural control of reproductive tissues in the female locust, *Locusta migratoria*

Angela Lange, Rosa da Silva

University of Toronto Mississauga, Mississauga, ON, Canada

Introduction: The spermatheca in the female acts as a repository for spermatazoa deposited by the male, and in the locust is situated dorsal to the lateral and common oviducts. In the locust, eggs mature in the ovaries and are ovulated into the lateral oviducts where they are held till a suitable oviposition site is found. At that time, aided by muscular contractions of the lateral oviducts, the eggs are propelled through the common oviduct and genital chamber and deposited in the soil. Contractions of the spermathecal sac lead to spermatozoa release, resulting in fertilization of eggs in the genital chamber. Coordination of the oviducts and spermatheca is clearly critical to the production of viable eggs.

Methods: Immunohistochemistry, neurobiotin backfilling and neurophysiological techniques have been used to examine the neural control of both the oviducts and spermatheca and the integrative actions of these two visceral muscles.

Results: Both structures are under central neuronal control incorporating neurons that express an array of peptide and amine phenotypes. Many of the phenotypes are common to both reproductive tissues. A neural loop ensures the coordinated release of spermatozoa when an egg passes into the genital chamber.

Conclusions: Central neurons control the muscular activities of the spermatheca and oviducts of the locust, allowing these tissues to work independently or in a coordinated and integrated fashion. This paper will discuss our understanding of the neural control of these reproductive tissues and their coordination.

‘Push-Pull’ - a chemical ecology-based IPM strategy for smallholder farmers in Africa

Zeyaur Khan

International Centre of Insect Physiology and Ecology (ICIPE), Nairobi, Kenya

With recent advances in our understanding of the chemical ecology of plant-insect and plant-plant interactions, we have developed new semiochemicals-mediated crop protection strategies to control insect pests and parasitic weeds in subsistence African farming system. Specifically, the presentation will highlight practical use of plants releasing semiochemicals to attract and/or ward off pest attack, to ensnare the attackers, to attract beneficial insects that will attack the pests, and, at the same time, to cause very effective suicidal germination and control of the African witchweed, *Striga hermonthica,* in cereals. Typically, the plants are deployed in a ‘push-pull’ (stimulo-deterrent diversionary) arrangement with rows of an attractive plant at the border and a repellent plant as an inter-crop with cereals like maize. The intercrop (e.g. the cattle fodder legume *Desmodium uncinatum*) was primarily selected because of novel allelopathic effects of flavonoid compounds in its root exudates on striga, some of which cause germination of striga seeds and others their subsequent development. There are now more than 12,000 smallholder families using the 'push-pull' approach in eastern Africa. The technology is improving their livelihood through increased agricultural productivity and improved environmental sustainability. In addition, it opens up significant opportunities for smallholder growth and represents a platform technology around which new income generation and human nutritional components, such as livestock keeping, can be added. To ensure long-term sustainability of the system, we are currently developing quality control protocols to monitor any potential changes in the semiochemicals produced by existing trap and repellent plants, and allelopathic agents produced by roots of desmodium intercrops. We are also exploring the possibility of broadening options to different farming communities through biotechnological transfer of biochemical traits associated with the systemic release of the defense chemicals from repellent plants to maize itself and those associated with striga allelopathy to edible legumes and, perhaps in the long term, to maize itself to create a new generation of weed-free maize plant.

The entomofauna of Greenland and its zoogeographical status

Jens Böcher

Zoological Museum, Copenhagen, Denmark

Greenland is an arctic area with a comparatively depauperate biota, the origins of which have been a subject of much interest and debate for more than a century. The expectation that the distribution and abundance of insects and arachnids at high latitudes will prove particularly susceptible to global climate change has recently added extra momentum to studies of the Greenland entomofauna, giving an updated stock-taking and continuous inventory of this fauna high priority. As a basis for such work the compilation of an identification manual of this fauna has been undertaken by the Entomology staff of the Natural History Museum of Denmark in collaboration with a large international specialist team. The revision of available museum holdings and new field work carried out in preparation for this publication have provided massive new information about the composition and distribution patterns of the Greenland entomofauna, now known to consist of about 1100 species.

Geological evidence points to a ”tabula rasa” at the height of the last glaciation, so that all Greenland taxa had to immigrate during the only 10.00 years of the Holocene. In spite of the position of the island, close to the North American continent, the Greenland faunas of particularly soil-bound taxa like Coleoptera, Collembola, Oribatida and Mesostigmata have sizable components of species of Palaearctic origin. A number of explanations of this strong Palaearctic element in the Greenland biota have been suggested, and these will be discussed in the light of the extensive new data and evidence from recent palaeo-entomological work.

Tracking butterfly flight with harmonic radar: Linking genotype, phenotype and performance

Kristjan Niitepõld, Otso Ovaskainen, Ilkka Hanski

University of Helsinki, Helsinki, Finland

Introduction: Many insects, including butterflies, use flight for both everyday purposes and dispersal. Flight ability may thus have fitness consequences in several ways. It has been suggested that certain phenotypes would be more likely to disperse, which clearly is the case in wing-dimorphic insects. We have been studying dispersal mechanistically in a wing-monomorphic butterfly species. We link together genetic variation in the *Pgi* locus, flight metabolic rate and flight in field conditions.

Methods: We measured the flight metabolic rate of common garden-reared Glanville fritillary butterfly (*Melitaea cinxia*) females using flow-through respirometry. On the following day an ultralight transponder was attached to the thorax of individuals which were released in an open heathland and followed using a harmonic radar. We recorded the flight paths of 66 females moving freely for several hours. A wing sample taken before the release was used to genotype the individuals for the polymorphic *Pgi* locus.

Results: Lab-measured flight metabolic rate was highly correlated with butterfly mobility in the field. An interaction between *Pgi* genotype and temperature was found both in the respirometry measurements and in radar-measured mobility. Also, mobility peaked at intermediate ambient temperatures in the field.

Conclusions: We have shown how variation at the genetic level may be correlated with flight in the field through the link of metabolic rate. The genotype being active in cool temperatures has in previous studies been shown to be most common in newly-established local populations in Finland. This supports the idea of mobile individuals establishing new populations, and suggests a mechanism for maintaining genetic polymorphism in a metapopulation.

Females do it better: Superior conditions for female development in a gall-inducing wasp

Netta Dorchin[1], John Hoffmann[2], Wendy Stirk[3], Miroslav Strnad[4], Johannes van Staden[3]

[1]Museum Koenig, Bonn, Germany, [2]University of Cape Town, Cape Town, South Africa, [3]Research Centre for Plant Growth and Development, University of KwaZulu-Natal, Pietermaritzburg, South Africa, [4]Palacky University and Institute of Experimental Botany, Olomouc, Czech Republic

Introduction: The pteromalid wasp, *Trichilogaster acacialongifoliae*, is a gall-inducing biological control agent introduced from Australia to South Africa against the invasive weed *Acacia longifolia*. Galls are induced in inflorescence and vegetative buds, and show striking differences in the abundance, position, and shape of larval chambers between the sexes. Females are found in spherical chambers at the center of the gall, whereas males, when present, are found in oval and much smaller chambers along the gall periphery.

Methods and Results: In a histological study of the galls we found significantly larger amounts of vascular tissues and stored metabolites around female chambers than around male chambers. These findings attest to an improved food supply and a higher metabolic activity around female chambers, a condition we attribute to the presence of phytohormones. To test this assumption, we used bioassays comparing Auxin- and Cytokinin-like activity in extracts of male and female larvae, and found significantly higher activity in females. Gall tissues originating from female chambers likewise showed higher phytohormone activity than tissues originating from male chambers.

Conclusions: Our data show that *T. acacialongifoliae* females are significantly more efficient than males in eliciting the gall induction response, resulting in improved nutritional conditions for their development. These physiological differences between the sexes are most probably responsible for the sexually dimorphic gall structures observed in this species. However, the source of the elevated phytohormone levels in the insect and gall tissues is currently unknown.

Larval-pupal parasitoids of the African wild silkmoth, *Gonometa postica* (Lepidoptera: Lasiocampidae) in the Mwingi Forests, Kenya

Ken Fening[1], Esther Kioko[2], Suresh Raina[3], Jones Mueke[4]

[1]ICIPE/Kenyatta University, Nairobi, Kenya, [2]ICIPE, Nairobi, Kenya, [3]ICIPE, Nairobi, Kenya, [4]Kenyatta University, Nairobi, and Democratic People's Republic of Korea

Introduction: *Gonometa postica* produces high quality silk, but is affected by parasitoids. This study seeks to assess the extent to which wild silk cocoon production is affected by parasitism and to study the development behavior of these parasitoids.

Methods: A survey of parasitism of *G. postica* larvae and pupae on host and non-host plants, and development of parasitoids were undertaken for two generations in 2006 at six field sites, three each in Imba and Mumoni forests of Mwingi, eastern Kenya. All freshly spun cocoons of *G. postica* were sampled at each site from a total of one hundred trees of the host plants and other non-host plants where they have migrated before pupation. The cocoons were kept individually in fine net-sealed plastic vials to determine percentage parasitism.

Results: Two dipterans and four hymenopteran larval-pupal parasitoids were identified from the two forests. They were all gregarious, endoparasitic koinoboints. The most common ones were *Palexorista* sp. (Diptera: Tachinidae) and *Goryphus* sp. (Hymenoptera:Ichneumonidae) with parasitism ranging from 1.8 – 32.7 % and 2.2 – 7.5 %, respectively. Parasitism varied significantly according to host or non-host plants, generations and sites. *Eurytoma transvaalensis* Cameron was thought to be a facultative hyperparasitoid of *Goryphys* sp. Multiparasitism was demonstrated for some species, as both *Pimpla* sp. and *Goryphus* sp. were obtained from the same cocoon of *G. postica.*

Conclusions: The current study has identified six larval-pupal parasitoids of *G. postica*.

Residual efficacy of aerosol insecticides in mills and warehouses

Frank Arthur, Thomas Phillips

USDA-ARS, Manhattan, Kansas, United States

Aerosol insecticides are receiving increased usage with the impending phase-out of methyl bromide in milling facilities. Some of these aerosols are also being applied in food warehouses. Questions arise as to the distribution of these aerosols and their residual persistence. Both of these components were examined to determine implications for insect pest management.

Concrete treatment arenas were constructed using the bottom portions of a plastic Petri dish, approximately 62cm2 in total area. These arenas were shipped to industrial cooperators, who exposed them to the label rates of aerosol insecticides, and then shipped these dishes back to the Grain Marketing and Production Research Center, Manhattan, Kansas, USA.. Residual efficacy was assessed by exposing different life stages of either *Tribolium castaneum*, the red flour beetle, or *Tribolium confusum*, the confused flour beetle.

Results show that the aerosols containing either methoprene or pyriproxyfen, both of which are insect growth regulators (IGRs), were highly effective on immature stages of both beetle species. The organophosphate diclhorvos offered little residual control.

Farmers' ethno-ecological knowledge of termites and their management in southern and eastern Africa

Gudeta Sileshi[1], Philip Nyeko[2], Philip O. Y. Nkunika[3], Benjamin M. Sekamatte[4], Festus K. Akinnifesi[1], Oluyede C. Ajayi[1]

[1]World Agroforestry Centre (ICRAF), Lilongwe, Malawi, [2]Makerere University, Kampala, Uganda, [3]University of Zambia, Lusaka, Zambia, [4]RIU (Research Into Use), Nkoola Institutional Development Associates, P.O. Box 22130, Kampala, Uganda, [5]World Agroforestry Centre (ICRAF), Lilongwe, Malawi, [6]World Agroforestry Centre (ICRAF),, Lilongwe, Malawi

Introduction: Termites are 'keystone' species in Africa as they play a dominant role in the way that managed and natural ecosystems function. Although less than 5% of the approximately 1000 termite species known in sub-Saharan Africa cause serious damage to crops and tree species, termites generally are regarded as "pests" in agriculture and forestry. Non-specialists approach their control as if a single pest were to be dealt with, which is often in sharp contrast with farmers' attitudes towards termites. Therefore, farmers' ethno-ecological knowledge may be valuable in designing more sustainable strategies for pest management and sustainable agriculture.

Methods: Data on farmers' knowledge, attitudes and management practices were collected using community meetings, participatory rural appraisal (PRA), individual interviews using structured questionnaires and direct observation by the authors in Zambia, Malawi, Mozambique and Uganda.

Results: Farmers perceived specific termites as the major causes of tree mortality and damage to staple crops such as maize, cassava and groundnuts, and they identified most of those that damage their trees and crops using local names, and applied various indigenous termite control practices. The strengths and limitations of farmers' ethno-ecological knowledge and termite control practices are discussed and recommendations for future research are given.

Phoretic arthropods of the red imported fire ant (*Solenopsis invicta*, Hymenoptera: Formicidae) in Central Louisiana

John Moser

USDA Forest Service, Pineville, LA, United States

A total of 4665 phoretic arthropods comprising 29 species were taken from red imported fire ant, *Solenopsis invicta* Buren (RIFA) alates that were preparing to fly from nests in Pineville, Louisiana. A wide variety of taxonomic groups were represented, including 2 insect- and 14 mite families. The arthropods fell into two classes -- those that may be truly phoretic with more than four specimens collected [13 species] and those appearing to be accidentally phoretic with 1-3 specimens collected [16 species]. The fact that over one-half of the species may have been "accidental" may mean that the alates were picking up mites from adjacent sources, such as grass, soil, tree bark; this suggests that many small arthropods may routinely be using phoresy as a dispersal mechanism. The arthropod with perhaps the highest total numbers was *Cyphoderus similis* Folsom a wingless insect, and the only phoretic species belonging to the Collembola. Twenty-three of the 29 species may be new; five of the common species are currently being described; another five species are future candidates for descriptions. Data analyses indicate that the more common species may actively persist in nests for the entire year. The scutacarid and pygmephorid associates may be associated with fungi. These and common associates from other families carried many types of hyperphoretic spores of fungi from inside the fire ant nests. All three of the laelapid mites may be important predators or parasitoids of individuals within the nests. *Histiostoma* n. sp. is a filter feeder consuming microorganisms, and the collembolan is possibly a general feeder. RIFA is native to Brazil, and we speculate that most of the common mite associates may also have originated there. *Trachyuropoda whitkombi*, at least, has been documented from RIFA nests of that country.

Area-wide IPM for commercial wheat storage

Paul Flinn[1], David Hagstrum[2], Carl Reed[2], Thomas Phillips[2]

[1]USDA-ARS, GMPRC, Manhattan, Kansas, United States, [2]Kansas State University, Manhatan, Kansas, United States

The USDA, Agricultural Research Service funded a demonstration project (1998-2003) for area-wide IPM for stored wheat in Kansas and Oklahoma. The project utilized two elevator networks, one in each state, for a total of 28 grain elevators. These elevators stored approximately 843682 metric tonnes of wheat, which was harvested from approximately 324000 hectares. During this study, thousands of grain samples were taken in concrete elevator bins. A vacuum-probe sampler was used to take ten 3-kg grain samples in the top 12 meters of each bin at grain elevators. Decision support software, Stored Grain Advisor Pro (SGA Pro) was developed. This software interprets insect sampling data, and provides grain managers with a risk analysis report that describes which bins are at low, moderate or high risk for insect-caused economic losses. Recommended treatment strategies and economic analysis are presented to the manager. The area-wide IPM program was superior to calendar-based management because it ensured that the grain in each bin was only treated when insect densities exceeded economic thresholds. This approach reduced the frequency of fumigation while maintaining high grain quality. Elevators that followed our recommendations reduced the number of bins they normally fumigated by at least 50%. A new grain-scouting company was started that is using SGA Pro and the sampling tools that were developed in this project.

Insect pest management in pulses in India

Chandra Srivastava

Banaras Hindu University, Varanasi, Uttar Pradesh, India

Introduction: Chickpea (*Cicer arietinum* L.) and pigeon pea [*Cajanus cajan* (L.) Millspaugh] are the two important pulse crops grown in India and are the major source of vegetarian protein to the millions of people in Indian sub-continent. Insect pests are the major biotic constraint to increase the production and productivity of pulses in India. These two pulse crops are attacked by more than 300 insect pests (> 60 on chickpea and > 250 on pigeon pea). *Helicoverpa armigera* Hubner is the most serious insect pests on chickpea and pigeon pea. Whereas *Melanagromyza obtusa* Malloch is also a serious pest of pigeon pea.

Methods: Experiments were conducted on larger plots and different modules were tested in farmers fields on both the crops. The treatments included cultural control, bio-rationals and judicious use of eco-friendly synthetic insecticides.

Results: Application of Neem Seed Kernel Extract (NSKE) at 5% concentration and HNPV @ 400 LE/ha managed the *H. armigera* on chickpea. Whereas on pigeon pea adjustments in sowing dates and crop maturity, application of eco-friendly synthetic insecticide and NSKE 5% minimized the damage *of H. armigera* and *M. obtusa*.

Conclusions: *H. armigera* on chickpea can be managed by combining the cultural control and use of bio-rationals. Whereas on pigeon pea, in addition to cultural control and bio-rationals, one spray of eco-friendly synthetic insecticide is required. By managing *H. armigera* on chickpea, the yield can be increased by 30-40%, whereas in pigeon pea the yields can be doubled by the successful management of *H. armigera* and *M. obtusa*.

The relative importance of snags and logs to the saproxylic beetle community in two forest types of the southeastern United States

Mike Ulyshen[1], Jim Hanula[2]

[1]University of Georgia, Athens, Georgia, United States, [2]USDA Forest Service, Athens, Georgia, United States

Numerous studies from Europe and Canada have demonstrated that saproxylic insects are sensitive to forest management practices that reduce the abundance and variety of dead wood. Yet this diverse community continues to receive little attention in the southeastern United States, a region supporting some of the most diverse, productive and intensively managed forests in North America. Research is needed to better understand the habitat requirements of saproxylic insects in this region if these species are to be retained for future generations. The primary purpose of this study was to compare the beetle communities inhabiting snags (i.e., standing dead trees) and logs of three common tree species (*Pinus taeda*, *Quercus nigra* and *Liquidambar styraciflua*) to determine the relative importance of these habitats to saproxylic beetles. Sampling took place in stands dominated by loblolly pine (*P. taeda*) as well as in mixed bottomland hardwood forests in the upper coastal plain of South Carolina.

The community ecology of tropical rainforest termites: a spatial analysis considering environmental and biotic interactions

Olivia Scholtz[2], Mairi Knight[2], Rod Blackshaw[2], Sarah Donovan[2], Paul Eggleton[1]

[1]Natural History Museum, London, United Kingdom, [2]University of Plymouth, Plymouth, United Kingdom

Introduction: Termites feed on organic material at various stages of decomposition, and as ecosystem engineers, their influence on soil properties may feedback into the termite community. We examined the spatial structure of termite feeding groups, soil and micro-habitat properties and other soil faunal groups, to consider the ecological interactions that are occurring within the termite community.

Methods: A one hectare plot, divided into 2 m x 2 m contiguous sample points, was surveyed in a tropical rainforest in Sabah, Borneo. At each sample point, termites were sampled from a soil pit (25cm x 25cm x 10cm deep), along with earthworms (considered their ecological analogues) and ants. Several environmental variables were also recorded. Spatial patterns for these variables were quantified, and spatially explicit associations analysed, using SADIE.

Results: The termite community was dissociated with soil moisture levels and under-storey vegetation. Soil feeding (SF) and non-soil feeding (NSF) termites, were associated with their respective food material, i.e. organic rich soil, and logs and sticks. The oral and/or faecal products on NSF that are worked into the soil profile, may provide a food material to SF, however no association was detected between the two groups. Predatory ants were associated with the termites, and a weak (non significant) association was found between SF and earthworms. The spatial scales of these variables indicate the complex interplay of environmental and biotic interactions.

Conclusions: It appears that food quality and availability is an important factor in structuring termite communities. However, this effect may be reduced by negative affects such as predation pressure.

Repellent activity of alligator pepper, *Aframomum melegueta* (Zingiberaceae) and ginger, *Zingiber officinale* (Zingiberaceae), against the maize weevil, *Sitophilus zeamais* (Coleoptera: Curculionidae)

Donald A. Ukeh[1], Michael A. Birkett[2], John A. Pickett[2], A. Jennifer Mordue (Luntz)[1]

[1]*School of Biological Sciences, University of Aberdeen, Aberdeen, Scotland, United Kingdom,* [2]*Centre for Sustainable Pest and Disease Management, Biological Chemistry Department, Rothamsted Research, Harpenden, England, United Kingdom*

Introduction: Maize, *Zea mays* L. (Poaceae), is an important source of carbohydrate in Nigeria. *Sitophilus zeamais* is a major insect pest of stored maize in the tropics. Essential oils and oleoresins extracted from seeds of alligator pepper, *Aframomum melegueta*, and rhizomes of ginger, *Zingiber officinale* were evaluated for their repellent activity against *S. zeamais* in the laboratory.

Methods: Vacuum distilled oils and oleoresins were tested against *S. zeamais* in a Pettersson olfactometer using 3 day old adults at 25 ºC, 65 % rh. The mean time spent and the mean numbers of entries made by the weevil to the test and control arms were assessed in 10 min duration.

Results: Olfactometer assays showed that *S. zeamais* adults were significantly repelled by vacuum distillates and oleoresins of *A. melegueta* and *Z. officinale* when tested individually ($p < 0.001$), and in combination with maize grains ($p < 0.05$). Bioassay-guided liquid chromatography of the distillates showed that the fractions containing polar compounds accounted for the repellent activity. Coupled gas chromatography-mass spectrometry (GC-MS), followed by GC peak enhancement and enantioselective GC using authentic compounds, revealed the identity of the 3 major compounds in the behaviourally active *A. melegueta* fraction to be (*S*)-2-heptanol, (*S*)-2-heptanyl acetate and (*R*)-linalool. A synthetic blend of the 3 compounds, prepared in a ratio (1:6:3) found in the distillate, was shown to account for repellent activity.

Conclusions: This research provides the scientific basis for the potential use of *A. melegueta* and *Z. officinale* in stored-product protection at the small-scale farmer level in Nigeria.

Odorant-binding proteins in insect vectors

Linda Field, John Pickett, Jing-Jiang Zhou

Rothamsted Research, Harpenden, United Kingdom

When insects respond to semiochemicals such as pheromones or host odours the first step is detection of the volatile cues by sensilla on the antennae. The odour molecules enter the sensilla via pores on the surface and are transported to the odour receptors (ORs) by odorant-binding proteins (OBPs). Many different putative OBPs have been identified in a range of insect species and there is some evidence of specificity between the proteins and the odour ligands.

We have used a 'MotifSearch' algorithm to identify genes encoding putative OBPs in the vectors *Anopheles gambiae* and *Aedes aegypti*. This had revealed a large number of genes for different classes of OBP some of which are specific to mosquito species and some of which show expression specific to female antennae and are therefore likely to be involved in the location of the correct host for the blood meal.

We will present data on the mosquito putative OBPs and techniques being developed to study their interactions with ligands. Preliminary experiments to identify similar genes/proteins in tsetse are also underway.

A first view of gall-inducer beta diversity in South America

Milton Mendonça

Departmento de Ecologia, UFRGS, Porto Alegre, RS, Brazil

Gall-inducing arthropods are useful for diversity sampling allowing recognition of arthropod and plant species through gall morphology. Galler diversity is almost always studied for alpha diversity only (species richness). Beta diversity (species composition) is nearly unexplored, and I provide examples where it can reveal important patterns. A dataset of 429 gall morphotypes from Rio Grande do Sul (RS) in subtropical south Brazil is analysed along with a few examples of data from the literature. RS gallers were sampled across 5 years in 8 localities and 42 trails with standardised 1h30min censuses, usually repeated visits (2 to 8 times) to trails with homogeneous vegetation. Samples covered 7 vegetation types: grassland, steppic savannah, restinga shrublands, humid forests, riparian forests, riparian forest edges (with grassland) and peat forest. Space is more important than vegetation type for beta diversity, although both factors were significant (ANOSIM tests: only savannah significantly differs from riparian forests, but most localities have significantly distinct species compositions). However, even between nearby (1 km apart) trails, galling fauna similarity can be low (20-40% species in common), except for savannahs (50-80% common species). Low similarity among close-by sites was found for cerrado and Pantanal in tropical Brazil, and Chaco in Argentina. Insufficient sampling is unlikely: for RS galls correlations between measures of sampling effort (trails and samples per locality) and similarity between nearby sites are non-significant (better sampled localities or vegetation have equally low similarities). This first assessment uncovers interesting ecological patterns that should be explored and considered in galler diversity hypotheses.

Control and modulation of salivary secretion in *Periplaneta americana*

Wolfgang Blenau[1], Britta Troppmann[1], Jeannine Witte[1], Otto Baumann[1], Arnd Baumann[2], Bernd Walz[1]

[1]University of Potsdam, Potsdam, Germany, [2]Research Centre Jülich, Jülich, Germany

The acinar salivary glands of the cockroach *Periplaneta americana* receive a dual innervation from the subesophageal ganglion and the stomatogastric nervous system. Acinar cells are surrounded by a plexus of dopaminergic and serotonergic varicose fibers. In addition, serotonergic terminals lie deep in the extracellular spaces between acinar cells. Recently, we could show that the gland is also innervated by neurons that contain GABA. Secretion in cockroach salivary glands is stimulated by dopamine and serotonin. Serotonin stimulates the secretion of protein-rich saliva, whereas dopamine causes the production of protein-free saliva. These observations are consistent with the view that protein-producing central cells of the acini respond only to serotonin, ion-transporting peripheral cells to serotonin and dopamine, and most duct cells only to dopamine. Thus, two elementary secretory processes, namely electrolyte/water secretion and protein secretion, are triggered by different aminergic transmitters. We characterized the pharmacological properties of dopamine- and serotonin-induced secretory responses by using receptor agonists and antagonists. PCR experiments with degenerate primers were performed in order to clone dopamine and serotonin receptor genes from *Periplaneta.* We obtained four PCR fragments of putative biogenic amine receptors. Meanwhile, three of them were cloned in full length. Here, we will focus on the serotonin 5-HT_1 receptor (Pea5-HT_1). Functional properties of Pea5-HT_1 were studied in stably transfected HEK 293 cells. Serotonin reduced cyclic AMP production in a dose-dependent manner. Pea*5-ht1* mRNA has a widespread distribution in various tissues including the salivary glands as shown by different techniques. In addition, we have cloned a cDNA fragment coding for nitric oxide synthase (NOS). NOS expression was proven in the salivary glands by using RT-PCR and NADPH diaphorase staining. Dopamine-induced salivary secretion was reduced by the application of NO donors.

Nest inheritance in the social wasp *Polistes dominulus*

Thibaud Monnin, Alessandro Cini, Vincent Lecat, Pierre Federici, Claudie Doums

Laboratoire Fonctionnement et évolution des systèmes écologiques CNRS UMR 7625, Université Pierre et Marie Curie, Paris, France

Introduction: We studied the potential conflict over nest inheritance in the social wasp *Polistes dominulus*. Colonies are initiated by 1 to 8 foundresses, of which 1/3 are unrelated. The alpha foundress monopolises reproduction, but one of the subordinate foundress may inherit the nest if alpha dies. Workers are daughters of alpha. Because workers can mate in *Polistes* they may oppose to an unrelated subordinate inheriting the nest, by favouring a sister worker instead.

Methods: We investigated this potential workers-subordinates conflict by analysing egg-laying and egg destruction in three sets of colonies: controls, colonies where brood was regularly removed to mimic the ageing of alpha, and colonies where alpha was removed. Colonies were video recorded continuously for 22 days. Relatedness was determined using microsatellites analysis.

Results: In control colonies alpha laid most eggs, and destroyed most of the few eggs laid by subordinates and workers. When brood was removed all wasps laid more eggs, especially workers. However, alpha retained a near-reproductive monopoly by destroying the other wasps' eggs. When alpha was removed, beta became the new alpha. She laid most eggs and destroyed the few eggs laid by other wasps. There was no difference between control colonies and colonies where alpha was removed, and no effect of relatedness.

Conclusions: There is no evidence of a conflict over nest inheritance, despite the potential high relatedness costs to workers. Colony level costs of conflict may favour a conventional nest inheritance by beta. Also, workers may leave the nest to initiate their own.

Monitoring phytosanitary insect pests and sharing pest information in tropical areas

Yulu Xia[1], Ronald Stinner[1], James Vankirk[1], Aunu Rauf[2], Merle Shepard[3], Michael Hammig[3], Phillip Chung[4], Shelby Fleischer[5], Stephen Crawford[5], Jon Voortman[5], Carltle Brewster[6], Jean Cobb[6], Pat Hipkins[6], Donald Mullins[6], James Westwood[6]

[1]North Carolina State University, Raleigh, NC, United States, [2]Bogor Agricultural University, Bogor, Indonesia, [3]Clemson University, Clemson, NC, United States, [4]Rural Agricultural Development Authority, Kingston, Jamaica, [5]The Pennsylvania State University, University Park, United States, [6]Virginia Polytechnic Institute and State University, Blacksburg, United States

Introduction: Fruit flies, whiteflies, and the cocoa pod borer (CPB) (*Conopomorpha cramerella* Snellen), are among some of the worst agricultural insect pests. It is critical to share information about these pests and monitor their distribution and populations on a regional, and global basis.

Methods and Results: This collaborative effort has involved three tropical regions: Southeast Asia (SA), the Caribbean Basin (CB), and West Africa (WA).

SA Project. This study focuses on sharing pest information about the CPB. CPB is a destructive cocoa pest in Southeast Asia only. It would be devastating to world cocoa production if it spreads to other cocoa production areas. Our efforts involve five areas: a) creating a knowledgebase of CPB; b) collecting and distributing CPB pest management technology; c) developing databases such as a Global CPB Expert Database, d) mapping of CPB worldwide; e) databasing general pest management information.

WA Project. Study scope includes a) developing a knowledge base of whitefly biology and dynamics, including alternative host plants, b) a pesticide residue and safety training website, c) developing an online mapping tool to provide dynamic descriptions of whitefly distribution in the region.

CB Project. Our effort is to develop an online fruit fly surveillance system for monitoring the five species of tephrid fruit flies in the region. An online data reporting and mapping system has been developed. Training sessions on sampling procedures and methods have been conducted and data collection is in progress. The current effort is focused on sampling and data reporting.

Phylogeny and antiquity of the bees based on combined molecular, morphological and paleontological datasets.

Sophie Cardinal[1], Atsushi Kawakita[2], Bryan Danforth[1]

[1]Cornell University, Ithaca, NY, United States, [2]Kyoto University, Kyoto, Japan

The traditional view of phylogenetic relationships of bee families has been recently contested by molecular data in favor of a topology where a paraphyletic Melittidae is sister to the remaining bees instead of Colletidae. In this study, we have expanded the molecular dataset to include 7 genes and all major lineages of bees with appropriate outgroups. The molecular dataset was combined with morphological data for a total evidence analysis. Phylogenetic relationships were estimated under parsimony, maximum likelihood and Bayesian optimality criteria. Increased taxon sampling within the family Apidae allowed us to incorporate fossil data to robustly estimate the antiquity of bees for the first time. Divergence dates were also estimated for all major bee clades. The antiquity of eusocial and cleptoparasitic behavior within bees is discussed as well as major shifts in diversification rates.

Simulation of mating disruption and mass trapping with competitive attraction and camouflage

John A. Byers

US Arid-Land Agricultural Research Center, USDA-ARS, Maricopa, AZ, United States

Introduction: Computer simulation was used to explore variation of key model parameters such as effective attraction radius (EAR) of lures, lure density, and female/male density on efficacy of mating disruption and mass trapping of moths and other insects.

Methods: QuickBASIC and Java program languages were used to simulate male moth movement as a correlated random walk during random encounters with EAR of lures of variable radius and density. Calling female moths of variable EAR and density were in competition with lures in attracting males that oriented in the EAR for various periods. Females could be camouflaged by lure EAR but were allowed to move positions at various rates.

Results: When male orienting time was constant regardless of EAR, the models indicated no difference in mating disruption efficacy between either a higher density of dispensers with smaller EAR, or a lower density of dispensers with a compensating larger EAR. However, when the orienting time was increased in proportion to dispenser EAR, then fewer dispensers with larger EAR were more effective in reducing female mating than were more numerous ones with smaller EAR. When costs of pheromone are substantial, however, more numerous dispensers of smaller EAR would be more economical since dose-response curves in previous studies indicate release rate must increase exponentially to achieve a linear increase in EAR. Mass trapping reduced mating more than mating disruption given equivalent conditions.

Conclusions: The models are useful in understanding which variables need be measured to predict a successful mating disruption or mass trapping program.

Possibilities and constraints to breeding potatoes resistant to aphids and aphid-transmitted viruses

Edward B. Radcliffe[1], Jeffrey A. Davis[2], Kathy L. Flanders[3]

[1]Department of Entomology, University of Minnesota, St. Paul, Minnesota, United States, [2]Department of Entomology, Louisiana State University, Baton Rouge, Louisiana, United States, [3]Department of Entomology and Plant Pathology, University of Alabama, Auburn, Alabama, United States

Advances in biotechnology over the past quarter century have transformed our understanding of insect plant interactions. Molecular and biotechnological approaches are now routinely used to supplement conventional plant breeding methodologies. These technologies provide opportunities for exploitation of genetic traits in wild solanaceous species not previously accessible by conventional breeding methodologies. We seek to develop potato breeding lines incorporating durable resistances to aphids (*Myzus persicae*, *Macrosiphum euphorbiae*) and viruses (*Potato leafroll virus*, *Potato virus Y*). Wild potato species (~190 spp. are recognized) represent a vastly underutilized resource, e.g., *M. persicae*-resistant genotypes are reported in ~40 potato spp. Somatic fusions offer one way to overcome these incompatibilities. Somatic fusions created to incorporate late blight resistance from *S. etubersum* and *S. bulbocastanum* yielded some progeny concurrently resistant to *M. persicae* and *M. euphorbiae*. Past progress in breeding potato for virus/vector resistance has been stymied by our inability to identify resistance except by using phenotypic screens. Gene mapping and identification of molecular markers can facilitate selection of quantitative traits. However, the practicality of using marker assisted selection to concurrently introgress multiple resistances, especially of traits quantitatively inherited (e.g. *M. persicae*, *M. euphorbiae*, PLRV) has yet to be demonstrated. For purposes of validating resistance, vector resistance is best measured in the laboratory using life table studies to measure antibiosis and EPG (electronic penetration graph) to measure antixenosis and elucidate feeding behaviors associated with virus acquisition and transmission. Virus resistance is best measured by field screening in the presence of inoculated viruses and augmented aphid populations.

Integration of *Heterorhabditis indica* with other biorationals for managing chickpea pod borer, *Helicoverpa armigera* (Hüb.)

Aralimarad Prabhuraj, Girish K. S, Shivaleela Shivaleela, Patil B.V

University of Agricultural Sciences, Dharwad, Karnataka, India

Introduction: A successful management strategy was developed against chickpea pod borer, *Helecoverpa armigera* (Hüb) by integrating locally isolated entomopathogenic nematode, *Heterorhabditis indica* (RCR) with other entomopathogens like *Helicoverpa* Nuclear polyhedrosis virus (HaNPV) and *Bacillus thuringiensis* (Bt) and botanicals.

Methods: Preliminary laboratory studies were conducted, to standardize the optimum dosage of nematodes required for field application, to evaluate the compatibility of nematode with entomopathogens and botanicals and their combinations. The optimum dosage of infectives was standardized to third (LC_{50} of 145 IJs/larva) and fourth (LC_{50} of 195 IJs/larva) instars based on the concentration mortality response.

Results: Persistence study on chickpea foliage in field condition indicated that, infectives along with 0.1 % glycerol survived better (80%) compared to other antidessicants. In compatibility studies, though nematode was compatible with other entomopathogens, but was susceptible to higher concentrations of aqueous leaf extracts of some selective botanicals. A series of laboratory bioassay was carried out to select best combinations of *H. indica* with other entomopathogens and botanicals against third and fourth instar *H. armigera* and these were tested in field for two consecutive years. Two year field evaluation indicated that, sequential application of *H. indica* + *Prosopis juliflora* (1 lakh IJs/l + 10%) at 50 and 75 days after sowing was superior with highest larval reduction (23.47%), minimum pod damage (11.27%) and maximum seed yield (19.24 q/h).

Conclusions: Combination of two biorationals either in sequential or simultaneous application resulted in better management of *H. armigera* compared to insecticidal application alone.

Study on insectivorous bats as potential predator of moths of sugarcane borers

Sunaryo Sunaryo, Koko Widyatmoko

PT Gunung Madu Plantations (Sugar Plantation), Bandar Lampung, Lampung, Indonesia

Introduction: Sugarcane moth borers (pyralids, Lepidoptera) are predominant pests of Gunung Madu sugarcane plantation, Lampung, Indonesia. Major control measures include augmentative releases of lab reared parasitoids. However, alarming peaks of borer population still exist occasionally, which shall be characterized by abundant moth flying at 1900-2100 hrs. Within such time some insectivorous bats were observed preying on borer moths and a significant predation was presumed to take place. This brought about the present study.

Methods: Net trapping was used to capture the bats for identification. Twenty specifically designed shelters were made and installed near water reservoirs in sugarcane fields. Monthly observations on shelter occupation were done to study bats' roosting habit. Feces of the predominant species were collected and examined to recognize and quantify the predation.

Results: Three predominant species captured by the net were *Taphozous longimanus, Pipistrellus javanicus*, and *Scotophilus kuhlii*. However, only *S. kuhlii* was observed occupying the shelters. An average of 4.4 bats occupied each shelter and 77% of total shelters installed were occupied. Examination on feces collected from *S. kuhlii* as supplied from net-trapping showed remains of organs of eight insect orders which include Lepidoptera, Coleoptera, and Orthoptera.

Conclusions: The study suggests that bats may settle down in man-made shelters, which may be manipulated to increase their role in controlling moth population. It also suggests that lepidopteran moth is an important constituent of bats' diet. The insectivorous bats could complement the ecological approach of controlling sugarcane moth borers at times when moth population is abundant.

The effects of pyrethroid resistance on transcription of metabolic enzymes in a major African malaria vector, *Anopheles funestus*

Riann Naguran[1], Hilary Ranson[3], Maureen Coetzee[1], Lizette L Koekemoer[1]

[1]Vector Control Reference Unit, National Institute for Communicable Diseases, Johannesburg, Gauteng, South Africa, [2]Division of Virology and Communicable Disease Surveillance, School of Pathology of the National Laboratory Service and the University of the Witwatersrand, Johannesburg, Gauteng, South Africa, [3]Vector Research Group, Liverpool School of Tropical Medicine, Liverpool, United Kingdom

Introduction: *Anopheles funestus* Giles is a major malaria vector in Africa, specifically South Africa. Insecticide resistance in this species had a major impact on malaria transmission in South Africa. Very little is known about the genes responsible in detoxification of insecticides in *An. funestus*. We aimed firstly to determine if the microarray *(*detoxification chip) developed for *An. gambiae* could be used on *An. funestus*. The microarray detoxchip was then used to investigate the effects of pyrethroid resistance in *An. funestus* on transcription of metabolic enzymes.

Methods: The pyrethroid resistant *An. funestus* colony used in this study, originates from Mozambique (Fumoz-R) while the susceptible colony (FANG) originates from Angola. RNA extractions, dye labeling, hybridization, scanning and data analysis were performed.

Results: This study showed that the detoxchip can be used to study transcriptional differences in other insecticide resistant species such as *An. funestus*. A number of genes were over-expressed in the pyrethroid resistant and susceptible strain of *An. funestus*.

Conclusion: This study showed that the *An. gambiae* detoxchip can be used to study transcriptional differences in other insecticide resistant species such as *An. funestus.* Overall the outcomes of this research identified differentially expressed genes in a pyrethroid resistant *An. funestus* strain. The results will provide information on alternative enzymes associated with pyrethroid resistance in this important malaria vector and aid in our understanding of this complex resistance mechanism.

Fossils and phylogeny: The evolution of termites

Michael Engel, David Grimaldi

[1]University of Kansas Natural History Museum, Lawrence, Kansas, United States, [2]American Museum of Natural History, New York, New York, United States

A study of phylogenetic relationships among major lineages of Isoptera is provided based on morphological and ethological data. For the first time an extensive sampling of fossil termites from the Tertiary and Cretaceous periods, including an abundance of "primitive" termites newly discovered and described during the last year. This comprehensive paleontological and neontological analysis recovers major patterns of diversification of termites during the Cretaceous and again in the middle Tertiary. Most Cretaceous taxa are found to represent stem groups to either the modern families or as intermediate between groups of families, including one genus as a stem group to all other Isoptera. Mastotermitidae falls relatively basal in the order, among a diversity of fossil taxa. Termopsidae and Hodotermitidae as widely defined were not recovered as monophyletic with components of these families emerging from a grade of living and fossil termites lineages leading to Kalotermitidae as closely related to the higher termites (Rhinotermitidae + Termitidae). There is relatively tight stratigraphic-rank correlation, with the earliest fossils falling more basal in the order. The analysis indicates that the higher termites, particularly the ubiquitous Termitidae radiated during the Tertiary.

Does temporal synergism increase the efficacy of natural pyrethrins against insect pests?

Anna Khot, Lin Field, Graham Moores

Rothamsted Research, Harpenden, UK

Insecticide resistance is a growing problem around the world. Resistance can be caused by a number of mechanisms, one of which is enhanced detoxification of the insecticide by metabolic enzymes.

Temporal synergism using piperonyl butoxide (PBO) has been found to inhibit some resistance-associated esterase enzymes, overcoming insecticide-resistance in different agricultural pests. This PhD project investigates the use of temporal synergism to increase the efficacy of natural pyrethrins against insect-pests.

In vivo bioassays have been performed to calculate the lethal concentration of natural pyrethrins required to give 50% mortality in the studied population (LC_{50}). These bioassays have demonstrated that the presence of PBO in a tank mix with natural pyrethrins can reduce the LC_{50} for natural pyrethrins. Experiments have also been performed using a pre-application of PBO prior to exposure to pyrethrins, although these results need further investigation. Results will be discussed.

Botanical extracts and other compounds have been screened for their ability to inhibit esterase enzymes using a novel assay. Extracts showing potential to inhibit esterase enzymes have been screened for their ability to inhibit mixed function oxidase activity and will be screened for their ability to inhibit glutathione *S*-transferases. Compounds performing well will be selected for trials *in vivo.*

Ground-dwelling spiders in two Quebec vineyards

Noubar J. Bostanian[1], Christopher M. Buddle[2], Charles Vincent[1], Elise Bolduc[2]

[1]Hortic.Dev.Centre, Agric.Agri-Food Canada, St.Jean-sur-Richelieu, Canada, [2]Dept. of Natural Resources, McGill Univ., St. Anne de Bellevue, Canada

Introduction: Spiders are important predators in almost every imaginable habitat. In vineyards the spider community is composed of arboreal and ground dwelling species. Most spiders are generalist predators. Individual species may not exhibit classic density-dependent control of pests. Nevertheless assemblage of spiders do regulate pest insect populations.

Materials and Methods: Spiders were collected in pitfall traps weekly from May to mid September in two vineyards. All spiders were identified to species. All data were compared using a mean number of spiders collected on a per-trap basis. Diversity comparisons were done using rarefied estimates of species richness (Ecosim software). Community composition was elucidated by analyzing individual pitfall data with detrended correspondence analysis (DCA). Species turnover was evaluated by completing a matrix of shared species by sample period. Temporal distribution of web-building species to hunting species was also evaluated.

Results: A total of 4600 spiders belonging to 97 species from 16 families were collected. Assemblages were similar between the two vineyards independent of environmental differences. Fallow fields and adjacent apple orchards is believed to result for a higher abundance of certain agrobiont species in one of the vineyards. *Tennesseellum formicum* (Emerton) Linyphiidae, showed high phenotypic variation and possibly its multvoltine life cycle is an adaptive behavior to be present in vineyards that are frequently disturbed. Species turnover was high between sample dates. Data on activity and species richness indicated that many species that differ in forraging mode are active all months of the growing season.

Conclusion: spiders in vineyards are well placed to prey on phytophagous pests and their populations should be conserved in vineyards.

Spatial synchrony in forest insect outbreaks: Why is it so ubiquitous?

Andrew Liebhold[1], Ottar Bjørnstad[2], Derek Johnson[3], Christelle Robinet-Makdoud[4]

[1]US Forest Service Northern Research Station, Morgantown, WV, United States, [2]Department of Entomology, Pennsylvania State University, University Park, PA, United States, [3]Department of Biology, University of Louisiana at Lafayette, Lafayette, LA, United States, [4]INRA, UR633 Zoologie Forestière, Orléans, France

Spatial synchrony refers to the coincident temporal variability in the abundance of geographically disjunct populations and is a characteristic of virtually all species of forest insects. For those forest insects that occasionally reach epidemic densities, it is the characteristic of spatial synchrony that determines their pest status because outbreaks occurring synchronously over large areas are likely to result in more substantial ecosystem and sociological impacts. Spatial synchrony can result from 1) dispersal of individuals among populations, 2) synchronous trophic (e.g., parasitism) effects and 3) synchronous stochastic (e.g., weather) effects. Unfortunately it is often difficult to identify the relative contribution of these mechanisms and synchrony observed in real populations is likely the result of several mechanisms. Temporal variability in weather is universally synchronous and this is a plausible explanation of the ultimate ubiquity of synchronous population dynamics. However, understanding synchronous dynamics requires identifying both the factors contributing to synchrony as well as those processes that desynchronize populations. These latter processes are poorly understood but geographical variation in density dependence and nonlinear dynamics are both probably important. In this paper many of these issues are explored using the gypsy moth, *Lymantria dispar*, in North America as a model system.

A mutualistic herbivore? Increased yield through herbivore specific cues

Katja Poveda[1], Maria Isabel Gomez[2], Andre Kessler[3]

[1]Göttingen University, Göttingen, Germany, [2]Universidad Nacional, Bogotá, Colombia, [3]Cornell University, Ithaca, NY, United States

Introduction: Herbivores are known to be an important ecological force via their typically negative effects on plant fitness, which have devastating economic consequences in agriculture. In a few cases, overcompensation has been shown to provide an apparent benefit to attacked plants, but the actual fitness consequences have been controversial and the mechanisms by which overcompensation occurs are unknown. Here we demonstrate that larval feeding by the Guatemalan potato moth (*Tecia solanivora*, Lepidoptera: Gelechiidae), one of the most economically important potato pests in Latin America, leads to a dramatic increase in potato tuber production.

Methods: In the field we evaluated the effect of *T. solanivora* larval feeding on potato tuber production. In greenhouse experiments we tested if larval feeding induces the growth of damaged (local response) or undamaged (systemic response) potatoes. We also tested if herbivore specific cues (regurgitant) in opposition to mechanical tissue damage are causing an increased potato production.

Results: Field-grown potato plants in the Colombian Andes attacked by low numbers of potato moth larvae produce a 2.5 fold higher marketable potato yield than undamaged plants. Greenhouse experiments indicate that this effect is induced by compounds in the larval regurgitant, rather than by mechanical tissue damage.

Conclusions: The possibility of using induced overcompensation mechanisms to increase the per-hectare yield of a major crop has the potential to yield high economic returns. This is particularly true for potato production, as potatoes are the world's fourth most important crop and generate global revenues in excess of 6 billion USD per year.

Reproductive success of subfamilies in the honeybee colony (*Apis mellifera*)

Robin F.A. Moritz

Institut für Biologie, Martin-Luther-Unniversität Halle-Wittenbegr, Halle/Saale, Germany

The honeybee queen (*Apis mellifera*) mates with an excessive number of males and has been reproted to store the semen of up to 50 males in her spermatheca throughout her lifetime. Consequently, the colony is composed of a large number of half-sib subfamilies sired by different fathers but having the same mother queen. This sets the stage for a high potential of intercolonial conflict among these subfamilies. Many adaptations have evolved to prevent conflict both between queen and workers and among workers. Nevertheless, intracolonial selection is a strong factor considerably affecting reproductive success of the various subfamilies in the colony. I will show how this process interferes at the various levels of intracolonial selection determining the selection of queens and reproductive workers. I will argue that this is an inevitable process and highlight how an evolutionary stable strategy can emerge in spite of sometimes huge selection intensities at the individual level in the colony. The interplay between individual, family and colony level selection, a multilevel inclusive fitness, is the key to understanding natural selection processes in honeybees.

Peptidomics of pheromone biosynthesis activating neuropeptide (PBAN)-expressing neurons of an insect

Susanne Neupert[1], Wolf Huetteroth[2], Joachim Schachtner[2], Reinhard Predel[1]

[1]Institute of Zoology, Friedrich-Schiller-University,, Jena, Germany, [2]Fachbereich Biologie, Tierphysiologie, Philipps-University Marburg, Marburg, Germany

Pheromone biosynthesis activating neuropeptide (PBAN) is a member of the FXPRLamide/pyrokinin (PK) peptide family and is encoded on the diapause hormone (DH)-pheromone biosynthesis activating neuropeptide (PBAN) gene. It belongs to the most extensively studied neuropeptides of insects and regulates pheromone biosynthesis in female moths by direct activation of receptors of the pheromone gland cells. Totally, five peptides (PBAN, DH, and α-, β-, γ-SGNP), all of which share a common FXPRL sequence at the C-terminus, were predicted from the *Manduca sexta*-DH-PBAN precursor.

In this study, we analysed the cellular expression of the PBAN and structurally related neuropeptides from neuroendocrine cells in the SEG of the adult tobacco hawk moth, *M. sexta,* for subsequent MALDI-TOF mass spectrometric analysis. Neuropeptides of the DH-PBAN gene were found to be expressed in cells of the mandibular (4), maxillary (10) and labial (2) neuromeres along the ventral midline in the SEG. The mass spectrometric analysis revealed the expression of numerous peptides from the DH-PBAN gene in all neuroendocrine FXPRL synthesizing neurons of the SEG. In contrast to the neurons of the mandibular and maxillary neuromeres which express only the products of the DH-PBAN gene, the cells in the labial neuromere also express products of the CAPA gene, which contains an additional FXPRLamide, CAPA-PK.

Delimiting baridine weevil evolution (Coleoptera: Curculionidae)

Steve Davis

University of Kansas, Lawrence, Kansas, United States

Weevils (family Curculionidae) are one of the most diverse groups of extant organisms, with approximately 60,000 described species. They are extremely important economically, being of great agricultural significance because they are associated with all major groups of plants and plant parts. The weevil subfamily Baridinae is one of the larger weevil lineages. It is distributed worldwide, consists of 548 genera, approximately 9,000 described species, and is considered most in need of systematic study. Most baridine taxa have not been studied since their original description and the generic definitions are in need of much refinement. Although the baridines undoubtedly form a cohesive group, the delimitations of this group also remain uncertain. In order to provide stability to the group and to define the major lineages, the first phylogenetic hypothesis, based on morphology, has been constructed. Because of the rather broad scale of this undertaking, examination of the evolution of many interesting characters has also been made possible.

Introduced bees in Australia – a control regime for integrated weed management.

Caroline Gross

The University of New England, Armidale, NSW, Australia

Introduction. *Apis mellifera* L. was introduced into Australia in the 1800s. The Apiary Industry is an integral part of the domestic and export market as Australian bee products and pollination services are in demand worldwide. Feral colonies of honeybees are present over much of Australia and in the last 20 years there has been much concern over the impacts of honeybees on native biota. In addition, the pressure of introduced pollinators on natural systems is considerable because increasingly apiarists require access to native vegetation to agist their colonies over winter. The impact of honeybees on weed invasiveness is an unquantified area in Australia and a novel area for investigation.

Methods. An evaluation of the impacts of honeybees on weed fecundity was undertaken using two key weed species, Scotch Broom (*Cytisus scoparia*) and Lippia (*Phyla canescens*) in the field and in a glasshouse.

Results. Feral honeybees are having a demonstrable impact on seed set in these weeds — in Scotch Broom a single worker bee is capable of effecting over 6000 seeds in one day; in *Phyla canescens* (Lippia) a pollen vector is also required to effect seed set and honeybees are the primary cause of a seed bank that can reach 100,000 germinable seeds/m^2 per year in dense infestations.

Conclusions. The incorporation of pollinator control is the next step for the integrated weed management of these species and one that will require cooperation from local apiarists. A design for a baiting station and protocols for installation are discussed.

Development of diagnostic dose for monitoring resistance of the Asian corn borer *Ostrinia furnacalis* Guenee to Bt corn in the Philippines

Edwin Alcantara

National Institute of Molecular Biology and Biotechnology, University of the Philippines (Los Baños), College, Laguna, Philippines

Introduction: One of the most critical components of a resistance management strategy for Asian corn borer (ACB) populations is the ability to effectively monitor the development of resistance to Bt corn.

Methods: Artificial diet surface overlay assays were carried out to estimate baseline susceptibility of ACB populations to Cry1Ab protein. Mortality data were analyzed by probit analysis. The upper fiducial limit of the LC_{99} was used as diagnostic dose for monitoring ACB resistance to Bt corn. The same ACB populations were bioassayed in the laboratory to validate the diagnostic dose of Cry1Ab protein.

Results: There was no significant difference in LC_{50} values estimated from bioassays of eight ACB populations collected from Luzon. The LC_{50} values ranged from 0.42 ng/cm^2 to 1.5 ng/cm^2. Likewise, three ACB populations from Mindanao had similar susceptibility to Cry1Ab protein. The Mindanao populations had LC_{50} values ranging from 1.44 ng/cm^2 to 2.37 ng/cm^2. The susceptibility of all the populations was not significantly different from the susceptible ACB reference strain maintained in the laboratory. Each of the twelve ACB populations responded with at least 99% mortality when assayed with the diagnostic dose (104 ng/cm^2) of Cry1Ab protein.

Conclusions: The Philippine ACB populations are homogenous in mortality response and are highly susceptible to Cry1Ab protein. A diagnostic dose of 104 ng/cm^2 Cry1Ab protein can be used for nationwide monitoring for ACB resistance to Bt corn.

Clues to the evolution and speciation of the *Diplolepis* (Hymenoptera: Cynipidae) complex provided by the world's most structurally complex gall on rose hips in eastern Turkey

Joseph Shorthouse, Aban Güçlü, Rüstem Hayat

[1]*Laurentian University, Sudbury, Ontario, Canada,* [2]*Atatürk University, Erzurum, Turkey*

Each of the approximately 42 species of Holarctic cynipid wasps of the genus *Diplolepis* induce structurally distinct galls on wild roses. *Diplolepis* are organ specific, with galls of most species occurring either on the leaves or stems. One of these wasps, *Diplolepis fructuum* (Rübsaamen), induces galls within the flowers and hips of the wild roses *Rosa canina* L. and *R. villosa* L. in northeastern Turkey. Eggs are attached to all organs within immature flowerbuds resulting in galls induced from achenes (seeds), anthers, the hypantium (hip walls), sepals, and petals. Oviposition errors result in galls induced on leaves and tips of shoots. Achene and anther galls are frequently so abundant they cause hips to rupture and turn flowers into masses of tissue four times their natural size. Consistent gall anatomy, regardless of the tissues attacked, illustrates the control gallers have over the development of their hosts. *D. fructuum* is closely related to the first galler of roses and the occurrence of its galls within all tissues of flowers and hips provides clues as to how current species of *Diplolepis*, with their anatomically distinct galls, may have evolved.

Colony relocation in the ant *Aphaenogaster senilis*: role of foragers and reminiscence of acquired experience

Aurore Avargues-Weber, Thibaud Monnin

Laboratoire Fonctionnement et évolution des systèmes écologiques CNRS UMR 7625, Université Pierre et Marie Curie, Paris, France

Introduction: We studied the pattern of colony emigration of the ant *Aphaenogaster senilis*, which reproduces by colony fission, and its ability to improve at emigrating through acquired experience.

Methods: Emigrations were triggered in the laboratory by opening the nest while providing a new nest 1.5 m away (n=10). We video recorded foragers and nurses entering or exiting this arrival nest. Six to eleven weeks later a second emigration was triggered to determine whether colonies improved their performance.

Results: Nest relocation was characterized by a synchronised emigration: the number of workers present in the arrival nest increased following a sigmoid curve. The duration of emigration was relatively constant between colonies, while the delay before emigrating varied. The queen relocated in the middle of the emigration, when many workers were on the move. When emigrations were repeated, the duration of emigration was unchanged but the delay before the emigration was much shorter.

Conclusions: *Temnothorax albipennis* colonies gain experience through migrating. This experience results from the individual experience acquired by foragers and lasts six days. In *A. senilis* the experience acquired lasted several weeks, and it was not due to experienced foragers since these had been removed. These differences may stem from *T. albipennis* nurses being transported by foragers while *A. senilis* nurses actively walk to the destination nest, so that only the latter gain experience by emigrating. This would also explain the longer reminiscence of experience in *A. senilis*, where experienced individuals are not only short lived foragers but also young nurses.

Islands in the Australian savannah: Population genetics of magnetic termite mounds

Judith Korb[2], Anna Schmidt[1]

[1]University of Regensburg, Biology I, Regensburg, Germany, [2]University of Osnabrück, Behavioral Biology, Osnabrück, Germany

The “Magnetic Termite” *Amitermes meridionalis* is restricted to a small part of northern Australia where it occurs in seasonally flooded areas and builds famous wedge-shaped mounds with an elongated axis that is orientated in a striking north-south direction. Despite its popularity not much is known about this species’ biology. Due to its restriction to seasonally flooded areas, it has a very patchy distribution. ‘Islands’ sizes range from a few m² with less than 10 mounds to several km² with several thousands of mounds all differing by their degree of isolation. We used nine variable microsatellite markers, specifically developed for this species, to (1) describe the colony structure of mounds and (2) to test how population size and degree of isolation influence the population structure of *A. meridionalis*. The genetic analyses revealed that each mound was inhabited by a single colony and that colonies were not polydomous. The number and distribution of alleles and relatedness estimates indicated that colonies were founded by one pair of reproductives which was often replaced by its inbreeding offspring. Within the islands, the observed heterozygosity was lower than expected and F-statistics indicated that there was a significant degree of inbreeding. How population size and degree of isolation influence population structure will be discussed in this still ongoing study.

Termites and mites: adaptive behavioural responses to infestation

Judith Korb[2], Alexander Fuchs[1]

[1]University of Regensburg, Biology I, Regensburg, Germany, [2]University of Osnabueck, Osnabrueck, Germany

Rapid adaptation to their hosts' defence systems usually allows parasites to keep the upper hand in the co-evolutionary arms race between hosts and parasites. However, although morphological and physiological adaptations are generally far slower in hosts than in their parasites, the former can rapidly respond to a parasite challenge by dispersal-related, adaptivechanges in their behaviour. We investigated whether the drywood termite *Cryptotermes secundus* altered its behaviour in response to an infestation with parasitic, astigmatic mites.

The frequency of the vital, dispersal-related behaviours allogrooming and proctodeal trophallaxis did not differ between colonies or between individuals with mites compared to without mites. However, activity levels were lower in mite-infested colonies and individuals spent more time resting and feeding when mites were present in the colony, irrespective of whether they were infested themselves or not. This behavioural pattern shown by individuals from infested mite-colonies is known to be associated with a development of *C. secundus* workers into winged dispersing sexuals. As dispersing individuals were less likely to have mites, this behavioural response to the mites' infestation might be an adaptive response to escape the deteriorating nest conditions.

The use of *Solanum oplocense* as a source of resistance to the Colorado potato beetle, *Leptinotarsa decemlineata* (Say)

Yvan Pelletier, David De Koeyer

Potato Research Centre, Fredericton, NB, Canada

The objectives of this study were to evaluate the genetic variability for insect resistance and to gather information on the mechanism of resistance to the Colorado potato beetle (CPB) of *Solanum oplocense*. Further information on the genetics and nature of the resistance was also gathered by studying hybrids during a few generations.

In field plots, the population density of all developmental stages of the CPB tended to be lower on *S. oplocense*. There was a reduction in "feeding" frequency for all larval stages and adults on *S. oplocense*. All larval stages tended to spend more time "resting" and "walking" on *S. oplocense* foliage than on potato. Adults "walked" more on *S. oplocense* foliage than potato. All five CPB life stages consumed much less foliage of the wild *Solanum* species than of potato. When caged with *S. oplocense*, the population of CPB decreased and egg production was greatly reduced compared to potato. Data on the evaluation of resistance in *S. oplocense* hybrid populations will also be presented.

Trypsin Modulating Oostatic Factor (TMOF), from reproduction to digestion

Dov Borovsky

University of Florida, IFAS, Vero Beach, FL, United States

Trypsin Modulating Oostatic Factor, a decapeptide (YDPAPPPPPP), was isolated from the ovaries of *Aedes aegypti* female mosquitoes. Initially the hormone was thought to stop ovarian development and act like a 'birth control pill' because injection of the hormone into blood fed females caused the arrest of ovarian development. When female guts were dissected and assayed, it became apparent that the hormone directly inhibits blood digestion and acts like a 'diet pill' and indirectly inhibits ovarian development.

TMOF has 7 prolines and resists proteolysis in adult and larval guts. The hormone easily penetrates the gut epithelial cells when it is fed to larvae and adult mosquitoes and binds a specific receptor that resides on the hemolymph side of the gut. After binding, the hormone turns off trypsin biosynthesis in the gut epithelial cells by stopping the translation of the trypsin message. TMOF was found to be effective against mosquito larvae, and several other agricultural pest insects, i.e. *Heliothis virescens* and *Diaprepes abbreviatus,*

The hormone was genetically engineered and expressed on the coat protein of TMV, in *Chlorella sp.* and *Chlorella desiccate*, in *Saccharomyces cerevisiae* and *Pichia pastoris* and in alfalfa plants. Feeding tobacco plants that were infected with recombinant TMV expressing TMOF or recombinant alfalfa plants to several agricultural pest insects caused inhibition of larval growth and trypsin biosynthesis. Feeding recombinant chlorella and yeast cells to mosquito larvae caused anorexia starvation and larval death.

These results, the genetic engineering of the hormone and the characterization of its receptor will be discussed.

Advances in the semiochemistry of cerambycid beetles

Jocelyn G. Millar[1], Lawrence M. Hanks[2], Emerson S. Lacey[1], Jardel Moreira[1], James Barbour[3], J Steven McElfresh[1]

[1]University of California, Riverside CA, United States, [2]University or Illinois, Urbana-Champaign IL, United States, [3]University of Idaho, Parma ID, United States

Introduction: The Cerambycidae are a large and diverse beetle family, with >25,000 described species. A number of species are important pests, both in their native ranges, but increasingly in new regions of the world where they have been accidentally introduced. Despite their importance, very little is known of their use of pheromones, and the chemistry of those pheromones.

Methods: Pheromones of a number of cerambycid species were collected from the headspace of confined beetles, and identified by spectroscopic methods. A matrix of likely pheromone chemicals was also synthesized and screened in field trials.

Results: Sex and aggregation pheromones of a number of cerambycid species were identified by the tandem strategy of isolation and identification of compounds from beetle extracts supplemented by screening of possible pheromone components. Most pheromones were male-produced, with males of some species producing >0.1 mg of pheromone per day. The species for which pheromones have been fully or partially identified will be summarized, along with the chemistry of the pheromone compounds. Some general trends and patterns of pheromone use in this family are beginning to emerge, and will be discussed.

Conclusions: Both contact and long-range attractant pheromones are widely used by cerambycid beetles. These compounds have enormous potential for use in IPM programs, particularly for detection of invasive species.

Chemistry and practical applications of pheromones of mealybugs infesting vineyards

Jocelyn G. Millar[1], J. Steven McElfresh[1], Jardel Moreira[1], Kent M. Daane[2], Walt Bentley[3]

[1]University of California, Riverside CA, United States, [2]University of California, Berkeley CA, United States, [3]Kearney Agricultural Center, Rarlier CA, United States

Introduction: Obscure, longtailed, vine, and grape mealybugs constitute some of the most important pests of viticulture worldwide. Their sex attractant pheromones have the potential to be of major use in detection, sampling, and possibly control of these pests. We report the identification, synthesis, and testing of the sex pheromones of each of these species.

Methods: Pheromones of all 4 species were collected in microgram amounts from cohorts of unmated females, identified by spectroscopic and microchemical methods, and synthesized for field bioassays.

Results: The pheromone of each species consists of a single component, and each pheromone has proven to be a highly unusual chemical structure, with all of them being molecules new to science. The pheromones are extremely attractive, with microgram doses attracting males for >8 weeks in the field. Quirks in the reproductive biology of each species may have major implications in the use of these pheromones in IPM programs.

Conclusions: The pheromones of pest mealybugs are likely to become important new tools for IPM, with pheromone lures being extremely attractive to male mealybugs for extended periods under field conditions.

Plant-mediated interactions linking foliar-feeding insects and root-feeding nematodes: ecological significance and underlying mechanisms

Ian Kaplan[1], Robert Denno[2]

[1]Cornell University, Ithaca, New York, United States, [2]University of Maryland, College Park, Maryland, United States

Introduction: Roots play a critical, but largely unappreciated, role in aboveground anti-herbivore plant defenses and root-leaf connections may therefore result in unexpected coupling between above- and belowground consumers.

Methods: Using the tobacco (*Nicotiana tabacum*) system we highlight two examples of this phenomenon. First, using nicotine-deficient mutant plants we tested the role of nicotine, a secondary compound that is synthesized in root tissue, in nematode-induced effects on aboveground herbivorous insects. Second, we used pulse-labeling (^{13}C) of plants followed by stable isotope analysis to assess the impact of foliar insect herbivory on the performance of root-feeding nematodes via plant source-sink dynamics.

Results: Although recent studies emphasize the role of induced defenses in plant-mediated competition between foliar and root herbivores, we demonstrate that leaf-root connections can generate the opposite effect, with positive interactions linking foliar and root consumers. Nematode root herbivory interfered with foliar nicotine expression, resulting in positive effects on aboveground phytophagous insects. Notably, nematode-induced facilitation only occurred on nicotine-expressing plants, and not on nicotine-deficient mutants. Foliar insect herbivory elicited a putative tolerance response whereby aboveground nutritional reserves were allocated to roots, resulting in facilitation of phytoparasitic nematodes co-occurring on the same host-plant.

Conclusions: Plants integrate roots in resistance and tolerance mechanisms for leaf defense, and such root-leaf connections inherently link the dynamics of above- and belowground consumers.

Potential of the wasp *Habrobracon hebetor* (Say, 1836) (Hymenoptera: Braconidae) as a biological control agent for *Corcyra cephalonica* (Stainton, 1865) (Lepidoptera: Pyralidae) in stored rice

Charles Adarkwah, Daniel Obeng-Ofori, Sabine Prozell, Mathias Schoeller, Christoph Reichmuth, Carmen Buettner

[1]Humboldt University of Berlin, Berlin, Germany, [2]University of Ghana, Crop Science Department, Accra Legon,, Ghana, [3]Biological Consultants Ltd, Berlin, Germany, [4]Federal Biological Research Centre for Agriculture and Forestry, Berlin, Germany

Habrobracon hebetor is a gregarious larval ectoparasitoid of several species of pyralids attacking stored grains. The potential of using *H. hebetor* for the biological control of *C. cephalonica* was assessed in rice stored in jute bags. 1 kg of uninfested rice grains was introduced into small jute bags measuring 18 cm x 16 cm. A total of 8 bags (4 bags treated with *H. hebetor* and 4 untreated) were included into the test in separate two chambers. Treated and untreated bags were placed in climatized chambers at the same climatic conditions of a temperature of 25°C and relative humidity of 65%. Sixty first instar larvae of *C. cephalonica* were released into all of the bags that were subsequently sealed and kept for 10 days to allow for the larvae to develop inside the jute bags. The individual bags were placed on a small pallet. Ten *H. hebetor* adults aged 2 days old were exposed for 12 days to four of the bags containing rice infested with larvae of *C. cephalonica,* respectively, within one chamber. Each treatment was repeated five times with control without parasitoids in a separate chamber. After the exposure period, the rice was transferred from the jute bags into 250 ml glass jars. The emergence of *C. cephalonica* was recorded daily in both *H. hebetor* treated and untreated rice samples until the 21st day. *H. hebetor* was able to locate its host in the bags with infested rice kernels and produced F_1 progeny. In the four untreated bag samples, the pest population developed normally into adult moths: on average out of five replicates 91.3% adults were found out of 60 introduced larvae. *H. hebetor* was able to significantly reduce the emergence of *C. cephalonica* in rice stored in jute bags. On average a percentage reduction of emergence (PRE) of 61.6 % was observed. The implications of these results with respect to the suitability of *H. hebetor* for the biological control of *C. cephalonica* in jute bags are discussed.

Seasonal abundance of *Cephonodes hylas* (Linnaeus) (Lepidoptera: Sphingidae) on Robusta Coffee in Ibadan, Nigeria.

Feyisare Okelana, Adebayo Odebiyi

[1]*Cocoa Research Institute of Nigeria, Ibadan, Nigeria,* [2]*University of Ibadan, Ibadan, Nigeria*

The Oriental bee-hawk moth *Cephonodes hylas* (L) (Lepidoptera: Sphingidae) is one of the major defoliator insect pests of robusta coffee *(Coffea canephora* Pierre ex. Froehner) in Nigeria.

Seasonal abundance of the eggs and caterpillars of the insect vis-a-vis the influence of some climatological factors (rainfall, temperature and relative humidity) was monitored by weekly random sampling of 100 coffee stands at two well-established and routinely managed robusta coffee experimental plots under different shade regimes. The plots are located at the southern block of the Headquarters of Cocoa Research Institute of Nigeria, Idi-Ayunre, Ibadan. The study period covered five years (1990-1994).

The results showed a marked seasonal variation in the population of the two life stages of the pest. Incidence of eggs and caterpillars of the moth was from March, which usually followed the onset of the early rains and commencement of leaf flushing in coffee. The insect is bivoltine, having two reproductive cycles per annum; the major population peak occurring in any of the months between March and July which coincided with the period of peak rainfall in the South-Western part of the country and minor peak around October/November when the minor rainfall peak occurred. Irregularity, cessation and decline of the early rains after its onset, often resulted in drastic drop in the population of the pest. Generally, there was a positive correlation between the prevailing temperature and incidence of the eggs and caterpillars at the two plots. Furthermore, the comparative"t" test analysis showed that significant differences ($P>0.05$) in the number of eggs and caterpillars of the moth existed in 1990 at the two plots and in 1991 for the eggs. A higher population of the two stages was often recorded in the unshaded (open) and actively rejuvenating coffee plots which abound in young flushes than in the heavily shaded plot where old leaves predominate, probably because the new flushes produced by the open plot made it more attractive to ovipositing females and more nutritive to young larvae of the pest.

While heavy shading adversely affected the yield of robusta coffee, appropriate shade regime which will minimize attack by *C. hylas* but result in optimum coffee yield needs to be investigated.

Manipulating butterfly wing patterns using over-expression and knock-down of candidate genes using transgenics

Antonia Monteiro[1], Diane Ramos[2], Bin Chen[1], Firdous Kamal[2], Ondrej Podlaha[1]

[1]Yale University, New Haven, CT, United States, [2]University at Buffalo, Buffalo, NY, United States

Many genes involved in wing development in *Drosophila* are expressed in novel domains in the butterfly wing that correlate with adult color patterns. In order to move beyond correlative studies in implicating a gene in the development of a color pattern, we have been exploring the effect of over-expressing or down-regulating several of these genes in the African butterfly *Bicyclus anynana*. We developed a novel piggyBac vector plasmid where candidate genes can be either inserted once, and used in over-expression studies, or inserted twice, in opposite orientation, and used in RNAi based knock-down approaches. We are using the heat-shock promoter from *Drosophila Hsp70* to activate gene expression in a controlled temporal fashion in *Bicyclus*, and also a laser-assisted heat-shocking system to provide localized over-expression of genes on the developing pupal wing. Our results show that global over-expression and down-regulation of candidate wing pattern genes have opposite effects on the adult color pattern, suggesting a functional role for these genes in wing pattern development. In addition, local heat-shocks can produce a different class of phenotypes relative to global heat-shocks, suggesting that juxtaposing cells with and without gene expression is an important parameter in the development of butterfly color patterns.

The evolution of eyespot number in *Bicyclus* butterflies: developmental mechanisms, sex, and imprinting

Antonia Monteiro[1], Kendra Robertson[2], Jeffrey Oliver[1], Andrea Hodgins-Davis[1], Andrew Goldman[2], Mayank Lahoti[2]

[1]Yale University, New Haven, CT, United States, [2]University at Buffalo, Buffalo, NY, United States

Bicyclus butterflies have diversified in mainland Africa and have evolved different wing patterns. Most wing pattern differences between species occur on the dorsal surface of the wings, a surface believed to be mostly functioning in sexual selection. Eyespot patterns are sometimes present on this surface, and their current species distribution implies that they have been “switched on” or “off” multiple times during the evolution of the genus. Here we propose both a developmental mechanism that can account for these “switches” as well as an ultimate sexual selection mechanism that allows new wing pattern mutations, involving variation in eyespot number, to be favored by members of the ancestral species. This mechanism can lead to assortative mating, and may facilitate speciation.

The importance of line thinning to arthropod conservation and ecosystem management in Japanese cedar (*Cryptomeria japonica* D. Don) plantations

MD. Abdul Maleque, Kaoru Maeto, Hiroaki Ishii, Shingo Taniguchi

Kobe University, Kobe, Hyogo Prefecture, Japan

Introduction: Overstocked conifer plantations in Japan, where management is lacking, support low understory biodiversity. Therefore, we investigated the effectiveness of a new silvicultural technique, line thinning (cutting trees in lines), on biodiversity restoration in overstocked *Cryptomeria japonica* plantations.

Methods: We investigated the effects of line thinning on microclimate, understory plant species diversity and insect assemblages. We compared the abundance and diversity of Coleoptera and Hymenoptera captured with Malaise traps from a line-thinned stand and an adjacent unthinned stand in two plantations: a low-elevation *Sugi* site (4 years since thinning) and a high elevation *Kuchiotani* site (6 years since thinning).

Results: In both plantations, more open canopy conditions resulted in higher maximum temperatures on the forest floor. The thinned stands supported greater understory plant species richness and biomass than the unthinned stands. Important functional groups of Coleoptera (*e.g.*, plant feeders, wood borers, rotten-wood feeders, root feeders, fungus feeders, dung feeders, and scavengers) and Hymenoptera (*e.g.,* pollen feeders, parasitoids, and predators) as well as many families of both orders were more abundant in the thinned stand than in the unthinned stand. Some coleopteran families were absent from the unthinned stands. There were strong positive relationships between coleopteran abundance and understory vegetation across sites. Most hymenopteran functional groups were positively correlated with both species richness and understory plant biomass in the plantations where understory vegetation was rich.

Conclusions: Our results indicate that line thinning increases the diversity of understory plants and arthropods, thereby enhancing ecosystem integrity in overstocked *C. japonica* plantations.

Microstructural characters in the systematics of Bostrichidae (Coleoptera)

Lan-Yu Liu[1], Klaus Schönitzer[2], Jeng-Tze Yang[1]

[1]Chung Hsin University, Taichung, Taiwan, Province of China, [2]Zoologische Staatssammlung München, Munich, Germany

Introduction: In order to find more taxonomically useful characters in the family Bostrichidae, we used an Environmental Scanning Electron Microscope (ESEM) to examine the micro-structural characters, such as hairs, punctures and tubercles of the middle part of the elytral disc. We expected to find new useful characters from these micro-structures.

Methods and Materials: We examined 78 species belonging to 3 subfamilies and 4 tribes by low vacuum ESEM. In order not to damage the old museum specimens, we did not dismount them and did not coat the surface of the specimens with gold or other metals.

Results: We studied the structures of the punctures, tubercles and hairs under the ESEM and described them in relation to their shape, density and the location of the insertion of the hairs.

Conclusions: Our work not only found more taxonomical useful characters in the micro-structures on the surface of specimens, but showed that we can now examine the specimens under ESEM without any damage.

Ecology and management of three rice planthopper species in the Yangtze Delta, China

Jia-an Cheng, Zeng-rong Zhu

Institute of Insect Sciences, Zhejiang University, Hangzhou, Zhejiang, China

Introduction: Modern agriculture relying on high yielding variety and agri-chemicals has resulted in more secondary pests, including *Laodelpdx striatellus* (SBPH), *Nilaparvata lugens* (BPH) and *Sogatella furcifera* (WBPH). The simultaneous outbreak of the three species in the new century indicates even higher risk in Yangtze Delta is coming. Ecological mechanisms and management strategy for reducing the risk were studied.

Methods: Field investigations and lab experiments were carried out to study interactions among the three species and environmental factors, understand mechanisms of mutualism causing simultaneous outbreaks and develop ecological strategy for managing rice planthoppers.

Results: Field investigations indicated that field competitions for food and space among the three species could be reduced by differentiations of seasonal development pattern and food nutrition. Coexistence of BPH and WBPH at certain level could promote their population parameters because of the changes of plant nutrition. Field evaluations on predation using McAb showed that time-lag of peak populations among the three species provided better chance for a late species to escape from predation. Differences in sensitivities of the three species to pesticides and effects of insecticides stimulating planthopper fecundity and reducing natural control made chemical controls for one species become alternative way causing resurgence for another species in same season. Therefore, one to one strategy for controlling planthopper resulted in outbreaks of three species simultaneously.

Conclusions: Planthopper management program should be designed based on understanding of interactions among three planthopper species and key strategy could be reduction of initial population size and growth rate using cultural practices.

Ghosts of invasions past: Non-target acquisition of native lepidoptera by parasitoids released to combat exotic tussock moths in North America

Dylan Parry

State University of New York, College of Environmental Science and Forestry, Syracuse, New York, United States

Introduction: The introduction of gypsy moth (*Lymantria dispar*) to North America in 1867 launched an ecological experiment still ongoing. Subsequent introductions of two additional lymantriids (*Euproctis chrysorrhea* in 1896 and *Leucoma salicis* in the 1920's) elicited an unprecedented biological control program that continued for more than 80 years. At least 50 parasitoids were released for control of these invasive tussock moths. I examined the acquisition of native North American Lepidoptera by these exotic parasitoids relative to their life-history strategies (generalist/specialist).

Methods: To assess non-target acquisition, I used controlled rearing of field-collected native Lepidoptera from natural and experimental populations coupled with analysis of literature. Field collections were also made from satin, browntail, and gypsy moth populations to survey the parasitoid complex.

Results: Of more than 50 parasitoids released for control of these invasive tussock moths, 14 species appear to be still extant in North America. Six are unique to gypsy moth, three to browntail moth, one to satin moth, and four species are shared by all three lymantriids. Acquisition of native hosts was dependent on life-history strategy and ranged from apparently zero in the tachinid *Townsendielliomyia nidicola* to nearly 200 species (*Compsilura concinnata*: Tachinidae).

Conclusions: Despite their presence in North America for 30-100 years, most parasitoids released as part of exotic tussock moth control programs have acquired few native species. The two notable exceptions (*C. concinnata* and the ichneumonid *Pimpla disparis*) are highly polyphagous in their native range and thus their effect on native biodiversity was predictable.

Overcoming host plant resistance and parasitoid attack: tri-trophic challenges for the large raspberry aphid

Carolyn Mitchell, Scott Johnson, Stuart Gordon, Nicholas Birch, Stephen Hubbard

[1]SCRI, Invergowrie, Dundee, United Kingdom, [2]University of Dundee, Dundee, United Kingdom

Introduction: This study investigated how the relative roles of bottom up and top down influences can be affected as the insect herbivore overcomes host plant resistance. This model system used the large raspberry aphid (*Amphorophora idaei*), the parasitoid (*Aphidius ervi*) and the red raspberry (*Rubus idaeus*). The resistance within the plant is underpinned by a single gene (A_{10}) which is absent in susceptible cultivars.

Methods: A survey of *A. idaei* in a raspberry plantation compared the number of aphids found on both resistant and susceptible cultivars. A series of laboratory experiments firstly compared the aphid performance on a resistant-challenged cultivar and a susceptible cultivar and secondly observed parasitoid performance and aphid behaviour on three cultivars with varying degrees of resistance.

Results: In the field, no aphids were found on the resistant-challenged cultivar but were regularly observed on the susceptible cultivar. In the laboratory, all four parameters studied: pre-reproductive period, total number of nymphs produced, longevity and r_m showed that the aphid preformed significantly better on the susceptible cultivar. Parasitoid attacking behaviour increased with aphid density but was lower on the resistant-challenged cultivar. The attack rate on the partially resistant cultivar was significantly higher than on the other cultivars. Aphids showed a greater tendency to drop from the resistant-challenged cultivar.

Conclusions: This study suggests there is a trade-off between bottom-up and top-down forces as insect herbivores become adapted to host plant resistance mechanisms.

The diminutive supercolony: Argentine ants of the southeastern United States

Grzegorz Buczkowski[1], Jules Silverman[2]

[1]Purdue University, West Lafayette, IN, United States, [2]North Carolina State University, Raleigh, NC, United States

Introduction: Native to Argentina and Brazil, the Argentine ant (*Linepithema humile*) is an invasive species that has become established on six continents and many oceanic islands. In several parts of its introduced range, including the western U.S., southern Europe, and Chile, the Argentine ant is unicolonial, forming extensive supercolonies.

Methods: We examined population genetic structure and intercolony aggression in two regions of the introduced range of this species in the United States: California and the southeastern U.S. Our results show that the southeastern *L. humile* population has high genotypic variability and strong intercolony aggression relative to the California population.

Results: In the California population, intercolony aggression was absent and 23 alleles were found across seven polymorphic microsatellite loci. However, in the Southeast, aggression between colonies was high and 47 alleles were present across the same seven loci in an equal number of colonies.

Conclusions: We suggest that distinctly different colonization patterns for California and the Southeast may be responsible for the striking disparity in the genetic diversity of introduced populations. Southeastern colonies may have descended from multiple, independent introductions from the native range, undergoing a bottleneck at each introduction. In contrast, the California supercolony may have originated from one or more colonies inhabiting the southeastern U.S., thus experiencing a double bottleneck. The differences in present-day distribution patterns between California and the Southeast may be due to the combined effect of two factors: lower winter temperatures in the Southeast and/or competition with another successful and widely distributed ant invader, the fire ant *Solenopsis invicta*.

Permethrin aerial ULV spray efficacy for controlling salt marsh mosquitoes and potential impacts on fish

He Zhong[1], Ed Hunter[2], Max Feken[3], Cate Brock[1]

[1]Public Health Entomology Research and Education Center, Florida A&M University, 4000 Frankford Avenue, Panama City, Florida 32405, United States, [2]Beach Mosquito Control District, 1016 Cox Grade Road, Panama City Beach, FL 32407, United States, [3]Florida Department of Agriculture and Consumer Services, Bureau of Pesticides, 3125 Conner Boulevard, Bldg. #6,Tallahassee, FL 32399, United States

Aerial ultra-low-volume (ULV) application of insecticides is widely used by mosquito control programs to control adult mosquitoes and reduce mosquito-transmitted diseases. Although permethrin is sprayed by truck as an adulticide in Florida, aerial applications currently are not permitted based on potential effects to field aquatic organisms, including fish. In 2007, we investigated the impact of permethrin residue on laboratory-reared mosquitofish, *Gambusia holbrooki* (Girard), following exposure to ULV aerial applications in Panama City Beach, Florida. The efficacy of the 5 field aerial spray trials was validated using adult salt marsh mosquitoes, *Ochlerotatus taeniorhynchus* (Wiedemann), placed in cylindrical exposure cages (over 50 female adult mosquitoes per cage) with 1 cage placed at each of the 12 sampling stations (9 treatment and 3 control stations). Non-target bioassays were conducted using 25 adult fish and 30 juvenile fish placed in separate plastic bins at each station. The ULV aerial applications were conducted by the Beach Mosquito Control District using a helicopter equipped with a high pressure nozzle spray system. Excellent mosquito control (> 90% efficacy) was obtained for all five trials. Also, no mortality differences were observed between treatment and control groups for either adult or juvenile fish after 120 hours. This research demonstrated that aerial applications of permethrin were effective against adult mosquitoes and did not result in adverse impacts on either adult or juvenile fish under the conditions of the study. We believe that when properly conducted aerial ULV application of permethrin should pose minimal risk to fish in the field.

Bees in bonnets, butterflies in stomachs, and ants in pants; how insects creep into culture

May Berenbaum

University of Illinois, Urbana, IL, United States

In some respects, it is remarkable that insects, a group that in real life is at best studiously avoided and at worst actively reviled, figure prominently metaphorically in most cultures around the world. Among the possible explanation for such cultural ubiquity is that, irrespective of location, it is virtually impossible on this planet to live an insect-free life, given their abundance, ubiquity, and close association with humans. Despite staggering differences in outward appearances and in lifestyle that may assail human sensibilities, remarkable similarities between humans and insects, particularly social species, have not escaped notice around the world. They are the only organisms that have colonized the planet to the extent that humans have, living everywhere people live (even on occasion hitching a ride on our bodies to do so). Historical and contemporary uses of insect societies to mirror aspects of human societies are provided.

A history of insect outbreaks — from Genesis to GIS

May Berenbaum

University of Illinois, Urbana, IL, United States

Insect outbreaks by their very nature command attention but, due to their inherently intermittent nature, they have proved difficult over the years to investigate experimentally. Although early hypotheses accounting for outbreaks tended to be essentially untestable (often involving in one form or another divine wrath or punishment), more recently a multitude of scientific hypotheses have been advanced--yet these, too, can be difficult to falsify. Cyclic variations in insect populations strongly suggest that some regulatory factor is in force, but just which regulatory factor remains an open question. A problem with many studies of population cycles in eruptive species is that they're pursued (and funded) at the peak of outbreaks and interest often disappears in the troughs. Moreover, dynamics of outbreak species, like many other aspects of insect life, might be idiosyncratic and difficult to generalize. Thus, it is not surprising that the nature of the forces affecting population sizes of insects has been the subject of some of the most polarized and vitriolic debates in insect ecology. As is often the case in insect ecology, however, both sides of each of the arguments may have merit, depending on species and circumstances.

All we are saying is give bees a chance — citizen scientists and pollinator decline

May Berenbaum

University of Illinois, Urbana, IL, United States

Worldwide, concern about pollinator declines has increased, and, where pollinator status has been monitored over time, as in Europe, reductions in numbers have been documented. The U.S. National Academy of Sciences Committee on the Status of Pollinators in North America, charged to evaluate apparent pollinator declines, concluded in October 2006 that, for most pollinators, there are simply no baseline data to allow assessments of changes in abundance and distribution. Among their principal recommendations was to begin monitoring programs with bees as a top priority due to their prominence as pollinators. This committee recommended involving citizen-scientists in such monitoring efforts, providing an extraordinary and timely opportunity for informal science education, particularly given the widespread attention in the popular media on colony collapse disorder and the nationwide disappearances of bees. Although the general public has an appreciation for bees and pollination, the level of detailed knowledge is low. Monitoring and conservation efforts require an educated public to differentiate between pollinating bees and predaceous stinging wasps. All too often, the typical reaction to the presence of anything striped and buzzing is to kill it. Thus, recruiting citizen scientists to pollinator monitoring efforts requires visual recognition and user-friendly color-guided keys rather than the more traditional collection and dissection to identify species. Such an approach is better suited in any case to conservation efforts. Components of a workable partnership between citizen-scientists and the professional science community that educates the public about pollinators and engages them in useful data collection are suggested.

Talking bugs — insects and ventriloquism

Hannah Leskosky

University Laboratory High School, Urbana, IL, United States

Ventriloquism is an ancient art form that, like magic, relies on misdirection to create the illusion that non-humans can engage in conversation. Despite the fact that some insects can actually communicate by sound, they rarely are used as ventriloquial figures. The main reason is most likely that the majority of the public don't usually think of "bugs" as "cute" or "funny" and ventriloquism is generally performed to entertain. In addition, because people generally don't know very much about their behavior, insects can be difficult for some audiences to relate to. However, insect ventriloquism has great potential not only for entertainment purposes but also to teach people about insects in an engaging way. Some entomological ventriloquism techniques will be demonstrated.

Efficacy of chemical insecticides in controlling the pea beetle (weevil) *Bruchus pisorum* L. (Coleoptera: Bruchidae) on field pea (*Pisum sativum* L.) in Ethiopia

Birhane Asayehegne, MC van Der Westhuizen

University of the Free State, Bloemfontein, Free State, South Africa

Introduction: The *Bruchus pisorum* L. has became very important insect pest on Pisum sativum L. in the northwest and northeast Ethiopia. For this newly occur insect pest for the region and the country on the crop and which is expanding its infestation in alarming rate to more field pea growing areas of the country, finding any control option was an urgent task.

Methods: The timely spraying of synthetic chemicals, one insecticide from each of, from carbamate, organochloride and organophosphate groups and three from pyrothroids group were used. The experiments were conducted on-farms for two consecutive years in randomized complete block design applying the insecticides with knapsacks.

Results: In the field control efficacy of the chemical insecticides among the groups and with in a group varied. Carbaryl 85% WP and Endosulfan 35 % EC more effective while Diazinon 60 % EC was less effective. From the pyrothroids, Alpha Cypermethrin and lambda cyhalothrin more effective compare to Deltamethrin.

Conclusions: In Ethiopia, where the small scale farming system dominant, in the absence of any immediate available means of control option it is revealed that a proper measure to use the lesser hazard to the environment but effective chemical insecticide(s) on the insect pest. Considering effective and economically sound chemical insecticide sprays at appropriate time based on the economic threshold level for the insect pest on the crop with proper operation of the sprayer in use is important.

Efficacy of chemical insecticides in controlling the pea beetle (weevil) *Bruchus pisorum* L. (Coleoptera: Bruchidae) on field pea (*Pisum sativum* L.) in Ethiopia

Birhane Asayehegne, MC van Der Westhuizen

University of the Free State, Bloemfontein, Free State, South Africa

Introduction: The *Bruchus pisorum* L. has became very important insect pest on *Pisum sativum* L. in the northwest and northeast Ethiopia. For this newly occur insect pest for the region and the country on the crop and which is expanding its infestation in alarming rate to more field pea growing areas of the country, finding any control option was an urgent task.

Methods: The timely spraying of synthetic chemicals, one insecticide from each of, from carbamate, organochloride and organophosphate groups and three from pyrothroids group were used. The experiments were conducted on-farms for two consecutive years in randomized complete block design applying the insecticides with knapsacks.

Results: In the field control efficacy of the chemical insecticides among the groups and with in a group varied. Carbaryl 85% WP and Endosulfan 35 % EC more effective while Diazinon 60 % EC was less effective. From the pyrothroids, Alpha Cypermethrin and lambda cyhalothrin more effective compare to Deltamethrin.

Conclusions: In Ethiopia, where the small scale farming system dominant, in the absence of any immediate available means of control option it is revealed that a proper measure to use the lesser hazard to the environment but effective chemical insecticide(s) on the insect pest. Considering effective and economically sound chemical insecticide sprays at appropriate time based on the economic threshold level for the insect pest on the crop with proper operation of the sprayer in use is important.

New reduced risk control approaches for area-wide pest management of fruit flies in the Pacific

Roger Vargas, Ronald Mau, Jaime Pinero, John Stark, Eric Jang

USDA-ARS-PBARC, Hilo, Hawaii 96720, United States

Introduction: In 1999, the United States Department of Agriculture, Agricultural Research Service, in cooperation with the University of Hawaii and the Hawaii Department of Agriculture, initiated the Hawaii Fruit Fly AWPM program to suppress fruit flies (Diptera: Tephritidae) below economic thresholds while reducing the use of organophosphate insecticides. Historically, protein-bait sprays and the highly attractive male lures, methyl eugenol and cue-lure, have been used with organophosphate insecticides (malathion and naled) for area-wide fruit fly control throughout the Pacific region. Through the AWPM program an effective Spinosad protein bait spray (GF-120 Fruit Fly Bait), a sprayable Spinosad male annihilation treatment (SPLAT ME and C-L) and a fipronil male annihilation station (Amulet ME and C-L) were developed and investigated as organophosphate insecticide substitutes for AWPM of melon and oriental fruit flies.

Methods: In field trials, GF-120, SPLAT, and Amulet were tested against oriental and melon fruit fly populations.

Results: Data suggested GF-120, SPLAT and Amulet reduced fruit flies, and in many cases were as effective as organophosphate treatments.

Conclusions: These fruit fly treatments offer environmentally friendly alternatives to present organophosphate formulations for area-wide suppression/eradication of fruit flies.

Addressing capacity needs in medical entomology for national disease vector control programmes in the Eastern Mediterranean Region

Abraham Mnzava

World Health Organization, Regional Office for the Eastern Mediterranean, Cairo, Egypt

Countries of the Eastern Mediterranean Region contribute disproportionately to the global burden of disease due to vector-borne diseases (VBDs). The Region is also experiencing the emergence/re-emergence of VBDs – including their seasonal and geographical expansion. Some of the factors responsible for this expansion: include climatic and technical (e.g. insecticide resistance) factors, rapid urbanization, population movement and inappropriate policies. For example, as a result of successful control of malaria, some countries withdrew vector control resources, both human and financial. In 2005, the 52nd session of the WHO Regional Committee for the Eastern Mediterranean – the highest policy decision body on health in the Region – reviewed this situation and took a number of decisions. While the Committee endorsed integrated vector management as the recommended strategy for rational use of vector control resources, it also recognized the need to strengthen national capacity in medical entomology and vector control for the successful implementation of integrated vector management. Through resolution EM/RC.52/R.6, the Committee requested the Regional Director of WHO to establish a regional MSc course in medical entomology and vector control in an attempt to address this problem. After a series of consultations with key national control programmes and regional and international research and training institutions, a course curriculum was developed and finalized. A hosting institution was identified and the first group of students will start the course in June 2008 at the University of Gezira, Sudan. With the continued support of partners and Member States, including their political commitment, it should be possible to start establishing capacity in medical entomology to meet the needs for successful implementation of integrated vector management in the Region.

Genomic analysis of chemical communication in honey bees

Christina Grozinger, S Kocher

North Carolina State University, Raleigh, NC, United States

Pheromonal communication is often considered to be stereotyped and innate, in terms of both the production and response to pheromones. However, production of pheromonal cues and responses to pheromones can be modulated by environmental context, physiological changes and/or the genotype, but the molecular mechanisms underlying these processes are relatively uncharacterized. *We are using genomic approaches to characterize the molecular mechanisms and pathways underlying modulation in the production of and response to queen mandibular pheromone (QMP).* QMP is rather unusual pheromone, in that it can cause both short-term changes in behavior and long-term changes in behavior and physiology. QMP also causes profound changes in brain gene expression, in a manner that correlates with its long-term effects on behavior and physiology. Furthermore, the short- and long-term responses QMP can be uncoupled; thus, they appear to operate by different mechanisms. We are now expanding our studies to characterize how physiological and genotypic factors modulate response to QMP. Additionally, we have found that modulation of the mating process in honey bee queens alters the pheromone blend that is produced, and workers are responsive to differences in these blends. Finally, we are beginning to address the roots of pheromone-mediated behavior in social insects, by monitoring expression of QMP-regulated genes in other hymenopteran species with different social organizations, to determine if there are common underlying pathways related to queen control.

Ancient rapid radiations of insects: a major challenge for phylogenetics

James Whitfield

University of Illinois, Urbana, IL, United States

The phylogenies of many major groups of insects have been difficult to resolve using either molecular or morphological data, in part due to shortness of time spans between divergences for evolution to occur, and very long time spans after divergences for subsequent evolutionary changes to obscure the earlier ones. Another reason for difficulty in resolving some of the relationships using molecular data is the limited spectrum of genes so far developed for phylogeny estimation. For this latter issue, there is cause for current optimism based on rapid increases in our knowledge of comparative genomics. For morphological studies, fossil evidence has been helpful at times, but some critical periods of insect evolution are more poorly documented than others. Our knowledge of insect fossil history continues to improve and to be more effectively integrated with morphological knowledge of extant taxa and with estimates of divergence times based on molecular data. At least some historical patterns of divergence may, however, continue to defy our attempts to completely reconstruct them with confidence, at least using current strategies.

Does the bumblebee trade have a sting in its tail?

Thomas Ings, Lars Chittka

Queen Mary, University of London, London, United Kingdom

Bumblebees are second only to honeybees in their economic importance as crop pollinators. Increased global demand for bumblebees has been met by year-round production of a limited number of species (4 to 5 out of approx. 250 species). Even though these commercially reared species are targeted towards particular regional markets, there are many cases where importation of bumblebees for pollination involves introducing non-native species. While many bumblebees are used to pollinate crops grown under glass (e.g. tomatoes), they readily escape into the wild, and are increasingly being used to pollinate open field crops (e.g. fruit trees and strawberries). Such observations have lead to a number of concerns being raised about the trade in bumblebees.

Therefore, we examine some of the ecological risks associated with the seemingly indiscriminate movement of non-native bumblebees around the globe. We focus on one of the main commercial species, *Bombus terrestris,* as it has been introduced into countries where it is a non-native genus, species and subspecies. Case studies of bumblebee introductions are used to illustrate three major ecological risks associated with importation of non-native bumblebees: parasites/disease, competitive exclusion and hybridisation.

The evidence presented clearly indicates that the commercial trade in bumblebees does carry a real ecological risk. However, it is important to evaluate how significant that risk actually is before any meaningful recommendations can be made. Therefore, we finish with a discussion on how we might attempt to evaluate, and potentially mitigate, the three major ecological risks associated with importing non-native bumblebees for pollination.

Juvenile hormone in reproductive physiology and behavior of Lepidoptera: Intra- and interorganismal co-ordination

Maciej Pszczolkowski[1], Sonny Ramaswamy[2]

[1]Missouri State University, MO, United States, [2]Purdue University, IN, United States

Traditionally, juvenile hormone (JH) is regarded as a *status quo* factor of metamorphosis. In adults of many species, however, JH is a primary coordinator of reproductive processes. In our paper we present how JH co-ordinates reproduction of a promiscuous lepidopteran female in two ways: during interaction between two conspecifics (JH transfer from male to female) and within the organism of mated female (ovarial patency and egg development upon JH action).

We also address functional and evolutionary aspects of JH action in promiscuous Lepidoptera, and speculate on its contribution to species richness of this order.

Independent gains or reversals of highly eusocial behavior in the corbiculate bees? Visualizing conflict among multiple gene trees

Sydney Cameron

University of Illinois, Urbana, Illinois, United States

Introduction: The corbiculate bees comprise four tribes, three of which represent the major groups of highly social bees, including the stingless bees (Meliponini), bumble bees (Bombini) and honey bees (Apini). Orchid bees (Euglossini), the fourth tribe within the clade, are solitary or communal. Understanding the historical pattern of relationships among these taxa is important for a full understanding of the evolution of highly social behavior in bees. Yet their phylogeny has been a difficult problem to solve. In particular, rooting the corbiculate bee tree has been difficult, even with large numbers of nucleotide characters and multiple outgroups. Thus, the direction of social evolution in the group has been obscure.

Methods: Bayesian analyses of each of 12 nuclear and two mitochondrial gene fragments were run for phylogenetic inference. To visualize the conflict among the gene trees, the filtered supernetwork method was used to extract the most common recurrent phylogenetic signal from a set of taxonomically overlapping gene trees.

Results and Discussion: At mintrees = 6, the supernetwork is already greatly simplified, but still contains some splits that place an outgroup (*Centris*) within the ingroup. At mintrees=9, all reticulation within the network is gone, and the outgroups are seen to root the tree at the base of the Apini + Euglossini split. The most recurrent splits among the 14 gene trees, despite outgroup “noise”, are consistent with previous findings that Meliponini and Bombini are sister taxa, with the relationships still uncertain for Apini and Euglossini.

Wolbachia effects on insect hosts: evolving from a symbiont to a mutualist

Ary Hoffmann, Andrew Weeks

The University of Melbourne, Melbourne, Victoria, Australia

Wolbachia commonly spread through host insect populations by causing cytoplasmic incompatibility, often expressed as reduced egg hatch when uninfected females mate with infected males. Infected females are frequently less fecund as a consequence of Wolbachia infection. However, theory predicts that because of maternal transmission, these ‘‘parasites’’ will tend to evolve towards a more mutualistic association with their hosts. In *Drosophila simulans* in California, which represents the classic case of a *Wolbachia* infection spreading in nature, cytoplasmic incompatibility allowed the infection to spread through individual populations within a few years and from southern to northern California (more than 700 km) within a decade, despite reducing the fecundity of infected females by 15%–20% under laboratory conditions. Here we show that the Wolbachia in California *D. simulans* have changed over the last 20 y so that infected females now exhibit an average 10% fecundity advantage over uninfected females in the laboratory. The data demonstrate that fecundity-increasing Wolbachia variants are currently polymorphic in natural populations but the variants exhibiting a fecundity advantage are expected to become fixed over time.

Wolbachia effects on insect hosts: evolving from a symbiont to a mutualist

Ary Hoffmann, Andrew Weeks

The University of Melbourne, Melbourne, Victoria, Australia

Wolbachia commonly spread through host insect populations by causing cytoplasmic incompatibility, often expressed as reduced egg hatch when uninfected females mate with infected males. Infected females are frequently less fecund as a consequence of Wolbachia infection. However, theory predicts that because of maternal transmission, these ‘‘parasites’’ will tend to evolve towards a more mutualistic association with their hosts. In *Drosophila simulans* in California, which represents the classic case of a *Wolbachia* infection spreading in nature, cytoplasmic incompatibility allowed the infection to spread through individual populations within a few years and from southern to northern California (more than 700 km) within a decade, despite reducing the fecundity of infected females by 15%–20% under laboratory conditions. Here we show that the Wolbachia in California *D. simulans* have changed over the last 20 y so that infected females now exhibit an average 10% fecundity advantage over uninfected females in the
laboratory. The data demonstrate that fecundity-increasing Wolbachia variants are currently polymorphic in natural populations but the variants exhibiting a fecundity advantage are expected to become fixed over time.

Predicting the ability of insets to counter the effects of climate change through adaptation

Ary Hoffmann, Michael Kearney

The University of Melbourne, Melbourne, Victoria, Australia

Shifts in the distribution, abundance and phenology of invertebrate species in response to climate change are now well documented in the literature, particularly in Europe. In Australia climate envelope models predict changes in the distribution of many invertebrates including pests and threatened species currently restricted to high elevation sites. Yet insects and other invertebrates have the potential to counter the effects of climate change through physiological acclimation and through evolutionary adaptation. There are now several examples of evolutionary shifts taking place in response to climate change in flies and mosquitoes. Patterns of clinal variation highlight the potential of many widespread insect species including pests to evolve. New mechanistic models that consider the way environmental conditions predict the growth and reproduction of organisms can accurately incorporate the potential for adaptation and evolution. These models when coupled with quantitative genetic information can be used to accurately assess distribution and shifts persistence of threatened populations under climate change.

Attraction of male vine mealybug to the female structurally related pheromone components

Anat Zada, Hofit Kol-Mimon, Ezra Dunkelblum, Fabienne Assael, Alex Protasov, Zvi Mendel

Department of Entomology, Volcani Center, ARO, Bet Dagan 50250, Israel

Introduction: The vine mealybug (VM) *Planococcus ficus* (Signoret) is a worldwide pest, mainly of grapevine and figs. Two pheromone components, (*S*)-lavandulyl senecioate and (*S*)-lavandulyl isovalerate were identified in Israel from VM reared for several generations on potato sprouts, while in California only (*S*)-lavandulyl senecioate and (*S*)-lavandulol were identified.

Methods: Enzymatic separation of racemic lavandulol enabled us to assess the response of VM males in the field to the two enantioenriched pheromone components and lavandulol.

Results: A positive correlation between peak mealybug density and male capture was observed using racemic lavandulyl senecioate as bait, strengthening the usefulness of the pheromone traps for monitoring the pest. However, addition of racemic or the two enantiomers of lavandulyl isovalerate to lavandulyl senecioate decreased the capture of VM males in the field, while in the lab, this component attracted males. Both enantiomers of lavandulyl isovalerate displayed the same antagonistic activity. The addition of (*S*)-lavandulol to the pheromone resulted in shut-down of the traps while inhibition by its antipode, (*R*)-lavandulol, was moderate indicating a certain degree of chiral discrimination.

Conclusions: Racemic lavandulyl senecioate can be used for field work since the unnatural enantiomer of lavandulyl senecioate is benign and does not affect the activity of the pheromone. Recently, we found that in some vineyards males are also attracted to lavandulyl isovalerate, indicating the existence of VM pherotypes in the field.

The role of competition in structuring an insect metacommunity on oak (*Quercus robur*)

Ayco Tack, Sofia Gripenberg, Tomas Roslin

University of Helsinki, Helsinki, Finland

Introduction: Herbivore densities in nature are generally very low, perhaps reflecting the importance of indirect interactions mediated by the host-plant. To test this hypothesis, we investigate the relative importance of direct and indirect interactions in structuring the herbivore community on the pedunculate oak (*Quercus robur*).

Methods: We address indirect interactions at different spatial and temporal scales, and among both herbivorous insects and a pathogenic fungus. Experimental work on the strength of interactions is combined with observations on spatiotemporal patterns of co-occurrence of different taxa in nature.

Results: Both direct and indirect interactions among leaf-mining species seem to result in slightly elevated mortality rates. Nevertheless, the species do not seem to repel each other: long-term surveys reveal that leaf miners occur more often than predicted by chance on the same leaf, shoot, branch and tree.

Conclusions: This study does not support any major role for direct and indirect interactions in shaping local insect densities or local community structure. While such effects are certainly present, they do not seem strong enough to leave any significant imprint on what species occur where and at what densities. In contrast, there appears to be a strong role for spatial processes in shaping the structure of local insect communities.

The legacy of Melrose Highlands: Parasitoid drift and its unintended consequences for lepidopteran diversity in New England forests

Dylan Parry[1], George Boettner[2], Jennifer Selfridge[1], Brian Hoven[1], Joseph Elkinton[2]

[1]State University of New York, College of Environmental Science and Forestry, Syracuse, New York, United States, [2]University of Massachusetts, Amherst, Massachusetts, United States

Introduction: Decline and extirpation of numerous giant silk moth species (Saturniidae) has been apparent for several decades in New England. Several explanations have been proposed, but a seminal study [Boettner et al. (2000), Conservation Biology] strongly implicated an exotic parasitoid, *Compsilura concinnata*, introduced a century ago to control burgeoning gypsy moth populations in Massachusetts. To determine how robust these results were, we experimentally established populations of several additional lepidopterans within and outside of Massachusetts and quantified mortality.

Methods: Parasitism by *C. concinnata* was assessed in experimental populations of four saturniids (*Hemileuca maia*, *Anisota senatoria*, *Antheraea polyphemus*, *Callosamia promethea*) and a notodontid, *Datana ministra*. The saturniid experiments were conducted at multiple sites in both Massachusetts and New York.

Results: Parasitism of *A. polyphemus* and *C. promethea* by *C. concinnata* was very high in Massachusetts, validating the results of Boettner et al. (2000) but was significantly lower in New York, suggesting limitations to this hypothesis. For *H. maia* and *A. senatoria*, parasitism was low in both regions indicating that alternative single-factor or interactive mechanisms may be driving populations declines. Finally, parasitism in the gregarious notodontid *D. ministra* was very high suggesting that the effects of this parasitoid need to be assessed in other less charismatic lepidopterans.

Conclusions: *Compsilura concinnata* plays an important role in the decline of native macrolepidopterans in northeastern North America but high regional variance in its parasitism suggest that it is unlikely to be the only factor underlying the decline of this biodiversity.

Local ecological effects on the rate of spread of Argentine ants: Interspecific behavioral interactions and aggregation sites

Deborah M Gordon, Katherine Fitzgerald

Stanford University, Stanford, CA, United States

Introduction: The Argentine ant, *Linepithema humile*, is invasive in Mediterranean climates worldwide, with substantial ecological impact on native arthropod and plant communities. The factors that determine its rate of spread are not well understood. Argentine ants are seasonally polydomous, aggregating in the winter and dispersing into many nests linked by trails, in the summer. A colony, or set of connected nests, occupies about 200 m2 in northern California. Previous work suggests that the native winter ant, *Prenolepis imparis*, is one of few native species that effectively resists elimination by the Argentine ant. Both the Argentine and winter ants nest at the base of woody plants and tend scale insects to consume their honeydew.

Methods: We have monitored the distribution of Argentine and native ants in a 500-ha preserve in northern California for 15 years. Observations and experiments examined competition between *L. humile* and *P. imparis* and the formation of new colonies.

Results: Survey results show that competition between Argentine and winter ants is intense at the edge of the invasion front, where the distribution of ants at many sites alternates between the two species. We will discuss how priority of access to foraging area, and seasonal factors, influence the distribution of the two species, and how the availability of winter aggregation sites affects the rate of formation of new clusters of associated nests, or colonies.

Conclusions: The availability of sites for new colonies, and the dynamics of interspecific competition, influence the rate of spread of Argentine ant invasions.

Consequences of environmental change and globalization for *Dendroctonus valens* and its fungal symbionts: A case study

Nancy Gillette, Jianghua Sun, Donald Owen, Min Lu, Mike Wingfield, Diana Six, Xudong Zhou

USDA FS, PSW Research Station, Berkeley, California, United States

Dendroctonus valens and its fungal symbionts may become globally catastrophic as invasives riding a tide of climate fluctuation. *D. valens,* native to North America, is a polyphagous subcortical feeder adapted to collecting fungal spores; it is difficult to control using biological, cultural, insecticidal, or behavioral insect pest management methods. It feeds on all pine species within its range, where it vectors *Leptographium terebrantis* and related fungi to its hosts. It was accidentally introduced into China, where feeds on all pines with which it has come into contact, and is now expanding its range there. There are no apparent barriers to its spread westward across Eurasia, where there is a continuous, transcontinental corridor of pines. In addition, *D. valens* in North America has already acquired a European species of *Leptographium* from a beetle introduced from Europe, and is expected to acquire more new associations as it expands its Asian range. The consequences of these new associations for native and exotic pine forests are difficult to predict, but even in the absence of such new associations *D. valens* is expected to become a more serious pest with warmer and dryer global climates. In an effort to respond to these potentially disastrous new associations, we have embarked upon an international collaboration to characterize the existing *D. valens*/fungal symbioses using molecular methods to build a baseline of information so that future new associations can be more rapidly detected. This case study may provide a useful model for other new beetle/fungal associations.

Conserving narrow range endemic insects in the face of climate change: Options for some Australian butterflies

Timothy New

La Trobe University, Melbourne, Victoria, Australia

Many southern hemisphere butterflies of conservation interest appear to be 'point endemics' or 'narrow range endemics', and vulnerable because of ecological specialisation and poor dispersal capability or opportunity. Short–term, site-focused conservation efforts, however successful they may be, do not cater for range alterations likely to occur with climate change. Greater attention to assessing potential future distributions of such species along ecological gradients, predominantly of latitude and altitude, may help to counter this lack by selecting sites for translocations to be made decades or more into the future. Consideration of such assisted colonisations for selected species may be a worthwhile addition to current conservation planning, with the possible options differing according to the species' current distribution pattern within the possible range.

Some possibilities for this approach are discussed, using examples from narrow range endemic butterflies in Australia. Such long-term strategies pose formidable problems in logistics and regulation, and may not be practicable widely. Designing and including conservation on this extended temporal scale, however, may help to focus current conservation efforts for wider beneficial effects.

Comparing Argentine (*Linepithema humile*) to big-headed (*Pheidole megacephala*) and native ants in their interactions with an extrafloral nectary plant: Who benefits?

Lori Lach[1], Richard J. Hobbs[1], Jonathan D. Majer[2]

[1]Murdoch University, Murdoch, WA, Australia, [2]Curtin University of Technology, Bentley, WA, Australia

Though Argentine ants (*Linepithema humile*) are strongly attracted to carbohydrate-rich resources, few studies have investigated relationships between Argentine ants and plants with extrafloral nectaries (EFNs). We compared benefits conferred upon and received from the EFN plant *Acacia saligna*, among Argentine ants, the invasive big-headed ant (*Pheidole megacephala*), and native ants. Twelve pairs of *A. saligna* were planted in each of eight urban bushland sites: two with Argentine ants, two with big-headed ants, and four matched nearby uninvaded sites. Argentine ants were observed on 83-92 %, big-headed ants on 30-80%, and native *Iridomyrmex* spp. on 58-92% of plants in their respective sites. Trophobionts were only observed in sites with native ants. In sites with Argentine and big-headed ants, ant-allowed trees grew more phyllodes and branches than their paired ant-excluded trees, but these differences were not seen in sites with native ants. In laboratory experiments, we compared worker survival of Argentine, big-headed, and native *Iridomyrmex chasei* workers exposed to herbivorized or non-herbivorized *A. saligna* or controls. Ants given herbivorized plants had 7-11 times greater worker survival relative to unfed ants, but there were no differences in survival among the three ant species exposed to the same treatments. Ants with access to non-herbivorized plants had the same survival as unfed ants. Results suggest that the invasive Argentine and big-headed ants are more beneficial to *A. saligna* growth than native *Iridomyrmex*, possibly due to the native ants' mutualistic relationships with trophobionts on the plants; however, all three taxa can benefit from *A. saligna* extrafloral nectar.

Circatidal rhythm of locomotor activity in the mangrove cricket *Apteronemobius asahinai*

Aya Satoh[1], Eiji Yoshioka[2], Hideharu Numata[3]

[1]University of the Ryukyus, Okinawa, Japan, [2]Kobe Yamate University, Kobe, Japan, [3]Osaka City University, Osaka, Japan

Introduction: Mangrove forests are influenced by tidal flooding and ebbing with a period of about 12.4 h (tidal cycle). Mangrove crickets (*Apteronemobius asahinai*) forage on mangrove forest floors during low tide and rest on stems during high tide. The endogenous rhythm in their locomotor activity was examined.

Methods: Locomotor activity was recorded under constant darkness (DD) for 25 days and under a 12-h light/12-h dark cycle (LD) for the subsequent 22 days for 24 collected males, and under LD for 14 days and under DD for the subsequent 12 days for 18 collected males. The temperature was maintained at 25ºC.

Results: Under DD, most crickets showed a clear bimodal daily pattern in their locomotor activity for at least 24 days; the active phases of about 10 h alternated with inactive phases of about 2 h. The free-running period was 12.56 ± 0.13 h (mean ± SD, n = 11). Under LD, the activity was not entrained by the light–dark cycle; the bimodal rhythm was expressed in the scotophase but suppressed in the photophase. This endogenous rhythm was assumed to be a circatidal rhythm. On the other hand, the activity under constant darkness subsequent to a light-dark cycle was more intense in the active phase continuing from the scotophase than from the photophase of the preceding light–dark cycle; This indicates the presence of circadian components.

Conclusions: Two clock systems, i.e. circatidal and circadian, are involved in controlling locomotor activity in mangrove crickets.

Conservation of biodiversity using shelterbelts: consequences for biological control at local and landscape scales

Sagrario Gamez-Virues[1], Geoff Gurr[2], Anantanarayanan Raman[2], David Perovic[3], Helen Nicol[2]

[1]Pest Biology and Management Group, The University of Sydney, Orange, New South Wales, Australia, [2]E. H. Graham Centre for Agricultural Innovation, Charles Sturt University, Orange, New South Wales, Australia, [3]Pest Biology and Management Group, Charles Sturt University, Orange, New South Wales, Australia

Introduction: As a result of biodiversity lost from farmlands, shelterbelts and related non-crop habitats have become the main refuge and source of food for wildlife. This study investigated the effects of shelterbelt characteristics and landscape elements on the abundance and activity of arthropods within shelterbelts and adjacent pastures, both types of perennial crop.

Methods: Pitfall and sticky traps were used to assess diversity of arthropods within 18 shelterbelts of different plant diversity and habitat structure. Arthropods were also collected along transects from shelterbelts to adjacent pastures using vacuum sampling. Predation of pest arthropods was measured using sentinel baits along the same transects. Generalised linear models were used to analyse data. Area covered by isolated trees, cropped trees and dams, at three landscape scales, were also included in the analysis.

Results: Effects of plant diversity and habitat structure on the abundance of arthropods varied between species. However, diversity of arthropods was not significantly different between shelterbelts when using Shannon's diversity index. The abundance of minute parasitic wasps such as Mymaridae (2 spp.) and Trichogrammatidae (1 sp.) decreased when the distance from shelterbelts increased, but the abundance of other arthropods such as Aeolothripidae (1 sp.) and Formicidae (1 sp.) increased. Predation of pest arthropods significantly decreased with increasing distance from shelterbelts. Effects of landscape elements on the abundance of arthropods varied between species.

Conclusions: Shelterbelts offer the possibility to improve biological control of arthropods that attack trees and adjacent crops via manipulation of plant diversity and habitat structure.

Studies on the reproductive capacity and intraspecific competition of *Holepyris sylvanidis* (Hymenoptera: Betylidae), a larval parasitoid of *Tribolium confusum*

Cornel Adler, Cornelia Frielitz

JKI, OPV, Berlin, Germany

Introduction: *Holepyris sylvanidis* (BRETHES 1913) is a parasitoid on larvae of *Tribolium confusum*. The present study was carried out to gain information for mass cultivation.

Methods: 1-5 up to 4 d old mated females were placed into a plastic petri dish (diam. 55 mm) together with 5 larvae of *T. confusum* and hollow wheat grains for shelter at 25°C and 55 % r.h. After 24 h the females were transferred to fresh larvae and grains. The total experimental time was 4 d or covered the lifetime of females.

To determine the optimum number of hosts, a batch of 5, 10, 15 or 20 *T. confusum* larvae and hollow wheat grains were offered to one mated female in a plastic petri dish. Twice weekly the larvae and grains were replaced, the experiment was carried out for three weeks.

Results: With 1.6 eggs per day and female the highest oviposition rate was achieved when a single female was kept in the petri dish. This value dropped to 0.9 with two females and 0.4 with five females. Up to 52 eggs were laid per female in the presence of a male.

The highest number of eggs was laid with 10 larvae and wheat kernels present at a time. Within one week (and a total of 20 larvae offered) an average of 9.5 eggs was laid per female.

Conclusions: *H. sylvanidis* is a promising candidate to suppress mass development of *T. confusum* in the grain industry.

Studies on the reproductive capacity and intraspecific competition of *Holepyris sylvanidis* (Hymenoptera: Betylidae), a larval parasitoid of *Tribolium confusum*

Cornel Adler, Cornelia Frielitz

JKI, OPV, Berlin, Germany

Introduction: *Holepyris sylvanidis* (BRETHES 1913) is a parasitoid on larvae of *Tribolium confusum*. The present study was carried out to gain information for mass cultivation.

Methods: 1-5 up to 4 d old mated females were placed into a plastic petri dish (diam. 55 mm) together with 5 larvae of *T. confusum* and hollow wheat grains for shelter at 25°C and 55 % r.h. After 24 h the females were transferred to fresh larvae and grains. The total experimental time was 4 d or covered the lifetime of females.

To determine the optimum number of hosts, a batch of 5, 10, 15 or 20 *T. confusum* larvae and hollow wheat grains were offered to one mated female in a plastic petri dish. Twice weekly the larvae and grains were replaced, the experiment was carried out for three weeks.

Results: With 1.6 eggs per day and female the highest oviposition rate was achieved when a single female was kept in the petri dish. This value dropped to 0.9 with two females and 0.4 with five females. Up to 52 eggs were laid per female in the presence of a male.

The highest number of eggs was laid with 10 larvae and wheat kernels present at a time. Within one week (and a total of 20 larvae offered) an average of 9.5 eggs was laid per female.

Conclusions: *H. sylvanidis* is a promising candidate to suppress mass development of *T. confusum* in the grain industry.

Simulating causes and remedies for spider mite outbreaks in Canadian apple orchards

John Hardman[1], Wopke Van der Werf[2], Jeff Franklin[1]

[1]Atlantic Food and Horticulture Research Centre, Agriculture and Agri-Food Canada, Kentville, Nova Scotia, Canada, [2]Crop and Weed Ecology, Plant Sciences Department, Wageningen University, Wageningen, Netherlands

Introduction: In Nova Scotia, Canada, successful biological control of the European red mite, *Panonychus ulmi,* by the phytoseiid predator, *Typhlodromus pyri*, was soon followed by outbreaks of the two-spotted spider mite, *Tetranychus urticae*.

Methods: A combination of simulation modelling and orchard experiments were used to explore causes of outbreaks and to assess potential remedies (cultural, biological and chemical controls). The model is a modified Leslie matrix, which simulates the effects of weather, pesticides applications, immigration of mites into trees, and predation on the dynamics of *T. urticae* and *T. pyri* in apple trees.

Results: Orchard trials and simulations indicated that warm weather, higher rates of *T. urticae* immigration from the ground cover, and application of pesticides toxic to phytoseiids all contribute to rapid growth of *T. urticae* populations in trees. A major predisposing factor for outbreaks was the near absence in the tree canopy of *Neoseiulus fallacis,* an effective predator of *T. urticae*, likely because of competition from *T. pyri*. Furthermore, simulations indicated that failure of *T. pyri* to aggregate in prey patches greatly reduces the effectiveness of this predator. Also application of non-selective acaricides, those less toxic to *T. urticae* than to phytoseiids and to *P. ulmi*, the preferred prey of *T. pyri*, can actually worsen outbreaks.

Conclusions: Remedies suggested by the model include managing ground cover vegetation so as to minimize *T. urticae* immigration into trees and properly-timed application of selective acaricides, which are more toxic to *T. urticae* than to *P. ulmi* and phytoseiids.

Phenology of the European spruce bark beetle (*Ips typographus* (L.) (Coleoptera: Scolytidae) as the basis for modelling outbreak risk assessment in Triglav National Park, Slovenia

Maja Jurc, Nikica Ogris

University of Ljubljana, Biotechnical Faculty, Department of Forestry and Renewable Forest Resources, Ljubljana, Slovenia

Introduction: Large scale sanitary fellings due to spruce bark beetles (mostly *I. typographus*) were carried out in 1986/1987 and have increased since 1999; in 2003/2004 populations greatly increased in all parts of Slovenia. We developed a model of population dynamics and phenology of *I. typographus* for outbreak risk assessment as a tool for spruce bark beetle management in mountainous parts of Slovenia.

Methods: The research area was in a 130 years old forest community *Aposeri-Piceetum* on the plot of an intensive monitoring programme in Slovenia's Triglav National Park, 1397 m a.s.l.. We measured temperatures and moisture (T button, H button, Dallas Semioconductor) under the bark of old Norway spruce trees that were felled and left in stand gaps, from Feb. 2007 to Feb. 2008. We systematicaly collected 200×200 mm squares of bark from the felled trees and through analysis of bark beetles galleries we tracked spring swarming, start of parental, sister and filial generations, and brood development, as well as the beetle's natural enemies; we isolated entomopathogenic fungi from the beetles. We also collected data about direct solar radiation and other GIS data relevant to the research area. We developed a model using an M5' regression tree for better understanding of the complex ecological interactions involved in bark beetle outbreaks.

Results: The most important factor for brood development is the temperature under the bark, which changed drastically during the year, as well as during the day, and depended strongly on the position where measurements were taken on the log. We also found out that there is a significant influence of entomopathogenic fungi on the development of the beetles analyzed.

Conclusions: These modelling procedures can be used for simulation of the developmental stages of bark beetles if accurate data about their biology and phenology are available. A risk assessment of outbreaks, in combination with retrospective analysis of population dynamics, a topoclimatic model, and spatial visualization of the potential development and associated risks of *I. typographus* outbreaks, can be a useful tool for spruce bark beetle management in mountainous parts of Slovenia.

Humanity hastens host expansion: the autumn gum moth as an Australian example

Martin Steinbauer[1], Fredrik Östrand[2]

[1]Department of Zoology, La Trobe University, Melbourne, Victoria 3086, Australia, [2]Department of Ecology, Lund University, Lund SE-223 62, Sweden

Introduction: In the 1960s foresters identified *E. globulus* and *E. nitens* as preferred for pulpwood production and began greatly extending both species' geographic range. Coincidentally, both species are preferred hosts of the autumn gum moth, *Mnesampela privata* (Geometridae). Since then, *M. privata* has gone from uncommon to outbreak species and expanded its host range in the wild.

Methods: Field observations of oviposition on different species and families of eucalypts and generational changes in body weight were conducted in two experimental arboreta. These data were supplemented with laboratory bioassays of oviposition preference and larval survival and analyses of physical and chemical traits of leaves of different species and families of eucalypts.

Results: In both arboreta, the numbers of eggs on preferred and novel hosts increased between parent and offspring generations. This coincided with an increase in the weight of females between consecutive moth seasons. Field and laboratory studies revealed that females would oviposit on novel hosts if foliar monoterpenes and epicuticular waxes were comparable to those of preferred hosts. Some larvae pupated on all novel hosts tested with one exception (*Corymbia eximia*). Larval mortality was high on novel hosts whose leaves contained high concentrations of sideroxylonal as well as high concentrations of monoterpenes. These hosts may present larvae with toxic loads greater than those ingested when eating *E. globulus* or *E. nitens*. Only high leaf toughness was universally detrimental to larvae but such leaves are usually avoided by females.

Conclusions: Synchronicity of time of planting provides a superabundance of the leaf type (juvenile) preferred for oviposition. Plantations of non-endemic hosts sustain atypically large populations and facilitate generational increases in fitness. The dispersal of numerous, highly fecund females from localised outbreaks creates greater opportunities for oviposition on less preferred families and species growing near plantations. Exaptation of larvae for ubiquitous eucalypt secondary metabolites means that some will eclose on novel species only somewhat similar to *E. globulus* and *E. nitens*. Whether or not host races have arisen is unknown but the potential for further host expansion continues to grow.

The contribution of ecological insights to pest management of the larger grain borer *Prostephanus truncatus* (Coleoptera: Bostrichidae) in Africa

Rick Hodges

Natural Resources Institute, Chatham Maritime, Kent, ME4 4TB, United Kingdom

Prostephanus truncatus arrived in Africa from meso America in the late 1970s. It was a new beetle pest of stored maize grain and dried cassava roots with a distinctly different ecology and behaviour from the more familiar storage insects. It also caused much greater storage losses.

The development of pheromone traps for *P. truncatus* soon demonstrated that the pest was unusual in having major populations away from stores on woody hosts in the bush. Evidence that greater numbers of beetles dispersing by flight increased the likelihood of stores becoming infested emphasised the importance of large populations in the bush as a source of infestation of stored products; an apparently unique situation for a storage pest. This finding supported the use of a predatory histerid, *Teretrius nigrescens*, as a classical biological control agent. Although this predator is relatively ineffective in reducing the pest in infested stores, it offers considerable benefits by limiting populations in the bush and consequently lowering the scale of cross-over from the bush into stores.

The pest shows strong inter-annual variation in flight activity and a rule-based model has been developed to predict flight activity using climatic variables. Warning of years with higher flight activity indicate when there is greater risk of *P. truncatus* attack and this can be used to alert farmers to take pest management action before food losses become significant.

The effect of a blood meal on insecticide resistance in *Anopheles funestus*

Belinda Spillings, Lizette Koekemoer, Basil Brooke

Vector Control Reference Unit, National Institute for Communicable Diseases, NHLS;; Division of Virology and Communicable Disease Surveillance, School of Pathology of the National Health Laboratory Se, Sandringham, Johannesburg, South Africa

Introduction: Insecticide resistance has been detected in the southern African malaria vector *Anopheles funestus*, raising concerns for current vector control programs. At present, indoor residual spraying (IRS) using DDT and pyrethroids is an effective method for reducing the numbers of malaria vectors in South Africa. However, the portion of the population most affected by IRS is the blood feeding females, which is responsible for the transmission of malaria.

It has been suggested that blood fed females are able to tolerate higher levels of insecticide due to their increased body weight (vigor tolerance). Furthermore, the process of blood digestion activates a suite of enzymes responsible for detoxifying potentially toxic compounds present in the blood. We hypothesized that this period of increased detoxification could result in increased levels of insecticide resistance.

Methods: Cohorts of *An. funestus* females were divided into blood fed and unfed groups and exposed in Permethrin coated glass bottles. The blood fed group were given a blood meal 4 hours prior to exposure. Percent mortality was scored 24 hours post exposure and statistical analyses carried out.

Results: Our data shows that a significant increase in insecticide tolerance occurs in blood fed females from a pyrethroid resistant strain of *An. funestus.* A comparison of blood fed and unfed females from a fully insecticide susceptible *An. funestus* strain did not show any significant increase in insecticide tolerance.

Conclusions: The elevated level of resistance detected in blood fed females of the insecticide resistant strain suggests that the resistance mechanism may be directly enhanced by detoxification processes that are stimulated by the presence of the blood meal. These increased levels of resistance are currently being quantified through molecular techniques such as qPCR and microarrays.

Immunity and insect social systems

Rob Knell[1], William Hughes[2]

[1]Queen Mary, University of London, London, United Kingdom, [2]University of Leeds, Leeds, United Kingdom

Intuitively, we expect disease incidence and therefore investment in immunity to be greater in social than in solitary insects, because the increased contact rates with conspecifics in social groups will lead to higher transmission rates. Theory disagrees, however, suggesting that reduced contact rates between social groups can counter the increased contact rates within groups, leading to lower disease incidence in social species. A review of empirical data finds support for both points of view. We discuss the relationship between social system and contact rates in detail, and propose that the relationship between immunity and sociality will depend on the details of the social systems in question. In particularly, the longevity of the groups and the movement patterns of the animals in the groups will vary between different types of social insect and will have a pronounced effect on the patterns of disease incidence and therefore immune investment.

Period gene plays a role in circadian rhythm and photoperiodism in crickets

Kenji Tomioka, Yoshiyuki Moriyama, Tomoaki Sakamoto

Okayama University, Okayama, Japan

Introduction: Periodic expression of clock genes is now believed to be an essential part of the circadian clock in *Drosophila* and the circadian clock has been hypothesized to be involved in insect photoperiodism. However, these are still to be examined. In this study we investigated the role of *per* gene in circadian rhythm generation and photoperiodism using two cricket species, *Gryllus bimaculatus* and *Modicogryllus siamensis.*

Method:.We measured *per* mRNA levels with quantitative real time RT-PCR and knocked-down *per* mRNA levels by injecting *per* double-stranded RNA (dsRNA).

Results: In *G. bimaculatus*, *per* mRNA levels in the optic lobe showed a rhythmic expression both in light/dark cycles and in constant darkness (DD), with a peak in the late day to early night. Knocking-down of the *per* mRNA levels mostly resulted in a loss of circadian locomotor rhythms. The electrical activity of optic lobe efferents also became arrhythmic in the *per* dsRNA treated crickets. We next examined the role of *per* in the photoperiodic regulation of nymphal development in *M. siamensis*. We collected the eggs laid by *per* dsRNA injected females and examined development of the nymphs hatched from the eggs under long-day or short-day conditions. Under both photoperiodic conditions, the nymphs showed an adult emergence pattern neither for those of long-day nor for short-day conditions but similar to those kept in DD conditions.

Conclusion: These results strongly suggest that *per* plays an important role not only in the circadian rhythm generation but also in the photoperiodic time-measurement in the crickets.

An early-warning system for *Heteronychus arator* Fabricius (Coleoptera: Scarabaeidae)

Thomas Drinkwater

ARC-Grain Crops Institute, Potchefstroom, South Africa

H. arator adults that emerge from pupal cells during late summer and autumn overwinter as adults in maize fields and damage maize seedlings during the following spring. By capturing adult black maize beetles (BMB) during February to April in light traps and entering these numbers into a mathematical model, the size of the subsequent spring population could be estimated and used as an early-warning system. The occurrence of two severe pest outbreaks over the past six decades, namely in the late 1940's and late 1970's was also incorporated into the model. During February to April of the latter period more than 72 000 adults were captured in a single light trap in the affected area. This is the magnitude that could be considered an outbreak. Following this period a limited number of light traps were placed in the Heidelberg area, which provided sufficient data to successfully advise producers in that region for nine consecutive years. This advisory service was expanded in 2002 to include producers in all affected areas by placing light traps in a quarter degree grid pattern over the whole area. An inverse distance-weighted analysis with four nearest-neighbouring localities was done with the *Arcview 3.2* computer programme, based on the actual number of beetles captured every year at each locality. BMB has now been monitored through this early-warning system for 16 years. Lately the seasonal mean number of adults captured fluctuated between 190 and 2 150, which remains far below the levels expected to cause an outbreak. Producers were continuously advised accordingly and could therefore save up to R110/ha every year.

Evolutionary origins and local adaptations of a novel host-plant detoxification gene in butterflies

Hanna Fischer[1], Christopher Wheat[2], David Heckel[1], Heiko Vogel[1]

[1]Max-Planck-Institute for Chemical Ecology, Jena, Germany, [2]Pennsylvania State University, PA, United States

Introduction: The interactions between plants and their specialist insect herbivores provide an excellent opportunity to study the evolution of species interaction on a molecular level. Here we investigate a novel detoxifying enzyme (Nitrile-specifier Protein: NSP) in the butterfly family Pieridae. NSP redirects the hydrolysis of plant chemical defense glucosinolates to nitriles rather than toxic isothiocyanates in caterpillar guts, enabling them to feed on plants in the order Brassicales. The appearance of NSP coincides with the emergence of the Brassicales family and was followed by significantly increased diversification rates identifying NSP as a key evolutionary innovation.

Methods: Generation of cDNA libraries and genomic data sets allowed us robust phylogenetic analysis. Population studies on four wild *P. rapae* populations permitted us concluding on population structure of this butterfly species and on selection pressure acting on NSP.

Results: We found NSP to be a member of an insect specific gene family we characterized and named NSP-like gene family. Members of this family can be found across insecta. The NSP-like gene family evolution is a dynamic, ongoing birth death process. NSP and its ortholog are still subject to high rates of change, reflecting dynamic properties and possible adaptation to their plant counter part.

Conclusions: We have generated a broad sketch of the evolutionary origins and ongoing selection pressures of an adaptive trait, which facilitated an ecologically important host shift and the diversification of the Pieridae butterfly family. We provide direct evidence that gene duplication is one of the driving forces for speciation and adaptation.

The evolution of control strategies for trypanosomiasis and tsetse flies (*Glossina* spp.) in Africa (1908-2008)

Charles Kyorku

University for Development Studies, Northern Region, Ghana

Trypanosomiasis is a protozoan disease transmitted by blood sucking tsetse flies (*Glossina* spp.) in man and other vertebrate animals in sub -Saharan Africa. Owing to its debilitating and fatal effects on man and his animals, especially cattle, it is one of the major constraints on socio-economic development in the region.

The importance of this disease was realized by the colonialists at the turn of the 20th century. Since then various strategies have been employed to mitigate the situation. These included chemo-therapeutic and chemo-prophylactic treatment infections and attacks on the vector populations including vegetation (habitat), wild host (food source) destruction and insecticidal spraying of vector populations. The paper reviews the gradual changes in the control strategies for this disease over the century

For the first half of the century, the results of control campaigns have varied widely from total failure in most places to limited success in a few. To a large extent, this was due to the fact that there was very little knowledge on the biology, ecology and behaviour of the whole vector-parasite-host relationship.

The failure of insecticides, especially DDT, to achieve permanent control and other drawbacks, prompted scientists to intensify research into finding more acceptable, sustainable and long-lasting alternative control strategies.

Thus, over the past fifty years scientists have put in concerted efforts to achieve this. Today efficient odour-baited attracting mechanical killing devices have been developed. These have proved, through community based pilot control projects, to be very effective in drastic reduction of vector populations and hence disease prevalence. The one problem encountered by most of these small scale projects is reinvasion of the control areas by tsetse from neighbouring populations.

In the light of above, the African Union (AU) has formulated a policy for adoption by all African countries for the eradication of tsetse and trypanosomiasis – The African Tsetse and Trypanosomiasis Eradication Campaign. (PATTEC). The programme was launched in 2007 in many parts of Africa including Ghana.

The prospects for this giant undertaking are discussed.

Habitat manipulation in cotton IPM: Host plant utilization, host sequence, and host preference of *Lygus hesperus*

Megha N. Parajulee

Texas AgriLife Research and Extension Center, Lubbock, Texas, United States

A comprehensive research on ecology and behavior of *Lygus hesperus* (Hemiptera: Miridae) has been conducted at the Cotton Entomology Program Laboratory in Lubbock, Texas, USA, for the last seven years, with a focus on quantifying the biological parameters in relation to host plant utilization, non-cotton host plant sequence, and host preference affecting the likelihood of *Lygus* damage severity in cotton in vulnerable stages. The presentation will examine a multi-year regional survey work that elucidates the habitat complexity and intercrop relationship in *Lygus* movement between cotton and non-cotton hosts. Field surveys showed that several non-cotton hosts (alfalfa, Russian thistle, pigweed, sunflower, and grain sorghum) serve as sink for *Lygus* during the early summer months while *Lygus* move to adjacent cotton when these alternate host sources senesce or are less favorable for *Lygus*. Laboratory studies also showed that nymphal development and survivorship were better in non-cotton hosts compared with that in cotton fruits, particularly the young bolls. Immunological assays of field-marked *Lygus* also indicate that the non-cotton hosts such as alfalfa may serve as both sink and source for *Lygus* depending on the phenological stages of these hosts. Large, regional research is currently underway in the western United States to develop a predictive model to estimate *Lygus* severity in cotton fields as a function of non-cotton host plant diversity based on a source-sink relationship with cotton.

Commercial use of transgenic crops, their effect on biodiversity and natural enemies

Graham Head

Monsanto Company, St Louis, Missouri, United States

Over the past 11 years, the use of transgenic crops has grown dramatically, and now exceeds 100 million hectares on a global basis with substantial adoption in both developed and developing countries. Corn, soybeans, cotton and canola make up most of this area, and the most commonly used traits are insect resistant and herbicide tolerance. Over the past five years, the use of transgenic crops with multiple traits has grown particularly rapidly. This rapid adoption has brought many changes to agricultural systems, including significant changes and reductions in conventional insecticide use, reductions in tillage, and changes in cropping practices. In addition, ecological changes have occurred in these agro-ecosystems, with apparent suppression of a number of major plant pests through direct and indirect effects of the transgenic traits, increases in some important natural enemy populations, and flare-ups of several previously uncommon pest species. The reasons for these changes and their implications for the future will be discussed, with a particular focus on interactions between transgenic crops and biological control functions in agro-ecosystems.

A private sector perspective on IRM strategies for transgenic Bt crops

Graham Head

Monsanto Company, St Louis, Missouri, United States

Transgenic Bt crops were first approved for commercialization in 1995 and now have been commercialized in more than 15 countries. Insect resistance management (IRM) is an important part of the stewardship of these Bt crops, and therefore technology providers have proactively implemented IRM practices wherever these products have been introduced (making this the first technology for which IRM has been routinely and proactively practiced). The IRM plans for Bt crops include a number of standard elements, such as an appropriate refuge for the production of susceptible target insects, a program to monitor for resistance, and broad-based education for growers and other relevant groups. However, there also has been an increasing recognition that the IRM needs for Bt crops vary among countries because of differences in pest biology, farming practices, and farmer literacy and experiences. Locally adapting IRM plans has required local scientific studies and surveys of grower practices, and has resulted in a number of novel approaches being developed. Smallholder systems in developing countries have posed a particular challenge because of the scale and diversity of these agricultural systems. In such cases, IRM strategies are most effectively implemented through the technology providers rather than requiring individual farmers to carry out novel practices. Going forward, it is heartening that no instances of resistance evolution to Bt crops have yet been observed, but significant scientific and logistical challenges will continue to arise.

Bionomics of *Aedes albopictus* (Skuse) vector of chikungunya and dengue in the Indian Ocean

Delatte Hélène[1], Gimonneau Geoffrey[1], Triboire Aurelie[2], Fontenille Didier[3]

[1]IRD, Saint Pierre, Reunion, [2]CIRAD UMR PVBMT, Saint Pierre, Reunion, [3]IRD, Montpellier, France

Introduction: *Aedes albopictus,* is a worldwide invasive mosquito originating from Asia, considered as competent in transmission of arboviruses. It was first described in La Réunion (an island of the South West part of the Indian Ocean (SWIO)) in 1913. Since, it has become the dominant *Aedes* species and a serious threat to public health, especially during the two last arboviruses outbreaks of Dengue and chikungunya. Despite its pest status, data on the biology of this vector are scarce, especially the population present in SWIO.

Methods: Biological parameters in controlled conditions were studied for this population at 8 constant temperatures (5, 10, 15, 20, 25, 30, 35 and 40°C). Biological data obtained were modeled.

Results: The minimal threshold of immature stages development was found at 10.4°C and its optimum at 29.7°C. The shortest periods for immature development were found at 30°C, with in average of 8.8 days. The optimum intrinsic rate of growth (*r*) was observed between 25 and 30°C. The trophogonic cycles were also evaluated and the shortest cycles were found at 30°C (in average 3.5 days).

Conclusions: Those results pinpointed the ability of a female to take a blood meal, at a minimum 2 days after its emergence. This ability, its good vectorial competence for CHIKV and DENV, the high (ideal) temperatures of subtropical summers, plus the presence of enough viremic travellers with an arbovirus, can partly explain the two explosive epidemic transmitted by *Ae. albopictus* for DENV and CHIKV in the Indian Ocean in 1997-8 and 2005-6, respectively.

Biogenic amine action on motor circuits in *Drosophila* and other insects

Hans-Joachim Pflueger[1], Natalia L. Kononenko[2], Ricard Vierk[1], Bjoern Brembs[1], Frauke Christiansen[3], Carsten Duch[4], Heike Wolfenberg[1]

[1]Free University, Berlin, Germany, [2]NTNU, Trondheim, Norway, [3]Universitaet, Wuerzburg, Germany, [4]Arizona State University, Tempe, AZ, United States

Biogenic amines are important modulators of behaviour both in vertebrate and invertebrate animals, and act on the central and peripheral nervous system. In *locusts*, we examined the functional role of octopamine which is released from a special class of efferent neuromodulatory neurones innervating peripheral muscles, sense organs and glands. Octopamine released from these neurones (i) modulates the efficacy of neuromuscular transmission, (ii) regulates the energy metabolism (activation of glycolysis), and (iii) increases the sensitivity of mechanoreceptors. Thus, the whole organism is primed for more dynamic, long lasting actions.

Consistent with this hypothesis, different types of efferent octopaminergic neurones are differentially recruited (activated or inhibited) during motor behaviour in parallel to the motor networks, and that those which activate glycolysis in muscles are inhibited during behaviours in which energy is generated by lipid oxidation. *Drosophila* tßh-mutants which cannot synthesize octopamine from tyramine, exhibit severe flight deficits, and the results suggested a combined effect of both tyramine and octopamine onto the flight system of *Drosophila*.

Correspondingly, the effects of octopamine and tyramine on the alternating motor patterns of a fictive flight preparation of *Manduca sexta* were tested. If tyramine is perfused then a similar alternating rhythm like that from octopamine is evoked but the depressor motoneurones show a different firing pattern sensitive to yohimbine, a tyramine-receptor-antagonist. This suggests that both octopamine and tyramine differentially affect elevator and depressor motoneurones.

Finally, immunocytochemical studies reveal pure tyraminergic cell populations and an interesting compartmentalization within octopaminergic neurones dependent on behavioural activity.

Caste polyphenism in bees: New phenotypes from tinkering with old genes and conserved signaling pathways

Klaus Hartfelder

Universidade de São Paulo, Ribeirão Preto, SP, Brazil

The two basic questions, *why* and *how* alternative phenotypes such as the caste of social insects can arise have, so far, mostly been formulated under quite distinct perspectives. This has left a wide gap between approaches that explain the origin of the worker caste in Hymenoptera and the soldier/worker castes in termites in terms of fitness gains (ultimate reasons) on the one hand, and developmental regulation and reproductive physiology (proximate mechanisms) on the other. The current fusion of developmental and evolutionary biology, driven by the advances in developmental genetics of model organisms, now start to provide a common framework on how caste phenotyes can be built from basic mechanisms for insect development. I will illustrate this by examples on endocrine system functions in social bees (juvenile hormone and insulin signaling) and from comparative functional genomic approaches. Obviously, the latter are only first incursions into a novel field of research, but one of the main conclusions already emerging is that metabolic regulation is a key factor in caste development. A particularly interesting question is that of gene regulatory networks, that is, how gene expression patterns are integrated by the architecture of their cis-regulatory regions in the development and reproduction of the female castes. I will show how this question can be approached through position-specific matrix analysis and network theory.

Population biology of the lucerne flea, *Sminthurus viridis*, with applications for control

John Roberts, Andrew Weeks, Ary Hoffmann

Centre for Environmental Stress and Adaptation Research, University of Melbourne, Parkville, Victoria, Australia

Introduction: The lucerne flea is a major agricultural pest of crops and pastures throughout southern Australia and New Zealand. As control methods for this pest rely heavily on pesticides, there is a need for a sustainable IPM strategy. To provide the necessary biological information for such an approach, we are currently examining the lucerne flea's population biology and life-cycle, as well as investigating chemical and biological control methods.

Methods: Genetic markers were used to examine the population structure, migration potential and mode of reproduction throughout Australia. Laboratory bioassays were used to assess the efficacy of several chemicals against lucerne fleas. Field experiments investigating the life-cycle of the lucerne flea were also conducted.

Results: Allozyme markers indicate that Victorian lucerne flea populations reproduce sexually and have significant structure due to limited gene flow. Microsatellite markers have been developed for greater resolution of the population biology throughout southern Australia as variability in allozyme loci was low. Pesticide testing has found lucerne fleas to have high tolerance to several registered chemicals when compared to the co-existing redlegged earth mite, also a major agricultural pest. Longitudinal sampling of several populations suggests at least two generations per season with numbers peaking in autumn and spring. Experiments examining summer diapause in the lucerne flea are in progress to determine when over-summering eggs are laid during a season.

Conclusions: High pesticide tolerance in the lucerne flea supports the need for an IPM strategy. Further insights into this pest's biology will lead to more effective and sustainable control.

Assessing the impact of the spatial arrangement of non-crop vegetation in Australian cotton landscapes: incorporating connectivity in spatially specific landscape complexity analysis

David Perovic[1], Geoff Gurr[2], Anantanarayanan Raman[2]

[1]Charles Sturt University, Orange, New South Wales, Australia, [2]E.H. Graham Centre for Agricultural Innovation, Charles Sturt University, Orange, New South Wales, Australia

Introduction: Landscape complexity at a scale of several kilometres has previously been shown to strongly affect natural enemy conservation in cropping land. Our study investigated ecological insights which may be gained by including measures of connectivity into landscape analysis.

Methods: The relationship between non-crop habitats and natural enemy abundance in crops was compared using generalised linear models at scales of 120, 750, 1500 & 3000 m surrounding crops. Cost-distance measures were included in regressions to test the effects that the connectivity of these habitats have on the abundance of natural enemies in crops. Further, the degree to which each land-use type impedes, or facilitates, the movement of natural enemies through the matrix was tested by comparing cost-distance models with different cost structures.

Results: Connectivity metrics explained the majority of variation observed within crops for all taxa observed. 'Linear' elements such as shelterbelts and 'dispersed' elements such as isolated native trees on farms were shown to be important for creating connectivity between non-crop habitats and cotton crops. Cost-distance models which considered arable land to be more resistant to movement than other land-uses fitted arthropod data most significantly. Spatially specific analysis indicated that landscape structure affects different taxa at different scales: these differences reflected the dispersal capacity of each taxon.

Conclusions: While non-crop areas provide important habitats for natural enemies in agroecosystems; the spatial arrangement of these elements can greatly enhance ecosystem services by facilitating the movement of natural enemies into crops.

Astounding success in dengue control in Vietnam, using *Mesocyclops* and community-based methods

Brian Kay

Australian Centre for International and Tropical Health, Queensland institute of Medical Research, Brisbane, Australia

Introduction: In 2005 in Lancet 365 : 613-617, we reported a mosquito control strategy which incorporated four elements; (i) a combined vertical and horizontal approach which depended on community understanding and leadership, (ii) prioritized control according to the larval productivity of major habitat types, (iii) the usage of predacious copepods of the genus *Mesocyclops* as a biological control agent, delivered by (iv) communal activities of health collaborators, school children and the public.

Methods: From 1998-2000, we reported that our community based vector control program in six communes in the northern provinces of Nam Dinh, Hung Yen and Hai Phong had resulted in extension to another 37 communes by 2000-2003. From 2000-2003, we set up similar interventions in central Vietnam provinces of Quang Nam, Quang Ngai and Khanh Hoa and from 2004-2007, worked in the southern provinces of Long An and Hau Giang. In 2007, our team evaluated program sustainability in Nam Dinh, 7 years after project completion.

Results: For all interventions, eradication of *Aedes aegypti* was achieved in 40 of the 48 communes, with only small numbers of larvae detected in the others. In Nam Dinh province in 2007, these community-based programs were strongly led by local leadership and eradication status maintained. The setting up of micro-enterprise schemes towards the end of project completion in 2000 was used to stimulate community action and was thought to have played a role in ensuring sustainability. The direct cost of locally run programs in Nam Dinh was estimated to be 4 US cents per person per year.

Conclusion: This strategy is affordable and sustainable in northern Vietnam at least but should have application to other countries where large water storage containers are major contributors of *Aedes aegypti* and where there are local leaders and communities willing to take responsibility for controlling dengue.

Postembryonic development of Mantophasmatodea, with reference to antennal development

Mike Picker, Dorit Hockman

University of Cape Town, Cape Town, South Africa

Introduction: The first description of the life cycle of Mantophasmatodea is provided. Antennal development and structure are described and used as characters for an evaluation of interordinal relationships.

Methods: Newly hatched nymphs of field-collected *Lobatophasma redelinghuysense* were reared, providing a time sequence of head capsule measurements. SEM and light microscopy tracked the mode of antennal growth.

Results: The life cycle comprised six instars, with females having significantly larger head capsules from instar II onwards and a greater rate of development than males. Antennae of first instars comprised a smooth 4-segmented basiflagellum and a 7-segmented, sensillae-rich distiflagellum. Increase in number of annuli occurred in the basiflagellum only. Lengthening of the antennal flagellum was achieved by division of the first basal annulus, adding two annuli at each moult. Both number of annuli and unique segmentation pattern of the distiflagellum (alternating short and long annuli) remained constant until adulthood. The segmentation pattern of the adult antennae (comprising basiflagellum and a distiflagellum of 14 and 7 annuli respectively) was consistent for all 10 species examined, and thus considered to be stable within the order. Secondary subdivision of terminal basiflagellar annuli occurred from segment 8 onwards. The position of the secondary annular divisions was variable, and corresponded with intraordinal clades defined by molecular studies.

Conclusions: The mantophasmatodean antenna provided a number of characters, autapomorphic within Hexapoda. It bears little resemblance to that of putative sister-groups viz. Grylloblattodea, Mantodea and Phasmatodea. Instead, the mode of flagellar elongation and annulation is the same as that of Isoptera, Blattodea and Dermaptera.

Understanding the nutritional ecology of *Anopheles gambiae* in western Kenya and its possible impact on malaria transmission

Hortance Manda[1], Louis Clement Gouagna[2], John Beier[3], Woodbridge Foster[4], Ahmed Hassanali[1], John Githure[1]

[1]International Centre of Insect Physiology and Ecology, Nairobi, Kenya, [2]Institut de Recherche pour le Développement, Ouagadougou, Burkina Faso, [3]University of Miami, Miami, Florida, United States, [4]The Ohio State University, Columbus, Ohio, United States

Introduction: To provide for their energy needs, both sexes of adult mosquitoes require sugars which they acquire mainly from plants. This study investigated plant-feeding behaviour of *Anopheles gambiae* and its impact on their fitness and vector competence.

Methods: In Suba district, western Kenya, indoor resting *An. gambiae* were sampled and tested for their plant-feeding status. Their feeding responses on common plants growing around human dwellings and mosquito larval habitats were determined in choice and no-choice bioassays. Survival and fecundity were evaluated when feeding on plants. Mosquitoes fed on each plant species were experimentally infected and their infectivity determined.

Results: Up to 12% of females *An. gambiae* sampled had recently fed on plants. There was a preferential feeding pattern of *An. gambiae* on specific plants species. Flower was the most preferred part for feeding, but leaves and stems were most preferred in some plants species. Survival and fecundity of *An. gambiae* were increased when they fed on almost all preferred plants. This was positively correlated with the quality and quantity of sugars on those plants. Two plants species impeded the development of *Plasmodium falciparum* in the mosquito midgut, significantly reducing the prevalence of infection in mosquitoes, at a magnitude of >50% below mosquitoes fed on the control glucose. The adverse effects of plants on parasite development in the mosquito midgut increased on post-infection plant-feeding and were optimum on continuous plant-feeding.

Conclusions: The availability of certain plants species to *Anopheles* mosquito in endemic areas may affect mosquito population dynamics and malaria transmission.

Spatio-temporal distribution of Coleoptera in food mills

Pasquale Trematerra

University of Molise, Campobasso, Italy

Introduction: Geostatistical methods and spatio-temporal analisys can be a powerful tool for the understanding of many spatially-related phenomena.

Methods: By utilizing food-bait traps we evaluated the presence and the spatio-temporal distribution of insect-pests in an industrial semolina-mill.

Results: Insect specimens captured in the traps belonging to 14 *taxa*, mainly Coleoptera. The most abundant were *Tribolium confusum*, followed by *Typhaea stercorea* and *Tribolium castaneum*. *T.confusum* was collected on all the sampling dates, with peaks in the second half of June-beginning of July and in the first half of August. *T.stercorea* was most abundant from the second half of May to the beginning of July and in the first half of September. The presence of *T.castaneum* had a peak in June. For *T.confusum* the highest abundance foci were confined to the corners of the milling area and in the base of the adjacent walls of every floor. *T stercorea* was confined in the I and the II floors, the main moisture areas of the mill contaminated with mould. *T. castaneum* was observed in the upper floors of the mill. Of interest was the presence in the food-bait traps of *T.confusum* and *T.castaneum* adults in a mixed population with equal numbers of males and females; analysis of the spatio-temporal dynamics suggested that the distribution of the two sexes was almost the same during the sampling period.

Conclusions: The indications obtained were used in precision IPM procedures after the fumigation, based essentially on the improvement of good sanitation practices.

Precision IPM and spatial distribution of Lepidoptera pests of pome, stone and grape fruits

Pasquale Trematerra, Andrea Sciarretta

University of Molise, Campobasso, Italy

Introduction: Geostatistical methods can be a powerful tool for the understanding of many spatially-related phenomena.

Methods: The main objectives of our studies (from 1998 to 2007) were to determine, by pheromone traps, the temporal and spatial variation in distribution and abundance of *Cydia funebrana*, *Cydia pomonella*, *Cydia molesta*, *Anarsia lineatella* and *Lobesia botrana* inside and outside orchards, and to evaluate the importance of the presence of several host plants.

Results: *C.funebrana* (250 ha), kriging procedures showed that the number of males was lowest in the interior of plum orchard and highest around a ravine, near irrigation channels and hedgerows in the orchard surroundings.

C.pomonella (100 ha), spatial characterizations obtained illustrate that the high trap capture foci were confined to the productive apple orchards or in a small groups of apple trees. *C.molesta* and *Alineatella* (250 ha), were investigated inside small plots of stone fruit, plum, apple, pear and kiwi orchards, and outside in field crops, irrigation channels, hedgerows and a river. The main hot spot for both pests was in a stone fruit orchard. The river and the irrigation channels seem to act as barriers.

L.botrana (50 ha), was monitored in a hilly ecosystem where vineyards are surrounded by hedgerows, small woodlots, alternated with cereal and olive groves. The presence of males was not limited to vineyards, particularly at the beginning of the season, when most of the individuals were caught inside olive groves, while during the II and the III flight they concentrated in vineyards.

Precision IPM and spatial distribution of Lepidoptera pests of pome, stone and grape fruits

Pasquale Trematerra, Andrea Sciarretta

University of Molise, Campobasso, Italy

Introduction: Geostatistical methods can be a powerful tool for the understanding of many spatially-related phenomena.

Methods: The main objectives of our studies (from 1998 to 2007) were to determine, by pheromone traps, the temporal and spatial variation in distribution and abundance of *Cydia funebrana*, *Cydia pomonella*, *Cydia molesta*, *Anarsia lineatella* and *Lobesia botrana* inside and outside orchards, and to evaluate the importance of the presence of several host plants.

Results: *C.funebrana* (250 ha), kriging procedures showed that the number of males was lowest in the interior of plum orchard and highest around a ravine, near irrigation channels and hedgerows in the orchard surroundings.

C.pomonella (100 ha), spatial characterizations obtained illustrate that the high trap capture foci were confined to the productive apple orchards or in a small groups of apple trees.
C.molesta and *Alineatella* (250 ha), were investigated inside small plots of stone fruit, plum, apple, pear and kiwi orchards, and outside in field crops, irrigation channels, hedgerows and a river. The main hot spot for both pests was in a stone fruit orchard. The river and the irrigation channels seem to act as barriers.

L.botrana (50 ha), was monitored in a hilly ecosystem where vineyards are surrounded by hedgerows, small woodlots, alternated with cereal and olive groves. The presence of males was not limited to vineyards, particularly at the beginning of the season, when most of the individuals were caught inside olive groves, while during the II and the III flight they concentrated in vineyards.

Mechanisms of insecticide-resistance in hemipteran species: An overview

Graham Moores, Georgina Bingham, Ian Denholm, Lin Field, Kevin Gorman, Martin Williamson

Rothamsted Research, Harpenden, Herts, United Kingdom

Too often in the past various insecticide-resistance mechanisms have been specifically aligned with pest species. Hence, 'Dipterans possess target-site insensitivity whilst homopterans possess metabolic resistance'. The agricultural sucking pest insects are a prime example to repudiate the old adages, with populations from aphid and whitefly species demonstrating the full spectrum of resistance mechanisms.

Main consideration is given here to the Sternorrhyncha, in particular the global whitefly pest, *Bemisia tabaci,* and the prinicipal UK crop pest, *Myzus persicae*. Both species exhibit target-site resistance in the forms of modified acetylcholinesterase (MACE) conferring insensitivity to carbamates and organophosphates as well as knockdown resistance (kdr) conferring insensitivity to pyrethroids. Furthermore, both species exhibit metabolic resistance in the forms of enhanced/ modified enzyme activity due to esterases and/ or microsomal oxidases.

Molecular, biochemical and synergist studies using piperonyl butoxide and analogues have been utilised to characterise these resistance mechanisms. The latter allow informed decisions on the contributions from each metabolic component and have indicated the possible presence of target-site resistance to neonicotinoids in some strains of *B. tabaci*.

Synergistic enhancement of plant activators

Georgina Bingham, Lesley Smart, Toby Bruce, Barry Pye, John Pickett, Glen Powell, Simon Hodge, Graham Moores

Rothamsted Research, Harpenden; and Imperial College, Kent, United Kingdom

The development of insecticide resistance in a wide range of important insect pest species, together with the withdrawal of several widely used insecticides in Europe, poses a serious challenge to effective crop protection, leaving an urgent need for alternative control strategies.

A number of natural and synthetic compounds (plant activators) are able to induce effective plant resistance against insect pests by increasing the plant-defense chemistry. Such plant activators include DL-β-aminobutyric acid (BABA) and *cis*-jasmone.

Insects have metabolic enzyme systems that enable them to metabolise plant xenobiotics. These same enzyme groups may be enhanced, resulting in pesticide-resistance. Inhibitors of these enzymes can act as xeniobiotic synergists, and by allowing sufficient time for these inhibitors to fully inhibit the enzymes (temporal synergism), insect pests can be made sensitive to either conventional pesticides or activator-derived plant xenobiotics.

Since activator-primed plants have an enhanced ability to produce defensive xenobiotics and enzyme inhibitors leave the insect defenceless, a combined approach has demonstrated enhancement of the potency of plant activators. In crops that have relatively toxic secondary metabolites (such as potatoes, cotton, tomatoes and black mustard), the use of temporal synergism in conjunction with plant activator priming has resulted in low survival of *Myzus perisicae, Aphis gossypii* and complete control of *Bemisia tabaci* (insecticide resistant and susceptible strains) without the use of pesticides.

Vegetation context and the emergence of multi-predator effects

Andrew Wilby[1], Linda Anglin[2], Khalid Asiry[2]

[1]Lancaster University, Lancaster, Lancashire, United Kingdom, [2]University of Reading, Reading, Berkshire, United Kingdom

Introduction: Mechanisms underlying both positive (prey risk enhancement) and negative (prey risk reduction) effects of increasing predator species richness have been identified, and it has been argued that the relative expression of these mechanisms may be affected by the broader ecological context. Here we test whether plant density and species composition can alter the strength or sign of emergent multi-predator effects.

Methods: We subjected caged populations of the aphid *Metapolophium dirhodum* to *Chrysoperla carnea* larvae alone, *Adalia bipunctata* adults alone, and a combination treatment including both predator species. These predator treatments and a no-predator control where applied in three different vegetation contexts: low-density wheat, high-density wheat and a wheat and field bean mixture. Comparisons of control and treatment cages allowed calculation of the per-capita impact of each predator treatment on population growth in *M. dirhodum*.

Results: Both *A. bipunctata* and *C. carnea* caused a significant reduction in *M. dirhodum* population size. Prey suppression was not affected by plant density, but was significantly reduced in the wheat/bean mix compared with the wheat monocultures. Comparison of prey-suppression in mixed-predator treatment with expected suppression based on the single-species predator treatments revealed positive emergent effects in the wheat monoculture treatments (risk enhancement), but negative emergent effects (risk reduction) in the wheat/bean mix.

Conclusions: Plant species composition can not only affect prey population suppression, but can also moderate the sign and strength of multi-predator effects. Benefits of increased predator species richness may be determined, in part, by the vegetation context.

The evolution of termites: Fossils and phylogenetic patterns

Michael Engel[1], David Grimaldi[2]

[1]University of Kansas Natural History Museum, Lawrence, Kansas, United States, [2]American Museum of Natural History, New York, New York, United States

A study of phylogenetic relationships among major lineages of Isoptera is provided based on morphological, ethological, and paleontological data. An extensive diversity of fossil termites from the Tertiary and Cretaceous have been newly synthesized with living termite diversity, including an abundance of "primitive" termites. Most Cretaceous genera are stem groups to either the modern families or as intermediate between groups of families, including one genus as a stem group to all other Isoptera. Mastotermitidae falls relatively basal in the order, among a diversity of fossil taxa. Termopsidae and Hodotermitidae as widely defined were not recovered as monophyletic, with components of these families emerging from a grade of living and fossil termite lineages, leading to Kalotermitidae as closely related to the higher termites (Rhinotermitidae + Termitidae). A relatively tight stratigraphic-clade rank correlation was recovered, with the earliest fossils falling more basal in the order. The phylogenetic patterns have implications for the diversification of termites and their impact on the surrounding environment as they are the most efficient recyclers of carbon and breakdown the most abundant biomolecule – lignocellulose. Although termites arose early, perhaps in the latest Jurassic, and diversified into numerous primitive lineages, they remained a small component of the insect fauna and with apparently minimal environmental influence. Termites only appear to have begun to rise in diversity slowly after the origin of the Rhinotermitidae + Termitidae clade. The analysis indicates that the higher termites, particularly the ubiquitous Termitidae with their enormous, perennial colonies did not truly explosively radiate until the Tertiary and may have altered global patterns of carbon recycling.

Establishment of *Harmonia axyridis* in North America: A case for the enemy release hypothesis?

Ted Cottrell, David Shapiro-Ilan

USDA, Agricultural Research Service, Southeastern Fruit and Tree Nut Research Laboratory, Byron, GA, United States

Introduction: The establishment and quick spread of the exotic coccinellid *Harmonia axyridis* across much of North America has possibly been facilitated through reduced susceptibility to endemic pathogens. Susceptibility of the exotic coccinellid to pathogens was compared with susceptibility of native coccinellids.

Methods: We tested the laboratory susceptibility of endemic and exotic species of North American Coccinellidae to *Beauveria bassiana* derived from different sources and to different species and strains of entomopathogenic nematodes.

Results: Three endemic coccinellid species were susceptible to an isolate of *B. bassiana* originally isolated from one of the native species. However, another endemic coccinellid and the exotic *Harmonia axyridis* were not susceptible to this isolate. Similarly, the exotic *H. axyridis* was less susceptible to nematode infection than native species. Nematode reproductive capacity data also indicated lower host suitability in the exotic *H. axyridis*. **Conclusions:** Overall, our hypothesis was supported, i.e., low susceptibility to pathogens may have contributed to successful establishment and spread of *H. axyridis*.

Allozyme studies on *Helopetis theivora* (Hemiptera: Miridae) from Peninsular Malaysia

Rita Muhamad Awang, Tan Soon Guan, Siti Hajar Latipp

[1]Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia, [2]Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia, [3]Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia

Introduction: *Helopeltis theivora* is known as a pest of cocoa and tea in Malaysia. Polyacrylamide gel electrophoresis (PAGE) was used to determine the metabolic enzymes (25) involved in the development of resistance in *H. theivora*

Methods. Adults of *Helopeltis theivora* were collected from three geographical populations namely Bukit Cheeding, Banting, Selangor, Sg. Palas, Cameron Highlands and MARDI, Cameron Highlands, Pahang.

Results: 9 enzymes were detectable in *H. theivora*: α- and β- esterase (EST), xanthine dehydrogenase (XDH), leucine aminopeptidase (LAP), glutamate oxaloacetate transaminase(GOT), superoxide dismutase (SOD), glucose 6-phosphate dehydrogenase (G6PDH), aldehyde oxidase (ALDOX) and alkaline phosphatase (ALKP). Based on the phenotypes observed for these nine enzymes, alleleic frequencies were obtained which were in turn used to calculate the Nei's (1978) genetic distance coefficients among the three populations. The genetic distance coefficients were then used to cluster the populations by using UPGMA (unweighted pair group method with arithmetic averaging).

Conclusions: Dendogram cluster analysis grouped the Banting, Selangor and MARDI, Cameron Highlands populations together while the Sg. Palas, Cameron Highlands population clustered by itself. This clustering pattern could be due to the frequent spraying of insecticides at Sg. Palas over the past 5 years. For the Banting and MARDI populations, insecticides were not frequently sprayed when compared with the Sg. Palas, Cameron Highlands population. Our insecticide sensitivity studies showed that the Sg. Palas population was more resistant to insecticides than the Banting and MARDI, Cameron Highland populations.

Field performance of transgenic crops: do they frustrate biological control?

Gary Fitt

CSIRO Entomology, Brisbane, Qld, Australia

IPM must be founded on a thorough understanding of the ecology of pest and beneficial species and their interaction with the crop and surrounding non-crop environments. Biological control is often a focal component of IPM in crop production systems, although key pests often escape the control of natural enemies and require other interventions. Transgenic crops targeting key pests, such as Bt cotton, are rapidly emerging as one of those key interventions, particularly control for noctuid pests such as *Helicoverpa* spp.

This emerging era of insect resistant GM crops with potentially high efficacy against target pests has raised concerns among some IPM practitioners about direct or indirect impacts on natural enemies in ways which disrupt the synergy of biological control and partial host plant resistance, often regarded as an ecologically stable approach.

Experience in many parts of the world with Bt cottons, suggest in contrast that these GM crops offer real prospects for more sustainable, economically acceptable IPM with the integration of a range of non-chemical tactics. With the potential for dramatic reductions in pesticide, natural enemies clearly continue as an important component of these systems. Examples from Australia and other systems will be discussed.

Maintaining an appropriate balance and retaining the benefits of Bt cottons requires vigilant resistance management, sustained efforts to enhance beneficial species and non-disruptive, short residual pesticides for key sucking pests. Overall the stability of these systems will require mobilization of the whole farm environment and greater understanding of the flows of impacts and services between intensive cropping systems and the surrounding landscape.

Have Bt crops led to changes in insecticide use patterns and impacted IPM?

Gary Fitt

CSIRO Entomology, Brisbane, Qld, Australia

GM crops have now been commercialised for over ten years and currently over 100 million hectares are grown in 22 countries. By incorporating a powerful pest management tactic within the plant these *Bt* crops overcome some, but not all of the problems with timing and variable rates of application of insecticides, which reduce efficacy and often result in higher than necessary concentrations being applied than is necessary. This paper will present the current evidence for impacts of *Bt* crops, largely *Bt* cotton and *Bt* maize, on insecticide use and will reflect on their role in IPM. Analyses of *Bt* crop performance across a range from large-scale intensive production to smallholder production systems of varying levels of sophistication indicate significant reductions in insecticide input and in some systems, highly significant improvements in yield. However, economic performance is highly variable and seems dependent more on the market characteristics, support structures and culture of the systems in which *Bt* crops are deployed than on the *Bt* crops themselves. Given their specificity for key target pests and well demonstrated lack of impact on beneficial insects, *Bt* crops provide an important new platform for sustainable IPM systems, one that is compatible with a full range of other tactics. However, achieving that IPM outcome will often require ongoing education and extension support for farmers, particularly in smallholder systems, to ensure they can build confidence and gain sustainable benefit from a mix of new and established technologies in pest management.

On a temporal model for the Chikungunya disease: application for vector control

Frédéric Chiroleu[1], Yves Dumont[2], Caroline Domerg[1]

[1]Cirad, Saint-Pierre, Reunion, [2]Université de la Réunion, Saint-Denis, Reunion

Introduction: We propose a compartmental model to study the time course of the Chikungunya outbreak of 2005 in Reunion Island. Our aim is to take into account the effect of larvicide or destruction of breeding sites to control vector population, and estimate the possible influence on the epidemics of 2006.

Methods: We use a SEIR model with host population constant along time and compartments corresponding to the epidemiological states. We add a supplementary compartment for vectors, the larval stage, corresponding to the productivity of breeding sites. We calculate the basic reproduction number, R_0, and a function of R_0, R_C. We present simulations for some cities, considering the great number of micro-climates, and compare them to real data.

Results: R_0 can be written as the product of a host-vector acquisition rate, R_{HV} and a vector-host inoculation rate, R_{VH}. We show that a free disease equilibrium exists that is globally asymptotically stable under a threshold condition on R_C. It means that we can control the epidemics if, at any time, efficient vector control interventions are realised to lower R_C enough.

From the simulations, we explain why no outbreak appeared in 2005: R_{HV} was very small, and so R_0, corresponding, for instance, to a small transmission rate from infectious host.

Conclusion: From our model, and knowing the evolution of some biological parameters, like the transmission rate from an infectious host, we link the episode of 2005 with the big outbreak of 2006. Finally, we show that efficient interventions could have been useful to prevent the epidemic of 2006.

Evidence of a recent outbreak range expansion in winter moth in Fennoscandia

Jane U. Jepsen, Snorre B. Hagen, Rolf A. Ims, Nigel G. Yoccoz

University of Tromsø, Tromsø, Norway

The winter moth, *Operophtera brumata* is one of the most important insect herbivores in sub-arctic birch forest in Fennoscandia. The winter moth experiences cyclic outbreaks in parts of the species' distribution range every 9-10 yrs, with severe impacts on the birch forest ecosystem. Historical records indicate, that winter moth invasion into northern Norway is a recent event (first occurrences in Troms County around 1900). However, throughout the twentieth century the area experiencing regular outbreaks by winter moth (e.g. the species' outbreak range) has been restricted to low-altitude, coast-near forest in W-NW Norway. Through analysis of outbreak records covering more than a century, we document a recent north-eastern expansion of the outbreak range of winter moth, most noticeably occurring during the last two decades. Regular outbreaks now occur at the northern and alpine forest limit in NE Norway overlapping the outbreak range of the autumnal moth (*Epirrita autumnata*). Since population peaks of winter moth tend to lag 1-2 yrs behind those of autumnal moth, an increase in range overlap can be expected to lengthen duration of outbreaks. Satellite monitoring and ground data, obtained during the most recent (2000-2007) outbreak cycle in NE Norway, confirms that this is indeed happening.

Are there patterns in above and belowground insect herbivore interactions?

Katy Clark[1], Scott Johnson[1], Sue Hartley[2]

[1]Scottish Crop Research Institute, Dundee, United Kingdom, [2]University of Sussex, Brighton, United Kingdom

Introduction: An increasing amount of literature over the last decade has focussed on interactions between above and belowground insect herbivores. However, identification of patterns within the data has proved difficult owing to the wide range of both study systems and experimental setup. Meta analyses were conducted to answer questions relating to the effect above and belowground insects have upon one another.

Methods: A literature search was conducted, from which 62 observations in 22 relevant papers were identified. The data collected was used to determine: 1) How do belowground insects respond to aboveground herbivory on a shared host plant? 2) How do aboveground insects respond to belowground herbivory on a shared host plant? 3) How are different above and belowground feeding guilds influenced by herbivory through a shared host plant? and 4) How are different above and belowground orders influenced by herbivory through a shared host plant? Analyses were conducted using insect performance parameters.

Results: Preliminary results indicate that relative growth rate (RGR) and survival of belowground insects are negatively affected by aboveground insect herbivory; however, weight/size gain and abundance are not influenced. Insect herbivores aboveground had a negative impact on belowground root chewing insects, but did not affect belowground insect suckers.

Conclusions: Meta analyses provide useful insights into the overall interactions between above and belowground insect herbivores, however, further research in the field will strengthen the results.

Diapause termination in overwintering larvae of the peach twig borer *Anarsia lineatella* (Lepidoptera: Gelechiidae)

Petros T. Damos, Matilda Savopoulou-Soultani

Aristotle University of Thessaloniki,Faculty of Agriculture,Laboratory of Applied Zoology and Parasitology, Thessaloniki, Greece

The course of diapause development under field conditions for overwintering larvae of *Anarsia lineatella* (Zeller) (Lepidoptera: Gelechiidae) was studied in Northern Greece. For 3 years (2005-2007) hibernacula with overwintering larvae of *A. lineatella* were collected during the winter and early spring from peach orchards of the most important peach production regions of northern Greece (Veria: 40.32^{o}N and Velvendo: 40.16^{o}N). Each hibernaculum was considered as a sampling unit and on the day of sampling, all the collected material was transferred to the laboratory and placed individually in plastic cells at 20^{0}C, under long-day (16:8h L:D) or short-day (8:16h L:D) photoperiods. In all cases photoperiod had a significant influence on diapause development. Duration in days, from transfer from the orchard to the laboratory until first molt and pupation of larvae was significantly affected by sampling date. In addition, photoperiod and sampling date had also a significant effect on the number of molts until pupation and especially on early-collected larvae (mid and late December). In most cases short-day photoperiod maintained diapause for larvae sampled until late January. Thus, *A. lineatella* may complete diapause development in late January, but it will not break diapause until spring, when region specific temperatures are sufficiently high to induce diapause break.

Development and validation of models in forecasting the seasonal emergency and population dynamics of the peach twig borer *Anarsia lineatella* (Lepidoptera: Gelechiidae) in northern Greece

Petros Damos, Matilda Savopoulou-Soultani

Aristotle University of Thessaloniki,Faculty of Agriculture,Laboratory of Applied Zoology and Parasitology, Thessaloniki, Greece

Effective management of the peach twig borer *Anarsia lineatella* (Zeller) (Lepidoptera Gelechiidae) in Northern Greece's IPM orchards, depends mostly on successful timing of biorational insecticide application. The objective of this study was to develop and validate species-specific phenological models that reliably predicted male moth emergence and population dynamics of *A. lineatella* in Northern Greece. Male moths caught in pheromone traps and temperature data were collected over a 4 year period in the two most important peach production regions of northern Greece (Veria lat. 40.32^{o} N and Velvendo lat. 40.16^{o} N). The relationship between the cumulative percentage of males caught in pheromone traps and the relative degree-days was modeled. A 3rd order polynomial equation, a Weibull distribution function and a 3-parameter sigmoid equation were fitted to the data. Field data were compared with developmental and emergence data coming from an *A. lineatella* laboratory strain. Predicted versus observed data were compared and the model performance statistics of root mean square error (*RMSE*) and index of agreement (*d*) were applied in order to validate the models. According to the 3-parameter sigmoid model, approximately 90, 250 and 460 *DD* must be completed, after the first moth caught in early spring, for a 10, 50 and 90% of the overwintering population moth emergence, while for the second flight, approximately 1100, 1300 and 1600 *DD* must be completed, for a 10, 50 and 90% cumulative moth caught, respectively. Degree-day forecasting models significantly improve present strategies of IPM in providing an early prediction of the moth emergence and population course during cultivation season.

Intraguild predation and selection of best species of biological control agents for release

Jacques Brodeur

Université de Montréal, Montreal, Quebec, Canada

Guild interactions occur among species within the same trophic level. Considerable attention has been given to intraguild predation among natural enemies in natural and agricultural ecosystems over the past decade. A common approach in biological control is the use of ecological theory to better interpret the prevalence, nature and outcome of guild interactions and, from a more applied perspective, to implement biological control programs. Of significance, understanding intraguild interactions is important to determine (i) the number and composition of species to release, (ii) the most suitable developmental stages of arthropods to be used, (iii) the timing of multiple releases, and (iv) the impact of biological control agents on non-target species.

Cotton pest management in Argentina

Oscar Antonio Peterlin

INTA, Santiago del Estero, Argentina

In Argentina pest management varies according to cotton production systems. It can be differentiated the pest management between small and large producers, and among crops in semiarid, wet and irrigation conditions. The cotton crops of small producers surrounded by a rich flora and fauna biodiversity in general show less pest problems because the pest population's level does not require insecticide applications. The case for big producers is totally different since the biodiversity of their ecosystems is extremely low because the area used for cultivation is very large. In arid conditions, characteristics that affect the survival chances of predators and micro-hymenoptera, markedly increase pest problems. In conditions of high humidity, the more benign environmental conditions allow greater survival of beneficial fauna, and usually have less pest problems. In the areas of irrigation, the planting dates are very diverse (either early, intermediate, or late cotton crops). This situation increases the proliferation of some pests from early to late crops.

The recommended IPM for cotton crops varies for different situations, but generally it is based on the rotation of crops with soybeans and corn, reducing the crop cycle by using narrow and ultra narrow rows, creating conditions that increase the natural control from beneficial insects, planting cultivars that contains a protein from *Bacillus thuringiensis* (Bt) that protects the cotton plants from specific lepidopteron insect pests and using a systematic monitoring of the presence of pests to establish timely control with insecticides.

New Zealand as a Noah's Ark for British bumblebees

Gillian Lye[1], Roddy Hale[2], Dave Goulson[1]

[1]University of Stirling, Stirling, United Kingdom, [2]Lincoln University, Christchurch, New Zealand

British bumblebees were introduced into the South Island of New Zealand in ~1895 for the pollination of red clover (*Trifolium pratense*). Four British species became established (*Bombus hortorum*, *B. ruderatus, B. terrestris* and *B. subterraneus*) and all four spread rapidly throughout large areas of the South Island. Their success is largely attributed to the availability of several non-native plant species including many that are known to be favoured forage species of these insects within their native range. As a result, the increasing drive towards the eradication of non-native weed species in New Zealand is posing a huge threat to the bumblebees.

Due to their non-native status, there appears to be little concern over the loss of these species from New Zealand. However, these non-native bees are potentially of great importance in terms of conservation. New Zealand has been become a stronghold for *B. ruderatus*, a bumblebee that has suffered severe declines elsewhere, and since the recent extinction of *B. subterraneus* in the UK, the New Zealand population of this species now constitutes the only remaining individuals of British stock in the world. As a result, New Zealand bumblebee populations have been suggested as potential source populations for reintroduction into the UK.

However, this suggestion is based on the assumption that the New Zealand population is ecologically and genetically similar to the original UK population. I will present ecological and genetic data comparing these populations in order to assess the potential of New Zealand bumblebees for use in a reintroduction attempt.

Global distribution patterns of termite (Isoptera) evolutionary feeding groups

David Jones, Paul Eggleton

Natural History Museum, London, United Kingdom

Introduction: Recent molecular phylogenetic studies have revealed repeated acquisition, loss and reacquisition of major feeding habits among termites. Species can now be assigned to one of 40 evolutionary feeding groups (EFG) defined by independent acquisition of feeding habit, rather than using traditional non-taxon-specific feeding groups. Using this new framework, how does the number of species in each EFG vary within and among regions? What is the impact of land-use change on EFG composition within termite assemblages, and the consequences for termite-mediated ecosystem services?

Methods: Termite assemblages were sampled at 110 tropical and subtropical forest sites in five continents. The standardised sampling method gives a representative measure of the species density and composition of the local assemblage. A range of environmental variables were also recorded.

Results: Multivariate analyses show that assemblages in different regions have very different EFG structures, and significant differences in species density. "Region" is the main factor structuring assemblages, whereas ecological factors such as rainfall or altitude account for only a small amount of the variation. However, some EFG, particularly soil-feeders, are very sensitive to land-use change.

Conclusions: The use of EFG uncovers patterns that are not seen when using the traditional feeding groups. The greater resolution offered by EFG reveals distinct trajectories of termite assemblages within each region, and provides new insights into the links between termite cladogenesis, dispersal ability and the ecological constraints of different feeding habits. Furthermore, the loss or reduction of some EFG caused by land-use change will have negative impacts on soil processes.

Use of Google Earth to strengthen public health capacity and facilitate management of vector-borne diseases in resource-poor environments

Saul Lozano-Fuentes[1], Darwin Elizondo-Quiroga[1], Jose Arturo Farfan-Ale[2], Maria Alba Lorono-Pino[2], Julian Garcia-Rejon[2], Salvador Gomez-Carro[3], Victor Lira-Zumbardo[3], Rosario Najera-Vazquez[3], Ildefonso Fernandez-Salas[4], Joaquin Calderon-Martinez[5], Marco Dominguez-Galera[5], Pedro Mis-Avila[5], Michael Coleman[6], Natashia Morris[6], Chester Moore[1], Barry Beaty[1], Lars Eisen[1]

[1]Department of Microbiology, Immunology and Pathology, Colorado State University, Fort Collins, Colorado, United States, [2]Laboratorio de Arbovirologia, Universidad Autónoma de Yucatan, Merida, Yucatan, Mexico, [3]Servicios de Salud de Yucatan, Merida, Yucatan, Mexico, [4]Laboratorio de Entomología Medica, Facultad de Ciencias Biologicas, Universidad Autonoma de Nuevo Leon, San Nicolas de los Garza, Nuevo Leon, Mexico, [5]Servicios Estatales de Salud de Quintana Roo, Chetumal, Quintana Roo, Mexico, [6]Malaria Research Programme, Medical Research Council, Durban, South Africa

Introduction: Novel solutions are needed for improved management of vector-borne diseases in resource-constrained environments. Emerging free software providing access to satellite imagery and simple editing tools (e.g., Google Earth) complement existing Geographic Information System (GIS) software and provide new opportunities to: 1) strengthen public health capacity through development of information for city infrastructure; and 2) display public health and vector data directly on an image of the physical environment.

Methods and Results: We used satellite imagery freely accessible through Google Earth and a set of feature-making tools included in the software (allowing for production of polygons, lines, and points) to generate information for city infrastructure and to display disease data in a Dengue Decision Support System framework. Two cities in Mexico (Chetumal, Merida) were used to demonstrate that a basic representation of city infrastructure useful as a spatial backbone in a Dengue Decision Support System can be developed at minimal cost using Google Earth. Data layers generated included labeled polygons representing city blocks, lines representing streets, and points showing the locations of schools, health clinics etc. City blocks were color-coded to show presence of dengue cases. Google Earth-generated data (KML file format) were successfully imported as shapefiles into a GIS software. Benefits and limitations of using Google Earth are discussed.

Conclusion: The combination of Google Earth and free GIS software (e.g., The HealthMapper, SIGEpi) has tremendous potential to strengthen public health capacity and facilitate Decision Support System approaches to prevention and control of vector-borne diseases in resource- constrained environments.

Spatial modelling of human risk of exposure to vector-borne pathogens based on epidemiological versus arthropod vector data

Rebecca Eisen[1], Lars Eisen[2]

[1]Division of Vector-Borne Infectious Diseases, Centers for Disease Control and Prevention, Fort Collins, Colorado, United States, [2]Department of Microbiology, Immunology and Pathology, Colorado State University, Fort Collins, Colorado, United States

Introduction: Understanding spatial patterns of human risk of exposure to arthropod vectors and their associated pathogens is critical for targeting limited prevention, surveillance, and control resources (e.g., spatial targeting of vaccination, drug administration or education campaigns; use of sentinel sites to monitor vector abundance; identifying areas for most effective use of pesticides). Vector-borne disease risk can in many cases be modeled with high predictive accuracy using Geographic Information System (GIS)-approaches because abundances of vectors and pathogen reservoirs often are associated with environmental factors. Spatial risk models for human exposure to vector-borne pathogens, which ideally should have high accuracy for predicting areas of elevated risk without overestimating risk coverage, can be constructed based on epidemiological data or abundance of vectors or infected vectors.

Methods and Results: We will use four bacterial or viral vector-borne diseases occurring in the United States and with pathogen transmission by fleas (plague), ticks (Lyme disease), or mosquitoes (dengue, West Nile virus disease) to: 1) examine how spatial risk of human exposure to vector-borne pathogens typically is presented to the public health community and public; and 2) evaluate the utility of basing spatial risk models on epidemiological data relative to data for arthropod vectors or infected vectors.

Conclusion: Recommended future directions for vector-borne disease risk modeling in the United States include development of sub-county level spatial risk models combining epidemiological and vector data and use of simulation or analytical models to assess critical vector abundance thresholds required for enzootic pathogen maintenance.

Sex determination in the housefly: Variations on a common theme?

Daniel Bopp, Nicole Meier, Christoph Quinter, Regina Perez, Caroline Henggeler, Monika Hediger

University of Zurich, Zurich, Switzerland

Sexual development is based on a simple binary decision between two alternative developmental programs, male or female. Still, we only have begun to understand the underlying genetic control in a few model systems. In insects, this pathway has been most extensively studied in *Drosophila melanogaster*, and this work has provided deep insights into the molecular mechanisms that specify the sexual fate. However, it appears that an astounding diversity exists at the level of the instructive signal. Alone in the housefly, *Musca domestica*, several types have been described in natural populations, ranging from dominant male or female determiners to maternal cues. Since this spectrum, to a certain extent, reflects the dissimilitude of sex-determining cues described in insects, the *Musca* system appears particularly well suited for studying evolutionary diversification of this pathway. The different mechanisms in *Musca* are considered to have evolved in a relatively short period suggesting that the observed variations are discrete changes in an otherwise well conserved pathway. By identifying the components and their molecular functions in the *Musca* pathway, and by comparing them to those found in other fly species, we were able to define a basic mechanism that operates in most dipteran insects. This conserved core mechanism provides an ideal target for developing effective sexing strategies in programs that use the Sterile Insect Technique to control the spreading of pest fly species of medical and agricultural relevance.

Insecticide and fungal susceptibility of laboratory-reared *Anopheles gambiae* s.s. and *Anopheles arabiensis*

Christophe K. Kikankie[2], Lizette L. Koekemoer[1], Basil D. Brooke[1], Bart Knols[4], Maureen Coetzee[3]

[1]Vector Control Reference Unit, National Institute for Communicable Diseases of the National Health Laboratory Service, Johannesburg, South Africa, [2]School of Animal, Plant and Environmental Science, University of the Witwatersrand, Johannesburg, South Africa, [3]Department of Virology and Communicable Diseases Surveillance, School of Pathology, University of the Witwatersrand, Johannesburg, South Africa, [4]Laboratory of entomology, Plant sciences group, University of Wageningen, Wageningen, Netherlands

Introduction: Control of the main African malaria vectors *Anopheles gambiae sensu lato* and *Anopheles arabiensis* continues to rely heavily on the application of insecticides either by indoor residual house spraying or bednet impregnation. The development of insecticide resistance can undermine theses control strategies. Therefore, alternatives such as vector control with biological agents may be effective. Entomopathogenic fungi are being considered as a biocontrol agents for adult African malaria vectors. We carried out a study to assess the level of susceptibility to fungal infection of insecticide susceptible and resistant colonies of laboratory strains of *Anopheles gambiae* and *Anopheles arabiensis.* The entomopathogenic fungal strain tested was *Beauveria bassiana* under laboratory conditions.

Methods: Insecticide susceptibility tests against all four classes of insecticides recommended by WHO for vector control was performed according to the standard WHO bioassay protocol. Fungal susceptibility tests using hair rollers brushed with dry spores of *Beauveria bassiana* was performed on laboratory reared colonies of *Anopheles gambiae* and *Anopheles arabiensis*.

Results: Our data showed that there is no relationship between insecticide susceptibility and fungal susceptibility. All colonies showed complete susceptibility to fungal exposures despite some of them showing high resistance levels to insecticide.

Conclusions: These results provide hope for alternative control strategies other than use of insecticides. Investigations are underway to determine whether mosquitoes can be killed by fungi within the 14 day period before they become infective.

Biogeography and biology of the New Caledonian Chrysomelidae (Coleoptera)

Pierre Jolivet[1], Krishna K. Verma[2]

[1]Nat. Museum of Nat. Hist., Paris, France, [2]MP. Govt. P. G. Colleges, Borsi, Durg, India

Introduction: Probably 150 to 200 species of Chrysomelidae exist in New Caledonia and around 120 have been recorded and described. The majority of them belong to Eumolpinae. Endemism is extremely high, 10 subfamilies are represented and at least 3 species seem to be the result of vicariance. Eumolpinae seem to be polyphagous in majority, but Spilopyrini, as are many non-eumolpine genera, oligophagous and restricted to some plant families.

Methods: Most of the Chrysomelidae were collected with beating sheets, sweeping nets, Malaise, pitfall and interception traps in the plains and also in the mountains. Their biology has been studied on the spot and in the laboratory.

Results: As in Madagascar, New Caledonian fauna is disharmonious, but being smaller the island is much poorer in genera and species as compared to neighbouring land masses. Some subfamilies, as Sagrinae, Donaciinae and Clytrinae, are missing and Cassidinae are represented only by one species. Donaciinae are represented in Northern Australia, Southern New Guinea and in Indonesia. More subfamilies are missing in New Zealand, but archaic Sagrinae which are so abundant in Australia and, even represented in Madagascar, are missing in New Caledonia and New Zealand. As regards the Spilopyrini, those eumolpines are typically part of an old Gondwanan distribution and the tribe is represented in New Caledonia. Among other chrysomelids, Criocerinae, Cryptocephalinae, Chrysomelinae, some cases of vicariance (*Zira*) could be suspected, but most of the affinities of the fauna are with Australia, Sunda islands, and New Guinea. Passive introductions seemed to have been taking place since the Miocene. Affinities with New Zealand probably in some cases exist, since both archipelagoes are believed to have been linked for a short period in the past. An Eumolpine genus, must diversified in New Caledonia, *Dematochroma*, is spread from Lord Howe and Norfolk islands up to Timor in the north. As usual, quasi-polyphagy or oligophagy is the rule for many genera, but strict monophagy also exists. Development of archaic and Gondwanan Spilopyrini larvae have special features.

Conclusions: Biodiversity is high in New Caledonia, but the fauna is disharmonious, as it seems to include products of both vicariance and dispersal.

Studies on a major vector *Anopheles arabiensis* from Gwave, a malaria endemic area in Zimbabwe

Givemore Munhenga[1], Ron. T. Masendu[1], Basil. D. Brooke[2], Richard. H. Hunt[4], Maureen Coetzee[4], Lizette. L. Koekemoer[2]

[1]Department of Biological Sciences, University of Zimbabwe, P.O. Box MP 167, Mount Pleasant, Harare, Zimbabwe, [2]Vector Control Reference Unit, National Institute for Communicable Diseases, NHLS, Private Bag X4, Sandringham, Johannesburg, South Africa, [3]Division of Virology and Communicable Diseases Surveillance, School of Pathology of the National Health Laboratory Service and the University of the Witwatersrand, Johannesburg, South Africa, [4]School of Animal, Plant and Environmental Sciences, University of the Witwatersrand,, Johannesburg, South Africa

Introduction: A major obstacle that has evolved from malaria control programmes that utilize insecticides for vector control is the development of insecticide resistance. Despite decades of pesticide usage in Zimbabwe limited information on the susceptibility status of major malaria vectors is available. We investigated the susceptibility status and underlying resistance mechanisms in *Anopheles arabiensis* from a malaria endemic area in Zimbabwe.

Methods: Standard WHO bioassays, using 0.75% permethrin, 4% DDT, 5% malathion, 0.1% bendiocarb and 4% dieldrin were performed on wild-collected adult anopheline mosquitoes and F_1 progeny of *An. arabiensis* reared from wild-caught females. Molecular assays were carried out to identify *kdr* mutation. Biochemical assays to determine relative levels of non-specific esterases, monooxygenases, glutathione-S-transferases and presence of an altered acetylcholinesterase (AChE) were performed.

Results: *Anopheles arabiensis* was identified by PCR. Among the *An. arabiensis* females, 0.5% (n = 436) were positive for *Plasmodium falciparum*. WHO diagnostic tests showed 47% mortality on permethrin and 68% mortality on DDT. Insecticide susceptibility tests on F_1 *An. arabiensis* families showed an average mortality of 85.9% (n = 567) after exposure to 4% DDT and 69.8% (n=372) after exposure to 0.75% permethrin. Six families showed resistance to both DDT and permethrin. Biochemical assays of F_1 *An. arabiensis* families revealed comparatively high levels of monooxygenase (48%, n = 33, $p<0.05$), glutathione S-transferase (26%, n = 31, $p<0.05$) and general esterase activity compared to the reference colony. The *kdr* analysis by PCR revealed the presence of the East and West African mutations, but sequencing did not confirm these results.

Conclusions: The detection of permethrin and DDT resistances in *An. arabiensis* populations from Gwave has serious implications for malaria vector control in this area, particularly since Zimbabwe has reverted back to DDT for indoor house spraying. Use of mosaic insecticide application or rotational use of insecticides is recommended.

Signals and cues in the recruitment behavior of stingless bees: An introduction

Friedrich G. Barth

University of Vienna, Wien, Austria

Stingless bees are a large group of eusocial hymenopterans with several hundreds of species. In the tropics they play a role in pollination similar to that of honey bees in temperate regions. Stingless bees show a remarkable diversity of life styles and form colonies which depend on the cooperative activities of many individuals. Much of these activities focus on the acquisition and storage of food.

Since the pioneering work of Lindauer and Kerr (1958) numerous species of stingless bees have been known to effectively recruit nestmates to profitable food sources. In recent years behavioral experiments and research using modern instrumentation succeeded in identifying the properties and the origin of a number of signals and cues used by stingless bees either extra- or intranidally when exploiting food sources. Introducing the Symposium, our present knowledge of chemical (scent trail, food marks), mechanical (jostling, thoracic vibrations) and visual signals and cues, and their actual or potential communicatory significance will be reviewed and discussed. There is abundant evidence for a correlation between signals communicated during recruitment and the quality of the food offered at the food source. So far, however, there is no evidence for a "dance" or a similar behavior indicating that stingless bees can communicate the location of a food source using a "symbolic language".

Supported by the Austrian Science Fund FWF, project 17530 to FGB.

Synaptic circuits in the medulla neuropile of the *Drosophila* visual system

Ian Meinertzhagen, Lu Zhiyuan, Takemura Shin-ya

Dalhousie University, Halifax, Nova Scotia, Canada

Tracing the pathways for vision beneath the fly's compound eye has stalled for decades at the second neuropile, the medulla, the largest neuropile in the fly's brain. Exploiting its modular composition and previous reports of synaptic circuits in the first neuropile, the lamina, we have used 3D reconstruction methods from serial-section EM to identify cells morphologically with reference to previous reports from Golgi impregnation, or more recent genetic reporters using the Gal4/UAS system.

First, we reconstructed input terminals to the distal medulla from: lamina cells L1-L5, photoreceptors R7 and R8, medulla cell T1, and centrifugal cells C2 and C3. The morphology of these conforms to previous Golgi profiles, offering assurance that our reconstructions are complete.

Next, we identified the medulla cell targets of these input terminals. Three medulla synaptic targets of R7 and R8 probably signal colour information: Dm5 receives input from multiple UV-sensitive R7s; Tm5 and Tm9 receives input from R7 and R8, respectively, with both also receiving input from L3. Inputs to five different medulla cell targets from L1 and L2 segregate these two pathways, which play a crucial role in motion detection. L1 is reciprocally connected to L5 and presynaptic to at least two medulla neurons, while L2 is presynaptic to at least three medulla neurons that are not postsynaptic to L1, two of which form synaptic contacts in turn with L4. The L1 and L2 terminals are connected only by C2 and C3, which are possibly required to switch activity between these two motion-sensitive L-cell pathways.

Effects of mycorrhizal fungi on insect herbivores: a meta-analysis

Julia Koricheva, Alan Gange

Royal Holloway University of London, Egham, Surrey, United Kingdom

Insect herbivores and mycorrhizlal fungi are indirectly linked through their common host plant. Moreover, mycorrhizal presence has a wide range of morphological and physiological effects on plants that may change their quality as a food for herbivores. One might therefore hypothesize that insects may be affected by the plant mycorrhizal status. To test this hypothesis, we conducted a meta-analysis of 34 published and unpublished experiments that have examined effects of mycorrhizal colonization of the host plant on performance and density of insect herbivores as well as on the degree of plant damage. Density and consumption of chewing insects were higher on mycorrhizal plants, but this did not lead to higher plant damage presumably because herbivore survival tended to be lower on mycorrhizal plants. Mono- and oligophagous chewers benefited from mycorrhizal colonization of their host plants whereas performance of polyphagous herbivores tended to be reduced on mycorrhizal plants. Among sucking insects, phloem feeders benefited from mycorrhizal infection whereas performance of mesophyll and meristem feeders was lower on mycorrhizal plants. Type of mycorrhizae had no effect on chewing insects, but performance of sucking insects was increased more by arbuscular mycorrhiza (AM) than by ectomycorrhiza. We have concluded therefore that plant mycorrhizal colonization has a significant effect on herbivore performance, but the direction and magnitude of this effect depends on the type of herbivore and type of fungi. Plant mycorrhizal status, therefore, have to be taken into account in studies examining variation in herbivores performance between plants in the field.

Fungus pathogenicity, establishment of bark beetle populations and tree death

Francois Lieutier

Universite d'Orleans, Orleans, France

Since tree death seems necessary for their population establishment, tree killing bark beetles should be associated with highly phytopathogenic fungi. However, when compared to classical fungal pests, bark beetle associated fungi need a high density of inoculations to kill trees, and are thus moderately phytopathogenic. The explanation may be that a highly pathogenic fungus would kill and invade the tree very rapidly, making its tissues unsuitable for beetle brood development. With that strategy, a relationship between fungus pathogenicity and beetle aggressiveness should exist among bark beetle fungi. But it does not. Rather than fungus ability to kill trees, what is important for bark beetle populations in their fungal associations is fungi ability to stimulate tree reactions to aggressions, resulting in lowering the critical threshold of attack density above which beetle attacks succeed. Fungus ability to induce extensive tree reactions appears a better parameter of the efficiency of the association than the critical threshold of inoculation density. However, during natural attacks, beetles do not all vector fungi, and the number of fungal spores in each beetle certainly plays a role, making hazardous the evaluation of reaction stimulation through artificial inoculations. It can be accepted that the above strategy is really operating, and that it works through the ability of the fungus to stimulate tree reactions to aggressions. It is suggested however that the efficiency of the association for beetle population establishment results from three components: the fungus intrinsic ability to stimulate tree defenses, the percentage of contaminated beetles, and the inoculum level on each beetle.

Directed aerial descent in tropical canopy arthropods

Steve Yanoviak

University of Arkansas at Little Rock, Little Rock, Arkansas, United States

Worker ants in seven tropical genera use directed aerial descent to return to their home tree trunk during a fall. Field experiments focusing on the common Neotropical species *Cephalotes atratus* showed that the behavior is not accidental or location-specific, and that performance is partly a function of body size. Falling ants use visual cues to locate tree trunks, and the behavior is strongly influenced by reflectance properties of potential landing substrates. Ablation experiments and high-speed video recordings of falling ants suggest that the hind legs have the greatest influence on aerodynamic stability and control. Ongoing surveys show that the behavior occurs in a broad range of wingless arboreal arthropods, including basal hexapods.

Close-range host searching behaviour of the stemborer parasitoid *Dentichasmias busseolae*: Role of a non-host plant *Melinis minutiflora*

Linnet S. Gohole, William A. Overholt, Louise E.M. Vet, Zeyaur R. Khan

[1]Moi University, Eldoret, Kenya, [2]University of Florida, Florida, United States, [3]Netherlands Institute of Ecology (NIOO-KNAW), Maarsen, Netherlands, [4]International Centre of Insect Physiology & Ecology (ICIPE), Nairobi, Kenya

Introduction: Studies were conducted on the host searching behaviour of the pupal parasitoid *Dentichasmias busseolae* Heinrich (Hymenoptera: Ichneumonidae), which attacks the cereal stemborer *Chilo partellus* (Swinhoe) (Lepidoptera: Crambidae). The aim of the present study was to investigate how molasses grass influences parasitoid close-range foraging behaviour in a diversified habitat.

Methods: The behaviour of individual gravid parasitoids was observed in a semi-field environment of a diversified habitat that consisted of stemborer host plants (maize, *Zea mays* L. and sorghum, *Sorghum bicolour* (L). Moench (Poaceae)) and a non-host plant (molasses grass, *Melinis minutiflora* Beauv. (Poaceae)). Observations of its behaviour and location were recorded for 30 minutes using the computer software package, The Observer.

Results: *Dentichasmias busseolae* strongly discriminated between host and non-host plants with female wasps spending most time on infested host plants and least time on molasses grass. On the infested plant, the wasps spent more time foraging on the stem, the site of damage than other areas of the plant.

Conclusion: The results indicate that presence of the non-host plant does not hinder close range foraging activities of the parasitoid species.

Univoltinity in the winter aggregator *Encosternum delegorguei* (Hemiptera: Tessaratomidae) in relation to abdominal fat, food plants and predation

Cathy Dzerefos[1], Rob Toms[2], Edward Witkowski[1]

[1]University of the Witwatersrand, Johannesburg, South Africa, [2]Transvaal Museum, Pretoria, South Africa

Introduction: *Encosternum delegorguei* is an edible stinkbug eaten with delight each year by people in north-eastern South Africa and southern Zimbabwe. To ensure long-term sustainable harvesting of this insect, a better understanding of its life history and other aspects pertaining to survival are necessary.

Method: Outdoor insectaries were built to observe daily activity, commencement of copulation, oviposition behaviour and egg incubation from May 2006 to February 2007. Field observations under natural conditions were also undertaken. Abdominal dissections on six adults per month were done and fat content categorised from May to December.

Results: Dissections showed that abdominal fat content is highest in June at the onset of diapause. From September *E. delegorguei* commenced feeding on *Combretum imberbe, Combretum molle, Peltophorum africanum, Pennisetum clandestinum, Phaseolus vulgaris* and to a lesser degree *Dodonaea viscosa.* From late October to end of December 1 752 eggs were laid by 103 females. The mean number of eggs in 64 egg clutches was 27.38±13.91 (range of 2 to 56 eggs). The incubation time averaged 18.65±8.95 days (range of 7 to 37 days). Shade cloth (68.8%) was the most commonly used substrate for depositing eggs followed by *P. clandestinum* (12.5%), *C. imberbe* (7.8%), *P. africanum* (6.3%), *D. viscosa* (1.6%), *C. molle* (1.6%) and *Combretum erythrophyllum* (1.6%). The parasitoid wasp, *Anastatus* sp. (Family: Eupelimidae) infected 68.8% of the egg clutches deposited by captive females.

Conclusions: During winter *E. delegorguei* is in diapause in misty mountainous areas where it is secluded from cold winds but is able to imbibe condensed water. This first record of an egg parasitoid, *Anastatus* sp. suggests break up of winter aggregation at the landscape level may be essential to minimise infection and could be a factor causing sporadic harvests. Controlled laboratory conditions where humidity in particular can be controlled and parasitoids excluded are recommended for domestication.

Physiological mechanisms underpinning the rapid cold-hardening response

Richard Lee, Shu-Xia Yi

Miami University, Oxford, Ohio, United States

The rapid cold-hardening (RCH) response refers to a swift acclimatory process by which insects enhance their cold tolerance following brief exposure to moderate chilling. Recently, we obtained strong evidence that RCH occurs under ecologically relevant cooling rates and diurnal thermoperiods. Not only does this widespread response protect against chilling injury but it also preserves locomotor, courtship and mating performance during environmental cooling. During the past few years we have begun to unravel clues to the physiological mechanisms underpinning this response. The cell membrane is generally believed to be the primary site of chilling injury caused, in part, by thermotropic phase changes. During RCH levels of unsaturated phospholipid fatty acids increase in the cell membrane as does membrane fluidity, which should function to decrease thermotrophic membrane damage. In vitro studies revealed that isolated cells of several tissues can respond directly to cold (i.e. cold sensing) and undergo RCH, indicating that neuroendocrine mediation is not required. Further studies indicate that calcium is required in the signaling pathway leading to the RCH response; removal of calcium or blocking with an intracellular chelator diminishes cryoprotection by RCH. Cold shock induces apoptosis or programmed cell death. Presumably cold causes mitochondrial release of cytochrome *c* into the cytoplasm that triggers the apoptotic pathway. RCH blocks cold-induced apoptosis by up-regulating the anti-apoptotic protein Bcl-2 and inhibiting the activation of caspases. Supported by NSF grant IOB-0416720.

Bridging theory and practice: the role of service-learning in bringing entomology to the public

Marianne Robinette, Ray Noblet

University of Georgia, Athens, Georgia, United States

Introduction: Service-learning and study abroad opportunities are critical components of undergraduate education that create an environment of active academic engagement while bringing entomology to the public. Mutually beneficial and sustainable projects with community partners allow students to solve real-world problems through first-hand experience.

Methods: Integrating service-learning into the entomology curriculum at UGA provides students the opportunity to participate in developing and implementing entomological programs for the community both domestically and internationally.

Results: *Entomology Outreach & Service-Learning* is a course where students participate in developing entomological educational outreach programs. Examples of current service-learning projects include building an Apiary as well as an Outdoor Classroom at Classic City High School in Athens, GA. The apiary is used as a concept learning tool for biology, environmental stewardship, sustainable agriculture, entrepreneurship, economics and business classes. Honey is collected and sold to the community for school fundraisers and for sustaining the bee colonies. The Outdoor Classroom is an interdisciplinary service-learning project addressing the need for an innovative space for teaching and learning in all subject areas at the high school. *Insect Natural History in Costa Rica* is a course designed for students to enhance their global awareness of environmental and cultural issues through the use of insects as teaching tools, coupled with structured entomological public outreach experiences. While abroad, students build insect collections, conduct research-based field studies, and participate in entomological outreach activities at Costa Rican elementary schools.

Conclusions: Collectively these service-learning and study abroad opportunities have enabled our students to connect insect science with the public.

Insect resistant transgenic crops: An opportunity for biological control?

Franz Bigler[1], Joerg Romeis[2], Roy G. van Driesche[3], Barbara I.P. Barratt[4]

[1]Agrsocope Reckenholz-Taenikon Research Station ART, Zurich, Switzerland, [2]Agroscope Reckenholz-Taenikon Research Station ART, Zurich, Switzerland, [3]University of Massachusetts, Amherst, United States, [4]AgResearch Invermay, Mosgiel, New Zealand

Plant resistance to insects has played a major role in integrated pest management (IPM) since long, and its compatibility with biological control is principally not questioned. Natural enemies such as parasitic wasps and predators fulfil an important ecological and economic function by reducing herbivore populations and thus, they contribute to sustainable IPM systems. It is well established that plant resistance factors that affect herbivores also interact with natural enemies and consequently with the biological control function they provide. Similarly, host plant resistance derived from genetic engineering will have an impact on biological control. There is evidence today that the currently available transgenic crops that express Cry proteins derived from *Bacillus thuringiensis* (*Bt*) have no direct effects on natural enemies due to their narrow spectrum of activity. However, the fact that the target pests are efficiently controlled by the deployed *Bt* crops has inevitable consequences for natural enemies that specialize on these species as hosts or prey. Landscape level effects may occur for specialists if adoption of *Bt* crops provide area-wide reductions of target pest populations. On the other hand, it has become clear that in crop systems where the deployment of *Bt* varieties has lead to a decline in insecticide use, biological control organisms have benefited significantly. Consequently, in systems where *Bt* crops replace insecticides, this technology can contribute to natural enemy conservation and thus be a useful tool in IPM.

Understanding distribution patterns of invertebrates within inland drift sand areas using life-history tactics and feeding guilds

Marijn Nijssen[2], Hans Esselink[1], Marten Geertsma[2], Toos Van Noordwijk[2], Henk Siepel[3]

[1]Radboud University Nijmegen, Nijmegen, Netherlands, [2]Bargerveen Foundation, Nijmegen, Netherlands, [3]Centre for Ecosystem Studies Alterra, Wageningen, Netherlands

Introduction: European inland drift sands and their characteristic flora and fauna species are highly endangered. Understanding of mechanisms shaping species distribution patterns within these systems is necessary to develop restoration and conservation measures. To unravel the relative importance of different environmental variables life-history tactics and feeding guilds are used.

Methods: Invertebrates were sampled in 8 inland drift sand areas in The Netherlands using extraction of soil samples and pitfall traps. Sampling took place in 5 successive vegetation types which differ in aeolian dynamics, microclimate and food resources. Species specific traits on development, reproduction, synchronisation and dispersal were used to define life-history tactics for mites (Acari), springtails (Collembola), ants (Formicidae) and carabid beetles (Carabidae). Distribution patterns were analysed using multivariate methods.

Results: Within all study areas, similar distribution patterns of species and life history tactics were found. Life-history traits explaining most variance in distribution patterns for all studied invertebrate groups were timing of reproduction and diapause, high dispersal capability and speed of larval development. These traits were highly correlated with differences in aeolian dynamics. Herbivorous browsers dominated in early succession stages, while in older succession stages feeding guilds were equally distributed, implicating an increasing bottom-up regulation from food resources.

Conclusions: Use of life-history tactics and feeding guilds proofs to be a strong tool in analysing mechanisms of species distribution, facilitating comparison of different areas and different invertebrate taxonomic groups. Management should focus on aeolian dynamics in a gradient to stable vegetation for restoration and conservation of complete fauna communities.

Using EPG to compare acceptance by the spittle bug *Carystoterpa fingens* of four plant species

Manoharie Sandanayaka

The Horticulture and Food Research Institute of New Zealand Limited (HortResearch), Auckland, New Zealand

New Zealand is currently free of both *Xylella fastidiosa* (a bacterium that causes several diseases of agricultural, horticultural and ornamental plants) and its vector, glassy-winged sharpshooter (GWSS). Nevertheless, it remains vulnerable to invasion by both organisms. *Citrus sinensis*, *Coprosma repens, Hydrangea peniculata* and *Vitis vinifera* (grape), are four of many species in New Zealand known to be hosts of both GWSS and *X. fastidiosa*. The electrical penetration graph (EPG-DC) technique was used to compare their acceptance as food by the endemic spittle bug *Carystoterpa fingens*; one of the several xylem feeders may potentially act as a conduit for *X. fastidiosa* into native host plants. EPG waveforms representing main stylet penetration activities [pathway, xylem ingestion, resting, and non-probing phases] of 54 adults were recorded for 12 hours per insect. The durations and the number of events were analysed to compare host acceptance. The total probing times on grape were not significantly different from citrus but were longer than on hydrangea and coprosma. Non-probing times were longest on coprosma. The longest periods of xylem ingestion (total duration and the longest event) were recorded on grape and the shortest on coprosma. The shortest durations of pathway were recorded on grape. Citrus and hydrangea were intermediate and not significantly different from one another. The number of xylem ingestion events on citrus was significantly higher than grape, coprosma and hydrangea. It was concluded that grape was the best host, citrus and hydrangea were accepted and coprosma was the least accepted.

Controlling larval chironomids (Diptera: Chironomidae) in Australian rice crops using a commercial formulation of *Bacillus thuringiensis* var. *israelensis*

Mark Stevens, Glen Warren

E H Graham Centre for Agricultural Innovation (NSW Department of Primary Industries and Charles Sturt University), Yanco Agricultural Institute, Yanco NSW, Australia

Introduction: Some larval Chironomidae attack the roots of rice seedlings, and in Australia populations dominated by *Chironomus tepperi* Skuse can cause over 80% seedling loss if not controlled. We evaluated spray applications of Vectobac® WDG, a commercial formulation of *Bacillus thuringiensis* var. *israelensis*, as a potential control option.

Methods: Vectobac® WDG was evaluated in 2 replicated small-plot field trials at rates between 0.5 and 6 kg/ha. Larvae were sampled and extracted using soil coring and magnesium sulphate flotation. Samples were taken at 5 day intervals from 4 to 19 days after treatment. Larvae were divided into target (Chironominae / Orthocladiinae) and non-target (Tanypodinae) groups. Target group larvae recovered from selected treatments at 4, 9 and 14 days after Vectobac® WDG application were identified to species level. Seedling density was also assessed.

Results: Target group suppression was significant ($P < 0.05$) at all rates 4 days after application, and ranged from 39 to 92% over the full 19 days. Complete control of *C.tepperi* was achieved at rates over 1.25 kg/ha. Vectobac® WDG had no noticeable effect on non-target Tanypodinae. In the first trial plant establishment was significantly ($P < 0.05$) enhanced at all rates, however in the second trial no significant differences were found, presumably due to lower pretreatment larval densities.

Conclusions: Vectobac® WDG has the potential to provide highly selective control of pestiferous chironomids in rice. The optimal rate for Australian rice crops is approximately 1.5 kg/ha.

The effect of the entomopathogenic fungi *Beauveria bassiana* and *Metarhizium anisopliae* against the major malaria vector *Anopheles funestus* Giles

Joel C. Mouatcho[1,2], Basil D. Brooke[1,3], Bart Knols[4], Maureen Coetzee[1,3]

[1]National Institute for Communicable Diseases, Sandringham/Johannesburg, South Africa, [2]School of Animal Plan and Environmental Sciences, University of the Witwatersrand, Johannesburg, South Africa, [3]Division of Virology and Communicable Disease Surveillance, School of Pathology of the National Health Laboratory Service and the University of the Witwatersrand, Johannesburg, South Africa, [4]University of Wageningen, Wageningen, Netherlands

Introduction: The increase of malaria cases due to insecticide resistance in some malaria vectors as well as the impact of pesticides on the environment and non-target insects and animals has provided an impetus for the development of alternative forms of vector control using entomopathogenic fungi. We investigated the potential of *Beauveria bassiana* and *Metarhizium anisopliae* against laboratory strains of the major malaria vector *An. funestus.* We also determined the level of infectivity between a pyrethroid resistant (FUMOZ-R) and susceptible strain (FANG) of colonised *An. funestus.*

Methods: Mosquitoes were exposed to dry fungal conidia for 24 hours using World Health Organization exposure tubes. Mortality was recorded daily after exposure. Sporulation was checked on cadavers 2 days post mortality. Data were analysed using *Statistix7 Software.*

Results: *Beauveria bassiana* was found to be effective in killing *An. funestus* with mortalities ranging from 90%-100% after 15 days. A comparison of FUMOZ-R and FANG treated with conidia showed the pyrethroid resistant FUMOZ-R to be more susceptible to fungal exposure than the susceptible strain FANG. Conidia of *B. bassiana* produced 100% mortality in FUMOR-R and FANG within 15 and 22 days respectively while, less than 10% mortality occurred in corresponding unexposed controls. For *M. anisopliae* treatment, mortality rates were higher in FANG than in FUMOZ-R with 100% mortality obtained within 14-17 days for FANG as compared to >20 days for FUMOZ-R. An average of 90% fungal infected mosquitoes sporulated between 2-4 days after death.

Conclusions: *Beauveria bassiana* and *Metarhizium anisopliae* can be used as an alternative mode of vector control. The presence or absence of insecticide resistance is not likely to affect susceptibility to fungal infection in *An. funestus.*

The behavioural ecology of *Ciulfina* praying mantids

James O'Hanlon, Greg I. Holwell, Mariella E. Herberstein

Department of Biological Sciences, Macquarie University, North Ryde, NSW, Australia

Previous research into the ecology of praying mantids has investigated in great detail the population characteristics of particular species and their role as generalist predators that can have significant effects on arthropod community structure. The great majority of this research however has concentrated on a small number of temperate, northern hemisphere mantids occupying similar habitats with similar life history strategies. Understandably this is not representative of the diversity exhibited in the 2300 or so species of mantids found world wide. Tree running mantids of the genus *Ciulfina* differ from those previously studied in many ways including their population structure, habitat type, geographical distribution and evolutionary history. This presentation investigates the behavioural ecology of *Ciulfina* mantids and addresses their population characteristics, intraspecific interactions and mating behaviour.

Natural refugia using alternate hosts of the Asian corn borer (*Ostrinia furnacalis*) for insect resistance management of Bt corn in the Philippines: Possible strategies in tropical setting

Merdelyn Lit

UP Los Baños, College, Laguna, Philippines

Insect resistance management (IRM) is one of the basic requirements for a successful Bt corn production in a country. This is based on the premise that insect pests generally become resistant to high selection pressure such as the use of Bt corn. It is even more complicated if the premise considers the geographical location and corn production systems of the area.

IRM, however, in the tropical sense is governed by two important undelying factors: 1) the tropical corn growing conditions and 2) the tropical feature of the Asian corn borer, *Ostrinia furnacalis* (Guenee). How these two important components interrelate with each other is the basic framework for a sound and ecological insect resistance management in the tropics. Furthermore, for an effective IRM, basic studies on the Asian corn borer must be in place.

This paper will present the basic requirements for IRM to work in a tropical setting highlighting the important role of alternate hosts as natural refuge for susceptible ACB. Some previous and on-going studies will also be presented. It will review the important role of the different alternate weed and crop hosts of ACB in three cropping systems of the country and discuss possible strategies of unstructured or natural refugia in Bt corn IRM in our tropical setting.

These strategies are founded on the above basic requirements and will eventually gain a total advantage if we put nature and biodiversity in the over-all framework.

Wolbachia, bacteriophage WO superinfection and genetic diversity in the uzifly *Exorista sorbillans* (Diptera: Tachinidae)

Puttaraju Hosagavi Puttegowda, Guruprasad Nadipinayakanahalli Munikrishnappa

Department of Sericulture and Lifesciences, Bangalore University, Bangalore, Karnataka, India

Wolbachia pipientis is a maternally transmitted bacterium that often alters the life history of its hosts to maximize transmission to subsequent generations. The various alterations induced by *Wolbachia* are cytoplasmic incompatibility, parthenogenesis, sex ratio distortion, male killing, and feminization. Earlier studies have established that the Uzifly *Exorista sorbillans* a tachinid endoparasite of silkworm *Bombyx mori* harbour A and B *Wolbachia* supergroup. In the present study we detected infection frequency of *Wolbachia* and bacteriophage WO superinfection and their effects on the diversity of Uzifly collected from different geo climatic regions of India. The molecular profiling of infected populations was done by using the Randomly Amplified Polymorphic DNA (RAPD). The dendrogram constructed from un-weighted pair grouped method with arithmetic mean (UPGMA) and distance computed using Euclidean distance clearly estimated the genetic diversity between different populations of *E. sorbillans.* The genetic divergence observed could be the result of the geographic isolation among populations, but it could also be explained by the infection with the rickettsial bacteria *Wolbachia* pipientis and bacteriophage WO It is suggested that the interaction between cytoplasmic incompatibility (CI) inducing *Wolbachia* and its bacteriophage WO of Uzifly perhaps promoting the genetic diversity and speciation in the Uzifly, *E. sorbillans*

Are nitrogen driven changes in host plant quality responsible for the decline of butterfly species in NW-Europe?

Marijn Nijssen[2], Frits Bink[3], Arnold van den Burg[2], Gert-Jan van Duinen[2], Hans Esselink[1], Chris Van Swaay[4], Michiel Wallis de Vries[4], Henk Siepel[3]

[1]Radboud University Nijmegen, Nijmegen, Netherlands, [2]Bargerveen Foundation, Nijmegen, Netherlands, [3]Centre for Ecosystem Studies Alterra, Wageningen, Netherlands, [4]Dutch Butterfly Conservation, Wageningen, Netherlands

Introduction: Many butterfly species in NW-Europe show a strong decline while their host plants are still abundant. This is especially true for species of nutrient poor habitat types such as bog and heathland. There are several indications that changes in quality of host plants due to increased nitrogen deposition might be an important reason for this decline. Changes in host plant quality can be caused directly by increased availability of nitrogen or indirectly by decreased availability of minerals as a result of acidification. This causes imbalances between nitrogen content of the host plant in relationship to levels of minerals, essential vitamins and amino acids. These imbalances can have significant effects on development, survival and reproduction success of butterflies.

Methods: Pilot field studies were carried out for 7 butterfly species. Host plant quality and soil chemistry were analysed from field sites differing in nitrogen deposition level.

Results: Studies showed several nutritional imbalances for micronutrients correlated with soil nitrogen content, including lack of Ni which may cause ureum toxification in caterpillars. Imbalances were found in different host plant types, such as grasses, heather and oak. Feeding experiments for *Hiparchia* species (Lepidoptera: Satyrinae) on grass species *Corynephorus canescens* are now running to analyse the effects of nutritional imbalances on larval development, pupation and adult reproduction.

Conclusions: Host plant quality can change significantly due to nitrogen enrichment, though mechanisms behind these changes are yet unclear. Feeding experiments will be necessary to elucidate actual risks of nutritional imbalances to endangered butterflies.

Learning to escape robotic spiders: predator avoidance learning in bumblebees

Thomas Ings, Lars Chittka

Queen Mary, University of London, London, United Kingdom

Introduction: Learning is expected to be potentially more important in predator avoidance than foraging because a single mistake can be fatal. However, few, if any, attempts have been made to measure the dynamics of predator avoidance learning in a natural context. We therefore quantify predator avoidance learning of nectar foraging bumblebees using a novel, semi-natural, foraging paradigm.

Methods: We presented bees with an artificial meadow containing 16 remotely controlled flowers that could simulate a predation attempt by a crab spider by capturing bees as they fed. Avoidance learning and memory dynamics were measured for bees encountering dangerous flowers with either visible or camouflaged spider models. In addition, flight behaviour was quantified using 3D tracking software.

Results: All bees learnt to avoid dangerous flowers well, irrespective of the visibility of the crab spider models. Bees learnt to avoid visible spiders slightly better than camouflaged spiders, although the speed of learning did not differ. For both spider visibility treatments bees continued to avoid dangerous flowers without significant loss in performance over both middle (minutes) and long time scales (24 hours). The presence of camouflaged spiders on dangerous flowers led to subtle changes in flight behaviour: when rejecting flowers, bees flew slower and spent longer inspecting dangerous flowers than safe flowers.

Conclusions: Bumblebees are readily able to learn to avoid simulated predation attempts at flowers. When predators are difficult to detect they appear to compensate by slowing down inspection flights enabling them to maintain high levels of accuracy.

Phylogenetic relationships among Alysiini (Hymenoptera: Braconidae: Alysiinae); utilizing 28S, 16S, COI and ND1 markers.

Salmah Yaakop[1], Cornelis van Achterberg[1], Bin Abd. Ghani Idris[2]

[1]National Museum of Natural History, NATURALIS, Leiden, Netherlands, [2]Universiti Kebangsaan Malaysia, Bangi, Selangor, Malaysia

Introduction: Information on generic relationships among Alysiinae: Alysiini based on morphological and molecular data is very poor. It is important to answer several related questions, i.e the relationships among genera, genus groups and phylogenetic status in Opiinae in relation to Alysiinae is supposed to be the sister-group of Alysiinae (both are endoparasitoids of cyclorraphous Diptera). The monophyly or paraphyly of Alysiinae/Opiinae is still under debate.

Methods: Sequences of Dacnusini and Opiinae are included in the phylogenetic analysis as well as Exothecinae (*Colastes* sp.) and Gnamptodontinae (*Gnamptodon* sp.) the latter to do grouping the outgroups. Samples of Alysiinae have been taken from fresh and dried museum specimens for PCR and sequencing. For the phylogenetic analysis PAUP 4.0 and MRBAYES 3.0B4 have been used.

Results: According to the preliminary results from the combined trees (28S + 16S) five well defined groups in Alysiini (*Phaenocarpa*, *Asobara*, *Alysia, Cratospila* and *Aspilota*-group) are found and the results agree with the morphology and biology. *Alysia*-group (mining Diptera and rotting organic material) + tribe Dacnusini (mining larvae) are found to be the basal groups, followed by *Heterolexis* sp. (*Dapsilarthra* group, mining larvae) - *Neurolarthra* sp. (aberrant group, biology: unknown) - *Aspilota*-group (parasitoids of Phoridae), while *Cratospila*-group (biology: unknown), *Asobara*-group (fruits-infesting larvae and rotting organic material) and *Phaenocarpa*-group (attacking larvae in galls, fruits, rotting organic material and less also mining larvae) as the more derived groups in Alysiinae. Both protein-coding genes (COI and ND1) are found not to be very useful to resolve genus relationships in Alysiinae, but good for species groups in Alysiini.

Conclusions: Relationships in Alysiini has been largely resolved, but some nodes with moderate support. The results of the molecular analyses are more or less comparable with morphology and biology.

New challenges facing regulatory agencies and advances in technology, communication, and research to support these challenges

Terrence Walters

USDA-APHIS-PPQ-CPHST, Fort Collins, Colorado, United States

As globalization increases, the biodiversity of potential pests arriving at our borders are and will continue to increase. Today, regulatory personnel struggle to have the taxonomic knowledge, background, and just basic information on potential pests to support their required decision-making. The magnitude, the required breadth of taxonomic knowledge, and reference collections of specimens and images required for the biodiversity of potential pests that might enter our country can be rather overwhelming for our agencies. As trade products continue to diversify and as the number of trading partners continue to increase, regulatory agencies have to depend more and more on outside sources for up-to-date pest taxonomic, identification, and diagnostic information.

Regulatory agencies are now depending more and more on their trading partners and global databases for taxonomic and identification resources and information on potential pests arriving at ports. The world-wide-web is now allowing us an amazing opportunity to share our knowledge with our trading partners, as well as to access pest information from our trading partners and others from throughout the globe.

Our decision process on whether a pest is actionable or non-actionable depends heavily on the biology and taxonomic research communities, both nationally and internationally, and our collaboration with and support for them. Regulatory agencies are and will continue to require reporting from these communities to support the ever changing and evolving plant protection and quarantine environment. We are fortunate in that these communities are now re-inventing themselves to share their findings and results with the public using the latest in technologies and methods of communication.

Aboveground-belowground interactions: state of the art and current and future challenges

Martijn Bezemer[1], Jeff Harvey[2]

[1]Laboratory of Nematology, Wageningen University, Wageningen, Netherlands, [2]Department of Multitrophic Interactions, Netherlands Institute of Ecology, Wageningen, Netherlands

Studies exploring interactions between insects and plants over several trophic levels have traditionally focused on aboveground communities. However, ecologists are becoming increasingly aware that plants and insects are part of a complex multitrophic aboveground and belowground environment in which they closely interact.

We will provide an overview of recent developments in the field of above-belowground interactions and will highlight challenges that are currently being addressed. Using examples from a range of studies we will summarize (i) evidence for linkages between aboveground and belowground herbivorous insects and other soil dwelling organisms via a shared host plant, (ii) mechanisms that have been proposed to explain these interactions, (iii) how interactions between above- and belowground organisms can influence parasitoids and predators, and (iv) whether there is evidence for linkages between above- belowground multitrophic communities under natural conditions in the field.

A population perspective on plant-pollinator interactions

Steven Johnson

University of KwaZulu-Natal, Pietermaritzburg, South Africa

The Allee effect (reduced reproductive success in small populations) has been reported for several plant species. One possible explanation for this phenomenon is reduced attractiveness of small populations to pollinators. This is supported by evidence showing a greater degree of pollen limitation in small plant populations. Ecological Allee effects caused by pollen/pollinator limitation are an issue of concern for management of rare and endangered plant populations. On the other end of the scale are invasive plants that appear to be highly resistant to Allee effects. Surveys also show that invasive plants are often capable of self-fertilization. This is consistent with Baker's Law, but it is not yet known whether self-fertilization in colonizing plant species is important because obviates the need for pollinators or because of the shortage of mating partners during early stages of population establishment. In general, there is increasing evidence that pollination processes can impact on plant population dynamics.

The present and future role of insect-resistant genetically modified maize in IPM

Richard L. Hellmich[1], Ramon Albajes[2], David Bergvinson[3], Jarrad R. Prasifka[1], Zhen-Ying Wang[4], Michael J. Weiss[1]

[1]USDA-Agricultural Research Service, Corn Insects & Crop Genetics Research Unit and Department of Entomology, Iowa State University, Ames, Iowa, United States, [2]University of Lleida, Lleida, Catalonia, Spain, [3]Bill & Melinda Gates Foundation, Seattle, Washington, United States, [4]Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing, China, [5]Golden Harvest Seeds, Pine River, Wisconsin, United States

Commercial, genetically-modified (GM) maize was first planted in the United States (USA, 1996) and Canada (1997) but now is grown in 13 countries on a total of over 25 million hectares (>17% of area worldwide). The first GM maize plants produced a Cry protein derived from the soil bacterium *Bacillus thuringiensis* (*Bt*), which made them resistant to European corn borer and other lepidopteran maize pests. New GM maize hybrids not only have resistance to lepidopteran pests but some have resistance to coleopteran pests and tolerance to specific herbicides. Growers are attracted to the *Bt* maize hybrids for their convenience and because of yield protection, reduced need for chemical insecticides, and improved grain quality. Yet, most growers worldwide still rely on traditional integrated pest management (IPM) methods to control maize pests. They must weigh the appeal of buying insect protection "in the bag" against questions regarding economics, environmental safety, and insect resistance management (IRM). Traditional management of maize insects and the opportunities and challenges presented by GM maize are considered as they relate to current and future insect-resistant products. Four countries, two that currently have commercialize *Bt* maize (USA and Spain) and two that do not (China and Kenya), are highlighted. As with other insect management tactics (e.g., insecticide use or tillage), GM maize should not be considered inherently compatible or incompatible with IPM. Rather, the effect of GM insect-resistance on maize IPM likely depends on how the technology is developed and used.

Successes and challenges for the rearing of predatory heteropterans

Patrick De Clercq

Ghent University, Ghent, Belgium

Several predatory mirids and anthocorids are currently being marketed for augmentative releases, mainly in greenhouse crops. Augmentative biological control should be based on a cost effective and reliable production of high-quality natural enemies. In order to reduce costs related to tritrophic rearing systems, factitious foods and artificial diets have been proposed for the production of predatory bugs and some of these have found their way into practice.

Frozen eggs of *Ephestia kuehniella* are routinely used for the production of predatory anthocorids (*Orius* and *Anthocoris* spp.) and mirids (e.g., *Macrolophus* spp., *Dicyphus hesperus*, *Nesidiocoris tenuis*). These lepidopteran eggs constitute a factitious food that is often nutritionally superior to the natural prey. However, the cost of *E. kuehniella* eggs is still high (currently around 500 EUR per kg) and market availability has been under pressure from a continually increasing demand. Cysts of the brine shrimp *Artemia* spp. have been used to replace lepidopteran eggs in part of the production process of certain predatory heteropterans.

In addition, artificial diets have been developed, with a varying degree of success, for several species of predatory anthocorids, mirids and pentatomids, but the practical use of these diets is still in its infancy.

Besides animal foods, many predatory bugs require plant materials for moisture, supplementary nutrients or growth factors, or as an oviposition substrate. The development of artificial oviposition substrates constitutes a further challenge for the rationalisation of rearing procedures for mirid and anthocorid bugs that deposit their eggs into plant tissues.

Quality assurance of mass produced predatory bugs often requires time consuming assessments of developmental and particularly reproductive traits. In this respect increasing attention is given to the development of rapid tools to assess reproductive potential, including dissection tests and ELISA-based detection of yolk proteins.

Multi-trophic maintenance of herbivore populations: how plant secondary chemistry indirectly benefits parasitoid natural enemies.

Angela Smilanich[1], Lee Dyer[1], Deane Bowers[2], Jeff Chambers[1]

[1]Tulane University, New Orleans, LA, United States, [2]University of Colorado, Boulder, CO, United States

Introduction: In the ongoing investigation into the relative importance of various biotic forces maintaining herbivore populations, two main hypotheses have guided research: (1) herbivore abundance is maintained by natural enemies (predator regulation), and (2) herbivore abundance is maintained by host-plant resources, nutritional quality, and plant secondary chemistry (resource regulation). Although there is evidence in support of each hypothesis, no consensus has been reached as to which hypothesis is best supported or most general in application. Herbivore populations are most likely maintained by a combination of both predator-regulated and resource-regulated mechanisms. Currently, many questions remain regarding specific mechanisms by which predators and resources interact, and how these interactions function to maintain herbivore populations.

Methods: In this study, we addressed these questions by investigating how plant secondary metabolites disrupt an important herbivore defense against natural enemies, the immune response. Caterpillars with varying diet breadths were fed diets with high and low plant secondary metabolites.

Results: We found that increased concentrations of plant secondary chemistry negatively affected the caterpillar immune response. Effects were highest on sequestering specialist caterpillars. Similarly, metabolic output was greatest for caterpillars feeding on high concentrations of secondary metabolites.

Conclusions: Together, these results show that plant secondary chemistry can have a positive effect on parasitoids by disrupting the caterpillar immune response, indicating a multi-trophic level function for the maintenance of herbivore populations.

The effect of temperature and climate change on the distribution of bark beetle-associated fungi

Six Diana, Bentz Barbara

[1]Department of Ecosystem and Conservation Sciences, University of Montana, Missoula, Montana, United States, [2]USDA Forest Service, Rocky Mountain Research Station, Logan, Utah, United States

Introduction: The mountain pine beetle (MPB) is a serious forest pest in western North America. This beetle is associated with symbiotic fungi including two mycangial species, *Grosmannia clavigera* and *Ophiostoma montium*, which are important for host beetle development and reproduction. Due to above-average temperatures in the last decade, the beetle and its fungi have expanded their range northward and eastward in Canada. In this study, we looked at genetic diversity of *G. clavigera* collected from five sites in Canada and two sites in the US including sites within the newly expanded geographic range.

Methods: AFLP profiles from 170 fungal isolates were used to assess genetic variability within and among the populations sampled.

Results: Genetic variation was low in *G. clavigera*. There was higher heterozygosity and higher percentage of polymorphic loci in the Rocky Mountain (RM) populations than in the British Columbian (BC) populations. AFLP data indicated the presence of two genetically distinct groups (Group 1 and Group 2).

Conclusions: We found both Group 1 and 2 in the RM populations sampled, but only Group 1 in the BC populations. The presence of Group 1 in the newly expanded range of the beetle is likely due to expansions of beetles from BC northward as well as eastward into the RM region.

Tracing the origins of the praying mantises (Dictyoptera: Mantodea): Is their rapid diversification and the repeated occurrence of ecomorphic convergences linked to the Gondwanan breakup?

Gavin Svenson[1], Michael Whiting[2]

[1]New York State Museum, Albany, NY, United States, [2]Brigham Young University, Provo, UT, United States

A comprehensive taxonomic and distributional sampling of Mantodea (praying mantises), covering virtually all higher-level groups, was assembled to reconstruct the phylogeny for the order. Sequence data were generated from five mitochondrial and four nuclear loci (12S rDNA, 16S rDNA, 18S rDNA, 28S rDNA, Histone III, Cytochrome Oxidase I & II, NADH dehydrogenase subunit 4, and Wingless) for 331 mantis species along with ten cockroach and termite species as outgroups. Phylogenetic reconstruction using multiple methods recovered nearly congruent topologies. Only 7 of 14 families, 14 of 33 subfamilies, and 7 of 14 tribes were recovered as monophyletic indicating that phylogeny is largely incongruent with current mantis classification. Mapping biogeographic regions on the phylogeny demonstrated that our results adhere closer to geographic distribution than to the current classification. Specific patterns in distribution suggest that major morphological convergences have confounded taxonomist's ability to construct natural groups. Rather, we found that major mantis lineages diverged prior to the isolation of geographic regions and subsequent ecomorphic specializations within these regions led to convergences in morphology. Divergence time estimations place the origins of Mantodea at the beginning of the Jurassic with modern mantises originating on Gondwana during the Early Cretaceous. The first major divergences among modern mantises occurred with the splitting of South America and Africa. The subsequent breakup of other Gondwanan continents spurred numerous divergences within the order and led to the contemporary paraphyletic assemblages of taxa within each biogeographic region.

SimBeetle: Agent-based model for simulating red flour beetle in two-dimensional flour landscapes

Paul Flinn, James Campbell

USDA-ARS, Manhattan, Kansas, United States

Red flour beetle (*Tribolium castaneum*) is a common insect pest that infests flour mills. Over the last 80 years, dozens of mathematical models have been developed to simulate its population dynamics. Although these deterministic and analytical models predict general population trends, they are not able to simulate individual behavior and movement, and most don't include a spatial dimension. We developed a spatially explicit, agent-based model to better understand and predict beetle population dynamics in fragmented landscapes. Because an agent-based model allows for differences in agent behavior and interactions between agents, these models can be more realistic than deterministic models, and facilitates the testing of hypotheses about the consequences of stochastic factors and behavioral interactions. An object-oriented language was used to simulate the behavior of beetles. The model allows movement and distribution of individual beetles to be recorded. The model is a useful tool for predicting the effects of landscape structure on the stability of red flour beetle population dynamics.

Biological control of the Indianmeal moth on finished stored products using egg and larval parasitoids

Matthew Grieshop[1], Paul Flinn[2], James Nechols[3]

[1]Michigan State University, Lansing, Michigan, United States, [2]USDA-ARS, Manhattan, Kansas, United States, [3]Kansas State University, Manhattan, Kansas, United States

Biological control using hymenopteran parasitoids presents an attractive alternative to insecticides for reducing infestations and damage from the Indianmeal moth (*Plodia interpunctella*) in retail and warehouse environments. We examined the potential for using combinations of the egg parasitoid *Trichogramma deion* Riley, and the larval parasitoid *Habrobracon hebetor* (Say), for preventing infestations of *P. interpunctella* in coarse ground cornmeal, as well as the influence of packaging on parasitoid effectiveness. Treatments included one or both parasitoids, and either cornmeal infested with *P. interpunctella* eggs or eggs deposited on the surface of plastic bags containing cornmeal. *Habrobracon hebetor* had a significant impact on *P. interpunctella*, lowering populations by about the same magnitude in both open and bagged cornmeal. In contrast, *T. deion* did not suppress *P. interpunctella* in open cornmeal. However, when released on bagged cornmeal, *T. deion* significantly increased the level of pest suppression over bagging alone. When *H. hebetor* was added to bagged cornmeal, there was a significant reduction of live *P. interpunctella* compared to the control (70.6%) with a further reduction observed when *T. deion* was added (96.7%). These findings suggest that, in most cases, a combined release of both *T. deion* and *H. hebetor* would have the greatest impact because, even though packaging may protect most of the stored products, there are usually areas in the storage landscape where poor sanitation is present.

Decision support systems for prevention and control of vector-borne diseases

Lars Eisen[1], Michael Coleman[2]

[1]Colorado State University, Fort Collins, Colorado, United States, [2]Medical Research Council, Durban, South Africa

Introduction: Recent decades have seen both emergence of vector-borne diseases (VBDs) in new areas (e.g., Lyme disease and West Nile virus disease in North America) and resurgence of VBDs following relaxation of vector and/or disease control campaigns (e.g., dengue in the Americas, malaria in parts of Asia). Public health capacity to meet the threat of emerging VBDs has been found lacking even in developed countries capable of rapidly allocating significant resources to combat these diseases. Novel approaches are urgently needed for improved prevention of emerging and resurging VBDs as well as maintenance of a disease-free environment following successful eradication campaigns. The importance of the latter is highlighted by the recent commitment of major funding and public health agencies to eradicate malaria.

Methods and Results: We will explore the topic of using decision support systems to facilitate prevention and control of VBDs. This will include a discussion of the importance of clearly defining end-users responsible for prevention and control of VBDs and examples of decision support systems for dengue and malaria under development. Four VBDs representing tick-borne bacterial diseases (Lyme disease), mosquito-borne viral diseases (dengue, West Nile virus disease) and mosquito-borne parasitic diseases (malaria) will be used to illustrate problems and possibilities related to use of decision support systems to combat VBDs.

Conclusion: Decision support systems have tremendous potential to counter VBDs through improved capacity for data collection, entry, storage, retrieval, analysis, and display; and through evidence-based decision making and use of locally appropriate vector/disease control program strategies and methodologies.

Respiratory physiology as a tool for understanding ecological patterns in fleas

Boris Krasnov[1], Irina Khokhlova[1], Laura Fielden[2]

[1]Ben-Gurion University of the Negev, Beer-Sheva, Israel, [2]Truman State University, Kirksville, United States

Introduction: We present two case studies demonstrating how measurements of respiratory gas exchanges can be used to understand ecological phenomena in ectoparasites using fleas and their rodent hosts as a model system. The first study asked whether sexual and interspecific differences in jumping performance of fleas that appeared to be not related to differences in the morphometric of locomotory system are instead correlated with differences in metabolic rate (MR). The second study considered energy cost of blood digestion of the host-specific flea that fed on preferred and non-preferred hosts.

Methods: In the first study, we related metabolic rate to jump performance of fleas, where as in the second study we calculated energy expenditure of a flea during digestion of a single bloodmeal taken from preferred or non-preferred host. A flow-through respirometry system was used to measure CO_2 emission.

Results: (1) Differences in jumping ability between males and females were found to be correlated with sexual differences in mass-specific or mass-independent MR. Interspecific comparison showed that the length of jump in both male and female fleas was strongly affected by their mass-specific and mass-independent MR. (2) Fleas expended significantly more energy digesting blood of non-preferred host than blood of preferred host.

Conclusions: Respiratory measurements appeared to be a useful tool when studying ecological patterns.

Comparative acute toxicity of two herbicides, Paraquat and Glyphosate to the larvae of two caddisflies, *Aethaloptera dispar* and *Cheumatopsyche digitata*

Sylvester Ogbogu, Efere Obuotor

Obafemi Awolowo University, Ile-Ife, Osun State, Nigeria

Introduction: Glyphosate- and Paraquat-based herbicides are among the most widely used pesticides in the world. In this study, we compared the susceptibility of the larvae of two caddisflies, *Aethaloptera dispar* Brauer and *Cheumatopsyche digitata* Mosely (Trichoptera: Hydropsychidae) to the acute toxicity of two herbicides Glyphosate (Roundup®) and Paraquat (Gramoxone®) under static bioassay conditions.

Methods: The larvae were collected from the stream below a tropical rainforest reservoir outflow and acclimatized to laboratory conditions. They were then exposed to 500 ppm, 100 ppm and 10 ppm test concentrations prepared from 1000 ppm stock solutions of both herbicides in short-term static bioassay experiments.

Results: There was a dose- and time-dependent mortality with Paraquat, giving an LC_{50} of 60.40 ppm and 112.78 ppm for *A. dispar* and *C. digitata* respectively, at 24-h exposure. For glyphosate however, there was mortality at 15.35 ppm at 96-h exposure.

Conclusions: The results suggest that both herbicides are lethal to the caddisflies at the test concentrations although Paraquat was more toxic to larvae than Glyphosate. Therefore, their concentration before application must be considered to mitigate their harmful effects on non-target aquatic organisms such as caddisflies.

Biogeography of the mutillid wasps (Hymenoptera: Mutillidae)

Arkady S. Lelej

Institute of Biology and Soil Science, Russian Academy of Sciences, Far Eastern Branch, Vladivostok, Russian Federation

Introduction: The Mutillidae is a large family of solitary wasps which currently numbers 213 genera and about 4200 described (c. 6000 estimated) species. Their greatest diversity occurs in the tropical and subtropical regions of the world.

Methods: The distributions of 213 genera and 16 tribes, as well as the distribution and dispersal patterns of subfamilies, were analysed. Faunal similarities between six biogeographical regions were evaluated by using Sorensen's coefficient of similarity. The similarity matrix resulting from pair-wise calculations was then presented by Terent'ev pleiades. The higher classification of Mutillidae follows Lelej & Nemkov (1997).

Results: The current distribution of four basal mutillid subfamilies (Myrmosinae, Kudakrumiinae, Pseudophotopsidinae, and Ticoplinae) and the subfamily Myrmillinae supports the hypothesis that the primary differentiation of the family took place on the Laurasian continents. These five subfamilies had a Palaearctic origin, while Rhopalomutillinae, Mutillinae, Dasylabrinae, Ephutinae, and Sphaeropthalminae originated in the Afrotropical region. Myrmosinae and Pseudophotopsidinae are distributed mainly in the Palaearctic region, while Kudakrumiinae is Holarctic. The greatest diversity of the subfamilies Myrmillinae, Mutillinae, Rhopalomutillinae, Dasylabrinae, and tribe Odontomutillini (in Ephutinae) occurs in the Afrotropical, Palaearctic, and Oriental regions. Sphaeropthalminae dominates in the New World and Australian regions, while the tribe Ephutini occurs only in the New World.

Conclusion: The mutillid faunas of the Palaearctic, Oriental and Afrotropical regions are the most similar on the tribal and generic levels and represent the nucleus of the world fauna. The evolution of Mutillidae in the Palaeogene-Neogene was related to the formation of hemixerophytic (tropical, subtropical) and later hyperxerophytic (desert) biota.

Altruism in insect societies and beyond: voluntary or enforced?

Tom Wenseleers

Katholieke Universiteit Leuven, Leuven, Belgium

The extreme altruism of the social insect worker caste has puzzled researchers for decades. Inclusive fitness theory suggests that close relatedness has been key in promoting such altruism. Recent theory, however, shows that the intermediate levels of relatedness found within insect societies are too low to directly cause the extreme altruism observed in many species. Instead, recent results show that workers are frequently “coerced” into acting altruistically. For example, workers are deterred from laying eggs by egg killing, and female larvae are prevented from developing into queens by food control. This shows that the altruism seen in many modern-day insect societies may not be voluntary but enforced. In this talk I will argue that enforced cooperation in fact is a widespread phenomenon that occurs not just in insect societies, but also in social vertebrates, humans and interspecific mutualisms.

Pheromone guided recruitment to food sources by stingless bees

Stefan Jarau

University of Ulm, Ulm, Germany

Introduction: Stingless bees have developed a variety of signals that are used by foragers to inform their nestmates about the existence and/or the location of a food source. The most effective and accurate recruitment mechanism is the guidance of nestmates along a trail of pheromone spots deposited by foragers on a certain stretch from the food towards the nest.

Methods: In order to identify both the glandular source of these pheromones and their compositions in several species of stingless bees, artificial scent trail bioassays with both natural extracts and synthetic compounds were carried out along with chemical analyses of gland secretions.

Results: Extracts prepared from the bees' labial glands induced trail following behaviour, whereas mandibular gland extracts did not. The chemical analyses of labial gland secretions as well as the bioassays with synthetic compounds showed that the respective pheromone components are various carboxylic acid alkyl esters and terpene esters. Furthermore, for *Trigona corvina* and *Scaptotrigona pectoralis* it could be demonstrated that both the pheromone composition (relative abundance of single compounds) and its effect to elicit trail following behaviour are nest specific.

Conclusions: The trail pheromones of all stingless bee species studied so far by means of chemical analyses and artificial scent trail bioassays (*Trigona recursa*, *T. spinipes*, *T. corvina*, *Scaptotrigona pectoralis*) clearly are secreted from their labial glands. The nest specificity now demonstrated for two species probably helps to avoid competition for resources and, at least in the aggressive *T. corvina*, costly combats between foragers of different nests.

Ecology of cereal aphid – fungal pathogen interactions: A South African perspective with potential for inoculative-augmentation

Justin Louis Hatting

ARC-Small Grain Institute, Bethlehem, South Africa

Introduction: In South Africa, wheat (*Triticum aestivum*) is produced in winter and summer rainfall climates and is prone to attack by any of six cereal aphid species. Of these, the Russian wheat aphid, *Diuraphis noxia*, is considered the most destructive. Entomopathogenic fungi often cause natural epizootics among aphid populations, including those of *D. noxia*. Elevation-driven migration of aphids between South Africa and Lesotho as well as aphid behavioral traits were considered in formulating a hypothetical control strategy based on inoculative-augmentation of the entomophthoralean, *Conidiobolus thromboides*.

Methods: Fungal surveys were conducted employing direct (collection of mycosed cadavers) and indirect (collection and rearing of live aphids) sampling techniques over a four-year period. In-field pitfall trap data were used to qualify the spatial dynamics of aphid mobility leading to potential pick-up of fungal inoculum from soil surfaces.

Results: Eight fungal species known to infect and kill aphids were recorded, *i.e.,* the entomophthoraleans *Pandora neoaphidis*, *Conidiobolus thromboides*, *C. coronatus*, *C. obscurus*, *Neozygites fresenii*, and *Entomophthora planchoniana*. Two Sordariomycetes, *Beauveria bassiana* and *Lecanicillium lecanii* were also isolated. As host, *D. noxia* seemed highly suitable with six fungal species recorded. Compared to other cereal aphid species, observations revealed early-season activity for *D. noxia* and active aphid movement over soil surfaces within the crop.

Conclusion: Hypothetically, early-season migration of *D. noxia* from Lesotho into South Africa could be exploited through interventions increasing the level of latent and/or active infection in the crop environment. The novel use of a millet-based medium for inoculative-augmentation of *C. thromboides* is proposed.

Eukaryotic translation initiation factor 4A (eIF4A) of the diamondback moth, *Plutella xylostella*: a putative molecular target of CpBV15β, a polydnaviral protein derived from an endoparasitoid, *Cotesia plutellae*

Yonggyun Kim[1], Madanagopal Nalini[1], Seungbaeck Song[1], Jai-Hoon Eum[2], Sungsik Han[2]

[1]Andong National University, Andong, Korea, Republic of, [2]Korea University, Seoul, Republic of Korea

Initiation of translation is the most efficient step for regulation of protein synthesis, in which viruses are targeting the recruitment of mRNA to the 43S complex to form the 48S preinitiation complex. This process is accomplished by eukaryotic translation initiation factor 4F (eIF4F), which mainly consists of eIF4A (ATP-dependent RNA helicase), eIF4E (cap-binding protein), and eIF4G (adapter protein). Diamondback moth, *Plutella xylostella*, parasitized by an endoparasitoid, *Cotesia plutellae* (Hymenoptera: Braconidae), exhibits physiological alterations including immunosuppression, antimetamorphosis, and diversion of host nutrients. CpBV15β, a viral protein derived from *C. plutellae* bracovius, has been speculated to act as host translation inhibitory factor because of its homology with circumsporozoite, a malarian toxin protein to inhibit host protein synthesis. CpBV15β also exhibits amino acid sequence similarity to eIF4G at the interacting site with eIF4A, suggesting that its inhibitory action may bind eIF4A of *P. xylostella*. A positive clone corresponding to eIF4A was isolated from a cDNA library of *P. xylostella*. Using both RACEs, a complete eIF4A cDNA (1,700 bp) was cloned. It encodes 422 amino acid sequence with 47961.83 daltons and share high homologies with other eIF4As of *Bombyx mori*, *Drosophila melanogaster*, and *Apis mellifera*. The protein was expressed using a bacterial expression vector and purified by Ni-NTA affinity column. The purified eIF4A protein was injected into rabbit to raise polyclonal antibody. The antiserum reacted the purified protein and *P. xylostella* protein extracts. Immunoprecipitation assay showed that CpBV15β interacts with eIF4A in the parasitized *P. xylostella*.

Influence of potato plant preinfestation on its colonization by aphids

Philippe Giordanengo[1], Laurence Brunissen[1], Vincent Charles[2]

[1]Université de Picardie Jules Verne, Amiens, France, [2]Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu, QC, Canada

Introduction: The aphids *Macrosiphum euphorbiae* (Thomas) and *Myzus persicae* (Sulzer) (Homoptera: Aphididae) are serious pests of potato (*Solanum tuberosum* L.), notably in transmitting numerous plant viruses. Heterospecific interactions may occur between these two species as they are often observed at the same time on the same potato plant in the field. As aphid infestation is known to induce systemic changes in the plant, we investigated the effect of a previous infestation of a plant on its colonization by following aphids.

Methods: Behavioral (olfactometry and electrical penetration graph) and physiological studies were performed to evaluate the influence of plant conspecific (i.e. *M. euphorbiae*) or heterospecific (i.e. *M. persicae*) preinfestation on *M. euphorbiae*.

Results: We found that conspecific preinfestation altered olfactory and trophic parameters involved in behavioral steps of plant acceptance by aphids. In contrast, heterospecific preinfestation enhanced plant attractivity and aphid survival.

Conclusions: A previous infestation of potato plants by aphids, either conspecific or heterospecific, led to modified plant acceptance and life history traits for aphids colonizing the plant afterwards. Surprisingly, heterospecific preinfestation altered plant acceptance processes, probably inducing plant defense response. Conversely, heterospecific preinfestation favoured *M. euphorbiae* settlement and population development. Such effects of intraguild interactions and their ecological meanings are discussed.

Differential effects of the induction of direct plant defences on the development of a generalist herbivore and its solitary endoparasitoid

Rieta Gols[1], Jeffrey A. Harvey[2]

[1]Wageningen University, Wageningen, Netherlands, [2]Netherlands Institute of Ecology, Heteren, Netherlands

Introduction: Plants have evolved several defence mechanisms to prevent or reduce feeding by insect herbivores. Among these defences, plant allelochemicals have been shown to play an important role against insect herbivory. Levels of plant defences often increase in response to insect feeding and affect the performance of consecutive herbivore generations. Few studies have investigated the effect of induced plant defence on performance of parasitoids that develop inside insect herbivores. In this study, we investigated the effect of induced plant defence on a generalist herbivore and its larval endoparasitoid.

Methods: We examined the effect induced and non-induced food plants on the performance (survival, body mass development time) of a generalist herbivore (*Mamestra brassicae*) and its larval endoparasitoid (*Microplitis mediator*). Different wild populations and cultivars of *Brassica oleracea* were used as food plant for the herbivore and plants were induced by larval feeding of *Pieris rapae*.

Conclusions: The occurrence of sexual size dimorphism in *M. mediator* depends on the quality of the food plant on which the host has been feeding.

Interactions between generalist and specialist herbivores and their endoparasitoids on the invasive weed, *Bunias orientalis*

Jeffrey A. Harvey[1], Rieta Gols[2], Michael Reichelt[3], Roel Wagenaar[1]

[1]Netherlands Institute of Ecology, Heteren, Netherlands, [2]Wageningen University, Wageningen, Netherlands, [3]Max Planck Institute for Chemical Ecology, Jena, Germany

Introduction: Warty cabbage, *Bunias orientalis*, originates in western Asia but since the 1980s has become a highly invasive weed in parts of central and western Europe. However, it is still comparatively rare in some other parts of north- and south-western Europe, although it is on the 'black list' of plants to watch out for. Thus far, little is known about the factors underlying the success of *B. orientalis*. For instance, the insect fauna that feed on *B. orientalis* is poorly described, and the suitability of the plant to higher trophic levels, such as parasitoid wasps, is also unknown.

Methods: We conducted experiments with different populations of *B. orientalis* originating from two countries where it is an exotic, invasive pest (Germany, Sweden) and one where it is exotic but still rare (Holland). The growth, development and survival of specialist and generalist herbivores are described on German and/or Dutch populations. We then compared the development of a generalist herbivore, *Mamestra brassicae*, and its solitary endoparasitoid, *Microplitis mediator* on field-grown Dutch *B. orientalis* and a lab-grown cultivar (cv. Cyrus) of cabbage, *Brassica oleracea*. Finally, we compared the development of *M. brassicae* and *M. mediator* on plants originating in the 2 exotic invasive and 1 exotic non-invasive populations of *B. orientalis*. Larval preference for herbivore-induced and uninduced plants was also examined.

Conclusions: The results reveal significant variation in secondary chemistry and plant quality amongst the different populations as well as insect performance. We suggest that the various exotic populations may have different geographic origins.

Importance and distribution of the Mediterranean black fig fly, *Silba adipata*, McAlpine in South Africa.

Martin Wohlfarter[1], Elrita Venter[1], Jan Giliomee[2]

[1]Alternafruit SA (Pty) Ltd, Paarl, Western Cape, South Africa, [2]University of Stellenbosch, Stellenbosch, Western Cape, South Africa

Introduction: The Mediterranean black fig fly, *Silba adipata*, McAlpine (Diptera: Lonchaeidae) was recorded in South Africa for the first time from commercially grown figs (*Ficus carica*) late 2006. During 2007 various fig production areas in South Africa were monitored for this fly as part of a greater insect pest and disease survey on figs. The figures presented give an indication of the distribution of this fly as determined by the survey.

Methods: Commercial fig orchards and private backyard gardens were inspected for fruit damage for two consecutive seasons. *Silba adipata* attacks unripe to ripe figs, by ovipositing near or in the fruit ostiole. Larvae feed predominantly below the skin, causing a characteristic premature fruit ripening and internal decay. Twenty such infected fruit where randomly collected per orchard and larvae where reared in the laboratory. In addition to collections McPhail traps baited with Hexanol ($C_6H_{13}OH$) were used in the second season to attract flies and determine population densities.

Results: The occurrence of the fig fly is widespread in South Africa and in one particular orchard caused serious economic damage. Larvae emerged in mid November, suggesting first oviposition around end of October. Fruit damage was observed until late February. The reduction in infection can, however be attributed to targeted insecticidal application against Mediterranean fruit fly (*Ceratitis capitata*). Hexanol which was shown to be a potent attractant to *Silba adipata* in Greece (Katsoyannos & Guerin, 1984), only obtained limited success under commercial production in South Africa.

Conclusions: The Mediterranean black fig fly, *Silba adipata*, is an important new fig pest in South Africa, seriously affecting fruit quality. Its presence was established in the south western part of the country, but it is probably widely distributed all over South Africa. Unkempt orchards show the highest infestation, thus stressing the importance of sanitation practises.

Diversity and relationships of gall-inducing scale insects in South Africa

Penny Gullan[1], Lyn Cook[2]

[1]University of California, Davis, Davis, California, United States, [2]University of Queensland, Brisbane, Queensland, Australia

Introduction: More than 500 species of scale insects (Hemiptera: Coccoidea) are known from South Africa, but very few are reported to induce galls on their host plants. This contrasts with Australia and New Zealand, which have rich faunas of galling Coccoidea, especially in the family Eriococcidae. We use morphological and molecular information to estimate the taxonomic diversity and phylogenetic relationships of gall-inducing scale insects native to South Africa.

Methods: The number of gall-inducing scale insect taxa in South Africa was assessed based on a survey of literature plus recent collections made in the Eastern, Northern and Western Cape provinces. Nucleotide sequence data were obtained for gall-inducing species of soft scale (Coccidae), felt scale (Eriococcidae) and mealybug (Pseudococcidae) and added to a larger DNA dataset for each family to estimate potential relatives of the gallers. Undescribed species were recognized based on insect and gall morphology and DNA data.

Results: Only 13 species of native South African scale insects belonging to five families are known to induce galls, and those of the Asterolecaniidae are mostly nondescript stem pits. The gall-inducing *Calycicoccus merwei* is the only member of the Eriococcidae native to South Africa, and represents an isolated lineage. Two species (one undescribed) of *Cissococcus* are the only gall-inducing soft scales (Coccidae) in South Africa and are related to African non-galling coccids. The only two gall-inducing mealybug genera, *Diversicrus* and *Grewiacoccus* (Pseudococcidae), are not closely related. An undescribed leaf-galling species of armoured scale is reported from *Rhus* species in the Cape region.

Switch in the pest status and range of some true bugs (Heteroptera) due to landscape change and global warming in the neotropics

Antonio Panizzi, Daniel Sosa Gomez

National Soybean Research Center - Embrapa, Londrina, PR, Brazil

Introduction: During the last 40 years, a dramatic change in landscape along with increase in certain parameters indicating global warming has occurred in the neotropics, particularly in Brazil. As a result of this, changes in the species composition and abundance of true bugs (Heteroptera) associated with crops has been observed.

Methods: To demonstrate this, three species of heteropterans, the pentatomids, *Euschistus heros* (F.) and *Dichelops melacanthus* (Dallas), and the alydid, *Neomegalotomus parvus* (Westwood) associated with two major crops, i.e., soybean, *Glycine max* (L.) Merrill and/or corn, *Zea mays* L., were selected and analyzed. Data analyses were based on published records during this time accomplished with field observations.

Results: Results indicated that for all three species a tremendous increase in abundance and distribution has occurred in this time frame (last 40 years). This can be explained due to the expansion of these crops providing abundance of food, and to the massive adoption by growers of the no-tillage cultivation system that favor these species which spend part of their life on the soil surface feeding on seeds and/or using crop residues as shelter. In addition, the increase of minimum mean temperatures (over 1ºC during the last 40 years) and the less frequency of occurrence of frosts are probably favoring these neotropical species to colonize cooler areas of southern Brazil below the Tropic of Capricorn (latitude 23º 27'S).

Conclusions: The change in landscape and global warming are favoring the abundance of the true bugs analyzed.

Effects of short-term laboratory infestation of dried cassava variety TME – 7 by *Prostephanus truncatus* (Horn) (Bostrichidae: Coleoptera)

Popoola Kehinde

University of Ibadan, Department of Zoology, Ibadan, Oyo state, Nigeria

Introduction: Researches have shown that dried cassava varieties are relatively susceptible to *Prostephanus truncatus* (Horn) infestation, which results to about 70% lost in 4 months. This consequently affects a large percentage of the population from developing countries that depends of cassava as sources of food for high energy and income.

Methods: Laboratory studies were conducted to determine weight loss and nutritional status of the infested dried cassava chips (TME-7) and emergence rate of *P. truncatus* over an infestation period of 8 weeks.

Results: Cassava variety TME -7 mean weight loss (±SD) rose to 11.30% ± 4.01 (22.67%) with *P.truncatus* mean emergence rate (± SD) values were 9.93 ± 7.34, 18.53 ± 8.12 and 16.33 ± 6.75 for larvae, pupae and adults respectively. Nutrient proximate analysis conducted on infested TME-7 revealed the dried cassava nutritional status as follows: protein content was 1.30%; fat content recorded was 0.99%, while moisture content was put at 5.50%. Other parameters analyzed were ash content, which was 1.81%, and lastly, crude fiber and carbohydrate was 29.03%.

Conclusion: Dried cassava variety supports *P. truncatus* breeding, with appreciable damage to the crop. Breeding and damage have been implicated in the reduction of nutritional and market values of the dried cassava.

Variation and flexibility of egg discrimination in *Formica* ants

Heikki Helanterä

University of Helsinki, Helsinki, Finland

Social insects face the need to discriminate among different classes of brood in order to maximise their inclusive fitness. In the context of nestmate recognition of eggs workers potentially increase their inclusive fitness by discriminating against eggs laid by unrelated conspecific queens and unrelated social parasite queens. Workers of *Formica fusca*, an ant with highly variable queen number and a frequent target for temporary social parasite *Formica* queens, are able to discriminate against eggs laid by both conspecific and heterospecific alien queens. Our previous results also show that the diversity of eggs the workers experience in the spring affects their future acceptance of eggs from unrelated conspecifics. If this switch in discrimination also applies to eggs of social parasites, this suggests two ways how social parasites may increase the acceptance of their eggs by hosts. First, social parasites may get their eggs reared if they are laid early in the spring, during the period when exposure of workers to diverse eggs affects future acceptance. Second, workers in genetically diverse multiple queen colonies may be more likely to accept parasite eggs. We studied these scenarios using laboratory colonies of *F. fusca* and its sympatric social parasite *F. truncorum*. The results will shed light on the interplay of sociogenetic variation and the behavioural rules underlying recognition in moulding the accuracy of adaptation against social parasites.

Predation by larval *Agabus* (Coleoptera: Dytiscidae) on primary consumers in constructed freshwater wetlands

Lauren Culler, William Lamp

University of Maryland, College Park, Maryland, United States

After decades of wetland destruction for development and agricultural purposes, growing awareness by the public is providing support for their restoration. This support is often met with fear of mosquito annoyance and potential disease transmission since people associate areas of standing water with large mosquito populations. However, studies of macroinvertebrates in restored wetlands show that native wetland predators can suppress mosquito populations. At the Jackson Lane wetland restoration site on the Eastern Shore of Maryland, post-restoration monitoring data show a diverse community of macroinvertebrates with a high percentage of predator species. Predaceous diving beetles (Coleoptera: Dytiscidae) make up 16.9% of the taxa found, though account for only 5.1% of individuals. Adults and larvae of these beetles are known predators of mosquito larvae and we wanted to test if they are contributing to natural suppression of mosquito populations. We focused on *Agabus punctatus*, since these larvae are abundant when mosquitoes may be ovipositing as the wetlands thaw in late winter. A series of laboratory experiments are underway to test the feeding preference of this predator, and to specifically determine if mosquito larvae are an important component of its diet. Experiments address: (1) the performance of *A. punctatus* when fed on three different prey types (mosquito larvae, cladocerans, or copepods), (2) how the behaviour of *A. punctatus* and its prey influences prey selection, and (3) how intraspecific interactions among *A. punctatus* affect rate of prey consumption. Future experiments will address prey selection and the effect of predator density on the prey population.

The influence of maize phenologies and transgenic Bt maize on oviposition and injury to maize by European corn borer

Motshwari Obopile[1], Ronald B. Hammond[1], Peter R. Thomison[2]

[1]The Ohio State University, Wooster, Ohio, United States, [2]The Ohio State University, Columbus, Ohio, United States

Introduction: The European corn borer, *Ostrinia nubilalis* (Hubner), is a damaging pest of maize (*Zea mays* L.) throughout North America. Yield losses associated with *O. nubilalis* are estimated at more than $1 billion annually. A study was conducted to determine the influence of planting date and transgenic maize on oviposition by *O. nubilalis* and subsequent larval injury on maize.

Methods: Transgenic and non transgenic maize hybrids of different relative maturities were planted at three planting dates (early, mid, and late) each year. The study was carried out at the Northwest Agricultural Research Station near Hoytville and at Wooster, Ohio during the 2006 and 2007 cropping seasons. Egg masses, growth stages, and injury levels on stalks, foliar, and ears were recorded on 10 randomly selected plants.

Results: The egg density did not differ significantly between transgenic and non-transgenic maize. However significant differences were observed among planting dates and sampling dates, and with the sampling date by planting date and hybrid by sampling date interactions. Fewer eggs masses were laid on second planting than early and late plantings. Injuries on stalks, foliar and ears were significantly higher on non-transgenic maize. Significant differences were also observed between planting dates, and the planting date by hybrid interactions. The use of transgenic maize did not significantly improve yields in 2006, but did in 2007. Early planted maize yielded significantly more in 2006 but in 2007, yield did not differ significantly among planting dates.

Conclusions: The variability in the benefit from transgenic plants and planting dates makes recommendations difficult at this time.

Comparative aspects of life history regulation in honeybee and fruit fly

Thomas Flatt

Department of Ecology and Evolutionary Biology, Brown University, Providence, Rhode Island, United States

Hormones ensure the systemic coordination of physiological processes in response to environmental cues, from the cellular to the organismal level, and variation in endocrine pathways might thus play a major role in life history evolution. In the solitary fruit fly (*Drosophila melanogaster*), the neuroendocrine system (homologous to the mammalian hypothalamic-pituitary-gonad axis) integrates insulin-like signals, juvenile hormone (JH), and ecdysone signaling. This pleiotropic system coordinates major aspects of life history, including reproduction, stress resistance, immune function, behavior, and lifespan. Remarkably, a similar regulatory principle is found in the honeybee (*Apis mellifera*), a social insect distantly related to the fly. Like the fly, the bee uses a pleiotropic hormonal network to regulate a complex suite of social behavioral and life history traits, including behavioral ontogeny, foraging, pollen versus nectar preference, ovarian development, oxidative stress response, immunity, and longevity. Components of this complex network comprise JH, the JH suppressor vitellogenin, and possibly the insulin, target of rapamycin (TOR), and ecdysone signaling pathways. Together, the comparison of fly and bee suggests that a regulatory system of solitary origin has been co-opted by social insects and might have contributed to the evolution of social life histories. Here I review the endocrine regulation of *Drosophila* life history and draw parallels between this regulation in the fly and the bee. Well-established genetics and genomics in *Drosophila*, combined with the recent advent of RNAi, proteomics, and ease of physiological manipulation in the bee, promise to make such a comparative approach exceptionally powerful.

Different effects of three paracoprid dung beetles baased on their niche

Heason Bang[1], Joon-Ho Lee[2], Young-Eun Na[1], Min-Su Han[1], Ki-Ahn Noh[1]

[1]NIAST, Suwon, Korea, Republic of, [2]Seoul National University, Seoul, Republic of Korea

Introduction: Dung beetle act as removes dung on the ground from the soil surface. They bury the dung in the soil wherever they find it. This helps to accelerate the rate of the circulation of nutrients and to increase the productivity of grassland ecosystem. They use dung as their food and as their offspring. As the result of these activities there were noticeable changes in the soil. Different species of dung beetle were found in different soil layers.

Methods: In this experiment, three paracoprid dung beetles (*C. ochus, C. tripartitus and O. lenzii),* chemical properties, and microbial interactions were studied during the first and second month of dung decomposition. There were two kinds of pot these were the pot with beetles and the pot without beetle. The effects of three dung beetles in organic matter, total N contents, Ammonium N as well as on microbial population were assayed.

Results: After 3 weeks, each dung beetle accelerated nitrification. By dung beetle activity in each soil layer, microbial numbers were highly correlated to the organic matter and total N concentration of the soil. In 0-5 cm soil layer, *O. lenzii* treatment had the highest content of organic matter, total N and ammonium N, Otherwise in 10-30 cm soil layer, *C. ochus* treatment was higher than the other treatments.

Conclusions: Each three dung beetles contributed the changes in the chemical composition and microbiological activity of each soil layer as the result of using by their different ecological niche. Each dung beetle contributed the changes in the chemical composition and microbiological activity of each soil layer. This was the result of using their different ecological niche.

Regulation of cell migration by the gaseous messenger molecules CO and NO during formation of neural circuits

Gerd Bicker, Sabine Knipp

University of Veterinary Medicine, Hannover, Germany

Introduction: The formation of the insect enteric nervous system (ENS) provides a useful model to study the cell biology of neuronal migration. Neuronal precursors emerge from proliferative zones in the foregut epithelium and perform quite extensive cell migrations before they assemble into the neural circuits of discrete ganglia and nerve plexus.

Methods: Using small molecule compounds to activate or inactivate biosynthetic enzymes, we demonstrate that the gaseous messenger molecules carbon monoxide (CO) and nitric oxide (NO) regulate neuron migration in the locust ENS.

Results: CO is produced by heme oxygenase (HO) enzymes and has the potential to signal via the sGC/cGMP pathway. Here we show that inhibition of HO by metalloporphyrins promotes enteric neuron migration in intact locust embryos. This gain of function experiment in conjunction with the suppression of migratory behavior by chemical activation of HO strongly implicates the release of CO as inhibitory signal for neuron migration. Conversely, inhibition of nitric oxide synthase and application of the extracellular NO scavenger hemoglobin reduce cell migration. While migrating on the midgut, the enteric neurons express a transient immunoreactivity for HO.

Conclusions: The cellular distribution of NO and CO biosynthetic enzymes, together with the results of the chemical manipulations in whole embryo culture suggest CO as an intracellular messenger molecule that modulates transcellular NO signalling during neuronal migration. Thus we provide the first evidence that CO regulates neural development in a rather simple model insect.

Alternative foods for *Harmonia axyridis*

Nick Berkvens[1], Jochem Bonte[1], Dirk Berkvens[2], Koen Deforce[3], Luc Tirry[1], Patrick De Clercq[1]

[1]Laboratory of Agrozoology, Department of Crop Protection, Faculty of Bioscience Engineering, Ghent University, Ghent, Belgium, [2]Department of Animal Health, Prince Leopold Institute of Tropical Medicine, Antwerp, Belgium, [3]Flemish Heritage Institute, Brussels, Belgium

Introduction: The exploitation of available resources is an important factor determining the invasion success of an exotic species. An extensive range of arthropod species has been reported to be exploited by the polyphagous coccinellid *Harmonia axyridis*. However, little is known concerning the potential role of plant foods for the establishment potential of this invasive species. Our research investigated the developmental and reproductive success of *H. axyridis* on pollen.

Methods: A long-term laboratory population of *H. axyridis* and a melanic and non-melanic population of the species originating from field collected individuals in Belgium were used in this study. The insects were allowed to develop and reproduce on three diets: frozen eggs of *Ephestia kuehniella*, frozen moist bee pollen or an even mixture of the two.

Results: When fed a diet of pollen alone, 35-48% of the larvae of the field populations of *H. axyridis* successfully reached adulthood, albeit with a prolonged developmental time (31-49%) and a reduced adult body weight (37-68%) compared to individuals offered either diet containing *E. kuehniella* eggs. When fed exclusively on pollen in their larval and adult life, about 40% of the adult females of either field population were able to produce a small number of viable eggs.

Conclusions: The exploitation of pollen and other plant foods at times when insect prey is scarce, may offer a further competitive advantage to the non-indigenous coccinellid *H. axyridis* over native European predatory lady beetles that share the same niche and are less capable of using pollen as an alternative food.

Drosophila-Wolbachia symbiotic interactions: exploring the role of ankyrins

Panagiotis Sapountzis[1], Stefanos Siozios[1], Panagiotis Ioannidis[1], Aggeliki Saridaki[1], Haralabia Boleti[2], Kostas Bourtzis[1]

[1]Department of Environmental and Natural Resources Management, University of Ioannina, Agrinio, Greece, [2]Molecular Parasitology Unit & Light Microscopy Unit, Hellenic Pasteur Institute, Athens, Greece

Wolbachia are obligatory intracellular and maternally inherited bacteria that infect numerous arthropod as well as filarial nematode species. *Wolbachia* is considered as the most ubiquitous symbiotic creature on Earth and has major effects on host biology that are expressed through the establishment of symbiotic interactions and range from reproductive parasitism to mutualistic symbioses. The molecular mechanisms that mediate *Wolbachia*-host symbiotic interactions are currently unknown. However, the sequencing of the genomes of different *Wolbachia* strains (*w*Mel, *w*Ri) that infect insect hosts revealed an unusually large number of genes encoding proteins with ankyrin repeat domains. The role of these proteins is currently under investigation in different laboratories.

The present study investigated the distribution of ankyrin genes in different Wolbachia strains by PCR and Southern analysis. Semi-quantitative RT-PCR analysis was also performed on RNA extracts from different developmental stages and tissues (males, females, testes, ovaries, early and late embryos) of different Drosophila-Wolbachia expressing different reproductive phenotypes. Selected ank-proteins were expressed transiently in insect cells as GFP chimeras and their subcellular localization was analyzed by confocal microscopy.

Our results clearly indicate that most ankyrins present patchy distribution and expression patterns. In addition, the variation in the subcellular localization of the ank-proteins analyzed may reflect different roles of ankyrin proteins on the establishment of host-*Wolbachia* symbiosis and the induction of reproductive abnormalities such as parthenogenesis, feminization, male killing and cytoplasmic incompatibility.

Aspects of non-chemical control of pestiferous termites in agriculture and agroforestry: recent experiences from eastern and southern Africa

Philip Nyeko[1], Gudeta Sileshi[2], Ben Sekamatte[3], Philip Nkunika[2]

[1]Makerere University, Kampala, Uganda, [2]World Agroforestry Centre (ICRAF), Lilongwe, Malawi, [3]DFID, Kampala, Uganda, [4]University of Zambia, Lusaka, Zimbabwe

Introduction: A number of termite species are a major constraint in agriculture and forestry in the tropics. Losses of up to 100% have been reported on some crops and tree species in eastern and southern Africa. This paper summarizes studies recently conducted in the region to evaluate the efficacy of some non-chemical termite control methods in smallholder agriculture and agroforestry.

Methods: The potential of legume intercrops, legume improved fallows, protein and sugar-based baits, and the fungus *Metarhizium anisopliae* in the management of termites on maize and *Grevillea robusta* were assessed. Termite damage to maize and *G. robusta*, maize yields and the activity of termite predating ants were recorded.

Results: Intercropping maize with soybean, groundnut and common beans reduced termite attack on maize and loss of maize yield, and increased ant nesting in maize fields in Uganda. Maize grown in improved fallows suffered less termite damage and produced maize yields comparable with conventionally tilled and fully fertilized monoculture maize in eastern Zambia. Similarly, *M. anisopliae* reduced termite damage to maize and increased maize yield in Uganda. However, the fungus did not reduce termite attack on *Grevillea robusta* seedlings. Fishmeal bait increased ant nesting near maize plants and reduced termite attack on maize with consequent increase in maize yields.

Conclusions: There is a clear scope for non-chemical control of termites in smallholder cropping systems in eastern and southern Africa. However, more efforts are necessary to test such methods rigorously, develop specific recommendations relevant to smallholder farming conditions and appraise potential for commercialization.

Potential impact of *Cameraria ohridella* on maple: Is a host shift likely?

Sylvie Augustin[1], Christelle Péré[2], Carlos Lopez-Vaamonde[1], Romain Valade[1], Marc Kenis[2]

[1]INRA-UR633 Zoologie Forestière, Olivet, France, [2]Cabi Europe-Switzerland, Delémont, Switzerland

Introduction: The horse chestnut leafminer *Cameraria ohridella* is an invasive pest in Europe. This microlepidoptera, first discovered in Macedonia, almost exclusively develops on leaves of horse chestnut, *Aesculus hippocastanum*, but infestations have also been recorded on maples: *Acer pseudoplatanus* and *A. platanoides*. The fact that *C. ohridella* attacks and develops on *Acer* species might suggest that maple may be the ancestral host plant. As a consequence, we have studied the potential impact of this pest on maples, and we used a molecular phylogeny of the genus to reconstruct the ancestral host use and patterns of host shifts of *Cameraria.*

Methods: We sampled leaves on *A. pseudoplatanus* in Austria, Switzerland and France to investigate the impact of *C. ohridella* in relation to the distance to infested horse chestnut and to the arrival of the insect. In addition, a molecular phylogeny of 20 species of *Cameraria* was reconstructed using 2 genes.

Results: Our results showed that *C. ohridella* is mainly found on *Acer* at the vicinity of heavily infested horse chestnut. Females oviposit large numbers of eggs on maple, in contrast to other broadleaved species, but more than 80% of the larvae die in the first two instars. Attack rate and host tree resistance strongly vary between localities and individual maple. Attacks seem to increase slowly with time. Optimization analyses suggest that *Acer* is likely to be the ancestral host plant of *C. ohridella*.

Conclusions: These results suggest that *C. ohridella* could adapt to *Acer* species in the near future.

A phylogenomic odyssey within Hymenoptera: the utility of ESTs for resolving key Apocritan relationships

Barbara J. Sharanowski, John A. Walker, S. Randal Voss, Michael J. Sharkey

University of Kentucky, Lexington, Kentucky, United States

Introduction: Superfamily relationships within Hymenoptera have been exceedingly difficult to resolve using conventional morphological and molecular markers. Genomic scale methods offer an alternative approach to phylogenetic reconstruction, typically overcoming incongruence between single-gene trees and providing increased nodal support.

Methods: We sampled over 2000 clones from cDNA libraries from 7 disparate Hymenopteran taxa. Expressed sequence tags (ESTs) were edited, cleaned of vector sequence, and clustered into contigs under rigorous parameters. To discover orthologous genes in other taxa, we compared these sequences with Hymenopteran and other insect ESTs in public databases using stringent criteria. These EST-derived markers were used to build a large concatenated multi-gene data matrix for a subset of taxa across the Hymenoptera. The concatenated dataset and individual gene matrices were analyzed using both Bayesian and parsimony techniques.

Results and Conclusion: We present a robust and well-supported hypothesis of Hymenopteran evolution at the level of superfamily and clarify several long-contested relationships among putative infraorders within Apocrita. Our results demonstrate the power of a phylogenomic approach for resolving deep evolutionary divergences within the Hymenoptera. Additionally, we show how EST-derived markers analyzed in a phylogenomic perspective offer a complimentary technique to more traditional phylogenetic methods that utilize denser taxon sampling.

Concentration and mixture interactions change the nitric oxide production patterns in the antennal lobe of *Manduca sexta*

Alan Nighorn

University of Arizona, Tucson, AZ, United States

Nitric oxide synthase, the enzyme that produces nitric oxide in response to a calcium signal, is present in the olfactory systems of almost every animal examined to date. We are using the moth, *Manduca sexta*, as a model system in which to investigate the function of nitric oxide in the processing of olfactory information. Using electrophysiological and optical recording methods we have found that NO is present at low levels at basal states and is actively produced in a glomerular pattern in response to odor stimulation. The odor-induced nitric oxide is apparently confined within glomerular borders and its pattern of production is dependent on the concentration and context of the odor stimulus. We find that increasing the concentration of some odorants results in a loss of activity in some glomeruli rather than the simple addition that is expected. We also find that the overall levels of odor-induced NO production may be context dependent. The responses of male moths to general plant odorants may be enhanced in the presence of female pheromone. These results suggest that nitric oxide functions as an important and highly dynamic modulator of antennal lobe neurons.

The present and future role of insect-resistant GM cotton in IPM

Steven Naranjo[1], John Ruberson[2], Hari Sharma[3], Lewis Wilson[4], Kongming Wu[5]

[1]USDA-ARS, Arid-Land Agricultural Research Center, Maricopa, Arizona, United States, [2]Department of Entomology, University of Georgia, Tifton, Georgia, United States, [3]ICRISAT, Patancheru, Andhra Pradesh, India, [4]CSIRO Plant Industry, Narrabri, New South Wales, Australia, [5]IPP, Chinese Academy of Agricultural Sciences, Beijing, China

Transgenic cottons producing Cry toxins from *Bacillus thuringiensis* (*Bt*) control lepidopteran pests and were first commercially grown in Australia, Mexico and the USA in 1996. As of 2007, six additional countries (Argentina, Brazil, China, Colombia, India, and South Africa) now grow *Bt* cotton on a total production area of over 12.2 million hectares. The technology primarily provides highly selective and effective control of bollworms, the most damaging pests of cotton worldwide. Between 1996 and 2005 the deployment of *Bt* cotton reduced the volume of insecticide active ingredient used for pest control by 94.5 million kg and increased farm income through reduced costs and improved yields by US$7.5 billion, with most of the benefit accrued by farmers in developing nations. Reductions in insecticide use have broadened opportunities for biological control and recent meta-analysis has demonstrated that Bt cotton has little or no effect on abundance and interactions among functional guilds of non-target arthropods. Most other pest management tactics in Bt cotton have remained largely unchanged. Several non-target pests have become more problematic in *Bt* cotton fields in some countries largely due to reductions in insecticide use for target pests. Pre-emptive resistance management has helped to preserve the efficacy of the technology. New products are in the pipeline to improve the effectiveness of genetically modified cotton cultivars for resistance to lepidopteran and other pests. Debate over food and environmental safety, regulatory oversight, and farming community welfare are likely to continue as the technology moves forward with new crops and new adopting countries.

Phylogeography of post-Plesitocene population expansion in a fungus-gardening ant and its microbial mutualists

Alexander Mikheyev, Tanya Vo, Ulrich Mueller

University of Texas, Austin, Texas, United States

Although biogeographic forces, such as historical climate-driven range shifts, greatly influence the present day population genetic structure of animals and plants, the extent to they affect microbial communities remains largely unknown. We examined the effect of post-glacial expansion on the population structure of the northern fungus gardening ant Trachymyrmex septentrionalis and compared it with that of its two microbial mutualists: the lepiotaceous fungal cultivars and antibiotic-producing Pseudonocardia bacteria. The ant population genetic structure showed a pattern of population expansion and, similar to many other North American taxa, was sub-structured into eastern and western phylogroups, separated by the Mississippi river drainage, and which likely originated in the Pleistocene. Although dispersal limitation, as evidenced by isolation by distance was present in all three symbionts, east-west subdivision structure was absent from the microbial mutualist populations. While neither the cultivar nor the Pseudonocardia genetic structure was correlated with that of the ants, they were significantly correlated with each other. These results show that biogeographic forces act differently on macro- and microscopic organisms, even in the extreme case when mutualists are vertically transmitted from generation to generation and share the same joint ecological niche. The population structure of the ants appears to be significantly influenced by historical climate change, biotic forces such as pathogen pressure and the structure of microbial populations.

Effects of tropical forest overstory diversity on biodiversity of ground dwelling ants in West Africa.

S. Sky Stephens[1], Mike Wagner[1], Paul Bosu[2]

[1]Northern Arizona University School of Forestry, Flagstaff, AZ, United States, [2]Forestry Research Institution of Ghana, Ghana, West Africa, Ghana

Introduction: Interactions between forest type or complexity and organism biodiversity and other environmental services are poorly understood for most forest types. Forest plantations are typically viewed as biological deserts, having reduced biodiversity. However, the current literature base on biodiversity in forest plantations is based largely on inappropriate comparisons. Most biodiversity and forest type assessments have been of exotic tree species monocultures to native forest conditions. To better assess biodiversity and forest type we compare a gradient of forest plantations including an exotic species monoculture, a native species monoculture, a six native species polyculture and an eleven native species polyculture.

Methods: We assessed ground foraging ants (Hymenoptera: Formicidae) as biological indicators of overstory tree species diversity in four experimental plantations in Ghana, West Africa using pitfall traps. Collections were made over a 48 hour trapping period during the wet and dry seasons.

Results: Traditional diversity indices show increases in diversity in native versus exotic species monocultures. However, a ten fold increase in overstory species diversity, native species monoculture to eleven native species polyculture, ant species diversity only increased by nineteen percent. Functional group assessment was performed and shows more distinct trends in ant response to overstory species diversity.

Conclusion: Biodiversity may be impacted through the manipulation of overstory tree diversity and species composition in forest plantations. Biodiversity is influenced more by overstory tree species composition than diversity and can be maintained, manipulated and managed as a forest plantation management objective.

Trait-mediated effects of termites and vertebrate herbivores in East-African savannas.

Alison K Brody[1], Todd M Palmer[2], Dan F Doak[3]

[1]University of Vermont, Burlington, VT, United States, [2]University of Florida, Gainesville, FL, United States, [3]University of Wyoming, Laramie, WY, United States

Introduction: Understanding what governs the distribution, diversity and abundance of species has been a central theme of ecology for decades. In semi-arid landscapes, termites are one of the most conspicuous and ubiquitous modifiers of habitats. Through their foraging and mound-building activities, termites directly modify the basal components of the ecosystems and indirectly change the foraging patterns of vertebrate herbivores. In so doing, they exert strong direct and indirect effects on entire communities. Although the importance of termites to the structure and function of African savanna communities is almost cliché, few hard data exist on the magnitude and mechanisms of direct and indirect effects of termites in these unique and threatened ecosystems.

Methods: I quantitatively demonstrate the importance of termites (*Odontotermes* sp.) to the invertebrate community, and dissect their direct effects in enhancing soils important to the diversity of host plants from indirect effects mediated through vertebrate herbivores.

Results: Invertebrate density is significantly higher on termite mounds than off mounds. Invertebrate diversity, however, is often lower on mounds than off-mounds. Host plant density and diversity follow these same patterns as well. The interactive effects among vertebrates and termites on invertebrate communities remain to be fully explored.

Conclusions: Termites directly affect plants by enhancing soil quality and indirectly affect entire communities through altering the density and foraging patterns of herbivores and predators. Teasing apart these direct and indirect effects is critical to our understanding of East African savannahs in particular, and to our understanding of food web dynamics in general.

Sexual selection, species isolation and genital evolution in *Ciulfina* praying mantids

Gregory Holwell

Macquarie University, NSW, Australia

The rapid and divergent evolution of male genitalia in animal species with internal fertilization is a commonly observed evolutionary trend. Three hypotheses have been suggested to explain this pattern: pleiotropy, species isolation (lock-and-key) and sexual selection. Whilst pleiotropy and species isolation lack strong support, there is growing evidence for sexual selection as the driving force behind genital evolution. Here I present the results of experiments that explicitly test both the sexual selection and species isolation hypotheses in the praying mantid genus *Ciulfina*. I will discuss the influence of both the shape and size of male genitalia on copulation duration, sperm transfer and fertilization success, and suggest that genital morphology is under sexual selection in these praying mantids. I also present data relating to the role of male genitalia in reproductive isolation between *Ciufina* species.

Small scale dispersal models and habitat selection of the Argentine ant, *Linepithema humile*

Paul Krushelnycky[1], Stephen Hartley[2]

[1]U.S. Geological Survey, Pacific Island Ecosystems Research Center, Haleakala Field Station, Hawaii, United States, [2]School of Biological Sciences, Victoria University of Wellington, Wellington, New Zealand

Local dispersal of insects is mediated by fine-scale variation in the physical environment. Quantifying this influence is difficult in many cases, due to complex dispersal patterns, gentle climatic gradients, and the confounding effects of strong biotic interactions. However, invasive ants often spread through budding, greatly simplifying dispersal patterns and in some cases clarifying the role of physical factors in shaping these patterns. At Haleakala National Park, Hawaii, two disjunct unicolonial populations of the invasive Argentine ant (*Linepithema humile*) have been dispersing in this fashion for over 40 years, producing patterns consistent with the diffusion model of spread. At the same time, an absence of strong predators or competitors, combined with steep climatic gradients at this locale, permit an analysis of the influence of abiotic variables such as temperature and rainfall on the rate and direction of this spread. We discuss how quantification of abiotic factors, as well as biotic factors that affect the physical environment, and the use of tools such as degree-day models can help in understanding both local behavior (e.g. nest site selection) and supercolony-level invasion dynamics. The ultimate goal of this small scale modelling effort is to develop better capacity for regional predictions of invasion patterns.

Insect biodiversity of the North Pacific area

Arkady S. Lelej, Sergey Yu. Storozhenko

Institute of Biology and Soil Science, Russian Academy of Sciences, Far Eastern Branch, Vladivostok, Russian Federation

Introduction: The problem of the biodiversity of the World and its regions is widely discussed. Among about 1.6 million described living organisms in the World, the insects are the most numerous (950,000 species).

Methods: The insect database of the Russian Far East (RFE) which is based on "Key to the insects of Russian Far East" (19 books, 1986-2007) was analysed by common statistical methods.

Results: Three regions in the North Pacific Area have almost the same number of species: RFE (c. 31000), Canada (c. 30000), and Japan (c. 29000). The southernmost boundaries of RFE and Canada have the same latitude (42^{o} N), resulting in similar climates and vegetation belts, which in turn strongly influence the distributions and diversity of organisms. The similar number of insect species for Japan, in spite of a much smaller area, results from the more southerly position of Japan (up to 23^{o} N). The insect fauna of RFE is represented by 631 families of 31 orders. The largest orders are Hymenoptera (72 families, 9000 species), Diptera (120 families, 8000 species), Coleoptera (114 families, 5500 species), Lepidoptera (81 families, 5000 species). The number of families and species strongly increases from north to south: in the tundra of Chukotka 200 families and 1100 species of insects occur, while in the nemoral landscapes of Sikhote-Alin Mts there are 600 and 22500 respectively.

Conclusion: The insect diversity of the large continental regions in the temperate zone generally depends on latitude rather than area.

A supercolony of Argentine ants spans southern Australia

Elissa Suhr[1], Dennis O'Dowd[1], Stephen McKechnie[2], Duncan Mackay[3]

[1]Australian Centre of Biodiversity, School of Biological Sciences, Monash University, Melbourne, VIC, Australia, [2]Centre of Environmental and Stress Adaptation Research, School of Biological Sciences, Monash University, Melbourne, VIC, Australia, [3]School of Biological Sciences. Flinders University, Adelaide, SA, Australia

Argentine ants can form expansive supercolonies that may contribute to their ecological success in introduced ranges. We investigated the colony structure of Argentine ants across southern Australia using microsatellite analyses and intraspecific aggression assays. Eight nests in each of three cities (Adelaide, Melbourne and Perth) spanning 2,800 km were sampled. Two nests from the native range and nine nests from other introduced ranges worldwide were also genotyped. Intraspecific aggression was completely absent between nest pairs within or between cities across Australia. Australian populations of Argentine ants were characterised by widespread genetic homogeneity and little genetic structuring within and between cities relative to source populations. Analysis of molecular variance (AMOVA) revealed that most variance was explained within nests (84.9%). Some continent-wide population structure was indicated by genetic differentiation between cities (10.7%), whereas little variation within cities (4.5%) was detected. A model-based clustering analysis of Australian samples identified three genetic clusters. Individuals had partial membership in multiple clusters and nearly always shared similar membership coefficients within cities. However, one nest in Perth clustered with Adelaide and an admixture between Adelaide and Perth was suggested at another Perth nest. When Australian and potential source genotypes were compared, Melbourne and New Zealand clustered together but marked differences occurred with other samples. Overall, Argentine ants in Australia form an expansive supercolony characterised by absence of aggression and effective local gene flow but limited gene flow across the continent.

Preference and performance of the six toothed bark beetle *Pityogenes chalcographus* L. (Coleoptera : Scolytinae) on native and exotic Pinaceae species in France

Coralie Bertheau, Geraldine Roux-Morabito, François Lieutier

Universite, Orleans, France

Introduction: *Pityogenes chalcographus* L. (Coleoptera : Scolytinae) is one of the important bark beetle species in European forests where it causes damage mainly on *P. abies*. It is considered as an oligophagous insect recorded on indigenous and exotic Pinaceae. This work was carried out on different host trees species belonging to *P. chalcographus* host range. It aimed at firstly estimating the preferences and the performances of the insect on different host species, and secondly testing the role of the between tree taxonomic relatedness in the possibilities of beetle adaptation to various hosts.

Methods: Choice and no-choice assays were set up under laboratory conditions, using logs of five Pinaceae species belonging to *P. chalcographus* host range: two indigenous species (*Pinus sylvestris* L. and *P. abies*) and three exotic north American species (*Pinus contorta* Dougl., *Picea sitchensis* (Bong.) Carr. and *Pseudotsuga menziesii* Mirbel (Franco)). Attack densities, fecundity, survival rate and brood productivity were analyzed, and a morphometric analysis of the emerged adults was performed.

Main Results: *P. abies* was the most attacked host species and *Pinus* species the least ones. In all assays, fecundity and survival rates were significantly higher in *Picea* species than in other species. Brood productivity was the highest in *P. abies*. No difference in beetle size was observed between host species but males were significantly wider and shorter than females.

Conclusions: *P. abies* was both the preferred and the most suitable host species. The closest relative *P. sitchensis* appeared the best substitution host.

Spatial processes in predator-prey dynamics and their importance for biological control of phytophagous pests.

Gösta Nachman

University of Copenhagen, Copenhagen, Denmark

Introduction: Modelling is a popular tool to assess the role of natural enemies in biological control. However, many models assume that herbivorous prey and their natural enemies are homogeneously distributed within a crop, whereas most field studies actually show that both prey and enemies are patchily distributed. This means that predators locally may be confronted with densities of prey that differ significantly from average densities. Many predator species therefore tend to concentrate their searching efforts to areas where encounters with prey are most likely, although this also leads to more intensive intraspecific competition among predators.

Methods: In order to understand the consequences of spatial interactions on predator-prey dynamics, a spatially explicit model (called *DynaMite*) has been developed. It simulates biological control of an arthropod phytophagous pest (two-spotted spider mites) by means of a specialist predator (a predacious mite). The model incorporates prey and predator aggregation at two different spatial scales (within and between plants).

Results: Simulations show that aggregation of predators has a profound effect on their capacity to suppress the prey within individual plants, but increases the risk of local extinctions of both species, which in turn may destabilize the system at the larger (regional) scale. The rate of movement of predators between plants plays a key role in achieving optimal control.

Role of antennae in termite grooming behaviour

Aya Yanagawa[1], Fumio Yokohari[3], Kazuhiro Iiyama[2], Chisa Yasunaga-Aoki[2], Susumu Shimizu[2]

[1]Institute of Biological Control, Graduate school of Bioenvironmental Science, Kyushu University and Research Fellowship of the Japan Society for the promotion of Science for Young Scientist, Fukuoka, Japan, [2]Institute of Biological Control, Graduate school of Bioenvironmental Science, Kyushu University, Fukuoka, Japan, [3]Division of Biology, Department of Earth Science, Faculty of Science, Fukuoka University, Fukuoka, Japan

It is well known that social insects have been developed the social strategy, which provide them great benefits. Likewise, in disease resistance, there are some reports about the advantage of sociality, however it has not been identified enough.

We have studied disease resistance based on the social strategy using termite, *Coptotermes formosanus* Shiraki and entomopathogenic fungi. Since termites live in high density population and a high humidity habitat which has suitable properties for fungal infection, fungal diseases can be quite lethal. However, even though the soils contain resident populations of entomopathogenic fungi, it is difficult to find fungal epizootics in termite populations. Previously, we have suggested the termite protect themselves from entomopathogenic fungus by mutual grooming behaviour. Nest mates remove of foreign bodies, such as fungal conidia, from the cuticle and throw them away through licking the surface of cuticle by glossa. Then, we wondered what elicit them to this behaviour.

To make clear this, the role of antennae in grooming behaviour was examined since antennal contact is important as introduction of other social behaviours. Behavioural experiments were applied to examine whether termite antennae were actually involved in the function of grooming behaviour, and electrophysiological methods were applied to examine whether antennae can detect the entomopathogenic fungal odour. The result of our study indicates that termite antennae have a role to find foreign organisms on their body surface by odour, however it seems that it is not the only method to detect foreign organisms. (238)

Replacement cost estimates of insect pollination services

Mike Allsopp[1], Ruan Veldtman[2], Willem De Lange[3]

[1]Plant Protection Research Institute, Agricultural Research Council, Stellenbosch, South Africa, [2]South African National Biodiversity Institute, Cape Town, South Africa, [3]Council for Scientific and Industrial Research, Stellenbosch, South Africa

Introduction: The importance of insect crop pollination to commercial agriculture is unequivocal. However, whether this service is largely provided by wild pollinators (as genuine ecosystem service) or managed pollinators (as commercial service), and which of these requires immediate action amidst reports of pollinator decline, remains contested.

Methods: Traditionally the value of these services is expressed as the proportional dependence of a crop's total production value, with a portion assigned to managed pollination. These methods either under-estimate (by equating pollination service values to the direct cost of the service) or over-estimate (by equating pollination services values to a proportion of total production value) the service value. In addition, the use of general insect dependence factors and the proportional allocation to managed pollinators have been criticised as being neither based on published data sources nor being regionally specific. We propose and apply the notion of ascribing a more accurate value to the service by calculating the cost to replace it. We employed adjusted insect and managed pollinator dependence factors to estimate the value of replacing insect pollination services for the Western Cape deciduous fruit industry of South Africa.

Results: Using pollen dusting and hand pollination as suitable replacements, we show that current market prices under-value the service, while traditional proportional value estimates is seen to be inflated.

Conclusion: Market prices for pollination service do not reflect the true value of pollination service. This market failure could promote unsustainable landscape use as both managed and wild pollinators are dependent on natural and semi-natural landscapes for forage. Credible valuation of pollination services will aid in justifying investment in their conservation.

Attraction of nectar-seeking mosquitoes to inflorescence odours of *Silene otites* (Caryophyllaceae)

Umma Salma Jhumur[2], Katrin Silke Jahreiß[2], Stefan Dötterl[2], Andreas Jürgens[1]

[1]University of KwaZulu-Natal, Pietermaritzburg, South Africa; [2]University of Bayreuth, Bayreuth, Germany

Introduction: Although mosquitoes are known to visit diverse flowers for nectaring, little is known about the specific cues used by mosquitoes for finding nectar plants. In several investigations flower odours were described as effective attractants for mosquitoes, however, in none of the studies the compounds responsible for attraction were identified. An interesting system to study the role of floral volatiles for attracting nectar-seeking mosquitoes is *Silene otites* (L.) Wibel (Caryophyllaceae), one of only two plant species world-wide in which mosquitoes have been described as effective pollinators.

Results and Discussion: When offering naïve mosquitoes inflorescences of *S. otites* they immediately fly towards them, land on them, and suck nectar. Most of the odour compounds of *S. otites* are electrophysiologically active to both night-active *Culex pipiens molestus* and day-active *Aedes aegypti*. In electroantennographic studies with the 13 most common and abundant odour compounds *C.p. molestus* males and females responded similarly to dilution series but the strength of the responses differed among compounds. Linalool oxide and linalool evoked the strongest responses in male and female mosquitoes, and (Z)-3-hexenyl acetate was strongly active in females. Wind tunnel bioassays with antennal sensitive compounds and *C.p. molestus* revealed that mosquitoes responded to 14 compounds in different magnitudes (65-20%). Furthermore, the significantly higher attraction of conditioned mosquitoes compared to unconditioned ones in wind tunnel bioassays shows that mosquitoes can learn floral volatiles to find their nectar host plants.

Multiple predators sharing prey: Consequences of microhabitat specialization

Maurice W. Sabelis[1], Arne Janssen[1], Izabela Lesna[1], Nayanie S. Aratchige[1], Sara Magalhaes[1], Alexis Onzo[2], Rachid Hanna[2]

[1]University of Amsterdam, Amsterdam, Netherlands, [2]International Institute of Tropical Agriculture, Cotonou, Benin

Introduction: Most species of herbivorous arthropods incur the risk of being eaten by more than one species of predator. Despite sharing the same prey, these predator species may coexist by occupying otherwise separate micro-habitats. While intraguild predation may drive niche specialization (and avoidance of intraguild competitors), its occurrence decreases in frequency with progress in specialization. We therefore predict intraguild predation to play a less important role and multiple predator species to affect the density of their shared prey in a near-additive way.

Methods: To test this prediction we analyze various two-predator-one-prey (=herbivore) systems on plants. The predators are two species of phytoseiid mites frequenting different parts of the same plants (e.g. flower *vs* leaf of a sweet pepper plant; apex *vs* leaf of a cassava plant ; external *vs* internal part of a bulb; different areas under the perianth of a coconut) and we investigate how these predator species, either together or alone, affect the shared prey (thrips, spider mites, rust mites). Moreover, we analyze how the prey chooses between plant parts harbouring different predator species.

Results and Conclusions: From these studies we conclude that the two predator species together act on prey suppression in an additive way and – when at least one predator species has no access to the microhabitat of the other – they may even act in a synergistic way.

Factors promoting Argentine ant colony expansion

Jules Silverman, Robert John Brightwell

North Carolina State University, Raleigh, North Carolina, United States

The success of Argentine ant, *Linepithema humile*, invasions has been attributed to a combination of genetic, behavioral and ecological factors. We have explored intercolony interactions and the contribution of stable food sources as factors contributing to invasion success.

Unlike reports from most regions within its introduced range, Argentine ant colonies in our study zone, the southeastern United States, are relatively small and discrete and display varying levels of intraspecific aggression. We predicted, however, that if environmental constraints, e.g. low winter temperature, were relaxed and colony boundaries expanded fusion would occur between colonies that ultimately made contact. In laboratory and field experiments, most paired mutually aggressive colonies did fuse as evidenced by queen movement between nests. We found a direct relationship between both genetic and cuticular hydrocarbon similarity and colony fusion success.

We also determined that Argentine ant colony expansion is, in part, mediated by available food. When sucrose-containing stations were positioned along a transect into uninfested deciduous forest adjacent to infested urban landscape ants moved at least 50 meters into the forest and thereafter retreated when the food was removed. Also, *L. humile* moved nests towards or away from the base of trees containing honeydew-excreting scale insects, depending on whether access to scales was permitted.

Using terrestrial arthropods to refine and define forest management and conservation in Eastern Canadian Boreal forests

Timothy Work, Christopher O'Connor, Annie Hibbert, Simon Paradis

[1]Université du Québec à Montréal, Montréal, Québec, Canada, [2]CRSNG-UQAM-UQAT Chaire d'aménagement forestier, Rouyn-Noranda, Montréal, Québec, Canada

Introduction: The preservation of biodiversity and ecosystem functions within managed forests has been widely advocated by proponents of sustainable forest management. However, how best to implement and integrate silviculture and conservation objectives remains largely dependent on forest type, natural disturbance regime and species-level differences among arthropod communities. Within Eastern Canadian boreal forests, variations of both clear cutting and partial cut harvesting have been proposed as a means to reflect the variability of stand structures that remain following natural wildfires or large-scale insect outbreaks.

Methods: Here we present a synthesis of recent studies aimed at understanding how these newly proposed silvicultural strategies affect arthropod communities with an emphasis on the responses of soil microarthropods (Collembola), saproxylic organisms within both coarse woody material (CWM) (Diptera and Coleoptera) and recently burned stands (Coleoptera) and higher order consumers (Coleoptera: Carabidae and Staphylinidae, Araneae) to changes in overall stand structure and specific within-stand 'legacy' elements.

Results: These studies indicate that arthropods associated with detrital inputs (i.e (litterfall, snags and CWM), decomposition or detrital-based food webs are sensitive to changes in forest structure. These changes range from species-specific responses to factors relating directly to detrital input or microbial activity to overall community level differences based on interactions between harvesting and time since fire.

Conclusions: We believe these responses can be actively included in forest and conservation planning to define a subset of 'detrital-based' forest management that integrates long-term temporal impacts of silviculture with the functional roles of arthropod biodiversity.

Enemy-induced responses and their indirect effects on arthropod communities on plants

Maurice W. Sabelis, Arne Janssen, Izabela Lesna, Merijn Kant

University of Amsterdam, Amsterdam, Netherlands

Introduction: Interactions between plants, herbivorous and predatory arthropods depend on the direct effects of enemies on their victims, but also on the indirect effects induced by the enemy in its potential victim and thereby on the tritrophic system as a whole. For example, herbivorous arthropods may not only kill plants, but they may also alter the plant's antiherbivore responses and the extent to which plants facilitate the foraging of the herbivore's enemies (so called indirect plant defense). Another example is that predatory arthropods may not only kill herbivorous arthropods, but they may also alter the herbivore's antipredator responses and the degree to which the herbivore alerts the plant's direct and indirect defenses.

Methods: To analyse these effects and their consequences for arthropod communities we made good use of plant hormones that trigger direct and/or indirect plant defense responses and of plants in which genes underlying these defense responses are silenced or overexpressed.

Results and Conclusions: We review recent results of experiments with various tritrophic systems involving predatory mites, herbivorous mites or thrips, and plants (tulip bulbs, cucumber, sweet pepper, tomato) and show that induced responses can have dramatic effects on the structure of arthropod communities.

Remote Diagnostics – research and identifications from afar?

Michael Schauff

Plant Sciences Institute, USDA, ARS, Beltsville, MD, United States

With continuing globalization and increase availability of high speed internet access several groups have begun to develop technology to remotely view, manipulate, and photograph specimens. This technology offers several advantages over current practices In particular, these devices may cut shipping costs, allow for rapid examination of specimens during times of crisis, and make available archives of images that will help reduce the need to repeatedly examine valuable and fragile types and other specimens. It may also make it feasible for regulatory personnel to remotely sort and identify some specimens without the need for an on-site investigator present. One recently developed instrument is highlighted as an example of where this technology is headed. While still limited in some aspects this instrument is able to provide many of the functionalities required of a remotely operable platform. Many challenges remain. Among these are staffing issues, information technology security concerns, access rights of users, storage and archiving of images, and hardware costs.

Conclusion: Remote diagnostics has the capability to mitigate many of the traditional and most difficult obstacles to specimen-based research and identification of insects. While many challenges remain current work has shown the viability of the concept.

Predator-predator interactions: Impact on biological control of a shared prey pest in Africa

Alexis Onzo, Rachid Hanna, Maurice W. Sabelis

[1]International Institute of Tropical Agriculture, Cotonou, Benin, [2]University of Amsterdam (IBED), Amsterdam, Netherlands

Introduction: The issue of introducing single or multiple natural enemy species for classical biological control has been an area of intense inquiry in biological control of cassava green mite *Mononychellus tanajoa* in Africa. This is because this herbivorous mite is preyed on by several predatory mites including *Typhlodromalus aripo, Amblydromalus manihoti* and *Euseius fustis.*

Methods: In series of screenhouse and field experiments where predator species composition was manipulated at plant level, we determined the effects of single and two predator species on suppression of *M. tanajoa* populations and on population dynamics of predators. These trials were supplemented with field surveys.

Results: In screenhouse, either *T. aripo* or *A. manihoti* was sufficient for suppressing *M. tanajoa* populations, with *A. manihoti* being more efficient at high initial prey densities and *T. aripo* more efficient at low initial prey densities. Field surveys showed that presence of other predators, in addition to *T. aripo*, was associated with lower *M. tanajoa* densities. *T. aripo* densities were generally positively affected by the presence of other predators. In manipulative field trials, *M. tanajoa* densities were also relatively lower on plants harboring the key predator *T. aripo* and either of *A. manihoti* or *E. fustis* than on plants with one predator alone. Moreover, no predator species was negatively affected by the co-occurrence of the others.

Conclusion: Suppression of *M. tanajoa* populations was enhanced by the co-occurrence of *T. aripo* and other predators. Two predator species are therefore better than one for biological control of *M. tanajoa* in Africa.

Recognition cues for cooperation and conflict in ants: Interplay between uniformity and variability of cuticular hydrocarbons

Jelle van Zweden

University of Copenhagen, Copenhagen, Denmark

Social insects are the prime evolutionary examples of cooperation and therefore a central model system to test predictions of kin selection theory. Kin recognition is required for kin selection to occur. However, when multiple genetic lineages are present within the colony, accurate information on kinship may lead to internal conflict. The relative influence of genetic background on the variation in recognition cues has remained largely unresolved so far. I used a cross-fostering design to disentangle the different sources of variation in the hydrocarbon profiles of ants, and to obtain relative heritability measures for the different compounds. The results show that the relative abundance of linear alkanes can be highly variable within colonies and that these are the least heritable compounds on a colony level. In contrast, branched hydrocarbons are more heritable components and these are the compounds that are homogenized among nestmates. Hence, only parts of the hydrocarbon profile are uniform among nestmates and can be used for cooperation, whereas other parts remain variable, so that potentially these can be used for within-colony discrimination.

Is there a gradient of predation pressure on specialist caterpillars at different elevations in the North Eastern Andes of Ecuador?

Genoveva Rodriguez-Castañeda, Lee A. Dyer

Tulane University, New Orleans, United States

Introduction: Predation is thought to change as assemblages of predators and abiotic conditions change. We compared survival rates of *Eois olivacea* (Geometridae: Laarentinae) and the associated changes in predator assemblages across a complete gradient of elevation (400-3200m), on both native and experimentally introduced plants.

Methods: In two separate experiments, *E. olivacea* were exposed to natural predator assemblages for 24 hours at different elevations and in forests that varied in ant abundance. In the first experiment, the caterpillars were placed on their natural host plants, which were transplanted one hour prior to the experiment. In the second experiment, caterpillars were placed on a leaf from their natural host plant species, then this leaf was attached to *Piper* plant species that occurred on the understory of the different elevations.

Results: We did not find a significant linear elevational gradient in predation rates for *E. olivacea* when the caterpillars were placed on their native host (predation rate =52.059-0.0062*(elevation), r^2=0.043, P=0.15). However, for the second experiment, predation first decreased with elevation (400-1500m) (predation rate =110.355-0.0275*(elevation), r^2=2.94, P=0.0001) and then increased from 1600-2600m. Predation pressure was not significantly associated with ant presence/absence.

Conclusions: Predation gradients in this study were determined by the native community of mostly specialized predators associated with the local *Piper* species and not by the presence/absence of ants at the different sites.

The role of ecological stoichiometry in outbreaks of forest Lepidoptera

Eric Lind, Pedro Barbosa

University of Maryland, College Park, MD, United States

Ecologists have explained outbreaks of caterpillars in temperate forests using a variety of models to capture the temporal and spatial dynamics of pest populations. Dispersal patterns, natural enemy response, and disease are known to regulate these outbreaks at various scales. Yet a comprehensive understanding of how and where outbreaks begin still eludes researchers. Ecological stoichiometry, an emerging area of ecological theory, may aid in understanding outbreaks by examining the intersection between insect growth rates and elemental nutrient requirements, and plant elemental nutrient content. Growth rates of herbivorous insects are known to be constrained by the nutrient levels in their food, specifically by the high C:N or C:P ratios in plants, but maximum growth rates and elemental ratios both vary between insect species. Under the growth rate hypothesis of ecological stoichiometry, phosphorus may be especially important for maximizing individual growth rate, yet it has not been as well studied as nitrogen in forest insect systems. We measured elemental ratios of outbreak and non-outbreak Lepidoptera in eastern North American temperate forests to determine whether they differed in constitutive elemental ratios. We also examined the spatial pattern in foliar C:N:P in a riparian forest tree, sampling leaves during a localized outbreak of a forest pest (the fall cankerworm *Alsophila pometaria*). Both sets of data suggest the inherent nutritional mismatch between caterpillars and their host plants is more dynamic than has previously been recognized, and that the spatial variability of the availability of nutrients, especially phosphorus, may add to an understanding of where, and with which herbivores, outbreaks occur.

Breeding systems, dispersal and mate choice in the Formosan subterranean termite

Claudia Husseneder[1], Edward Vargo[2]

[1]Louisiana State University, Baton Rouge, Louisiana, United States, [2]North Carolina State University, Raleigh, North Carolina, United States

Introduction: A subterranean termite colony is initiated by a monogamous pair. The pair's fat reserves sustain the incipient colony. Partner relatedness determines the degree of inbreeding within the colony. Therefore, body size and relatedness of reproductives are expected to play important roles in determining colony founding success. We tested whether swarming individuals select partners according to size and whether they avoid pairing with relatives during tandem running.

Methods: From five swarm aggregations in New Orleans, Louisiana, both tandem pairs and single individuals were collected and their weights and head widths were recorded. Degrees of relatedness were determined by microsatellite genotyping.

Results: Males running in tandem with females had larger heads than single males. Weights of tandem running partners were positively correlated as were head widths. Pairing was random with respect to relatedness, showing no evidence of kin avoidance. Interestingly, females forming tandems with males had a higher degree of heterozygosity than females that remained single. Although there was no kin discrimination during partner selection, there was little inbreeding due to long dispersal distances and due to genetic differentiation between the sexes. The dispersal distance of alates was sufficient to provide mixing of an average of 13 colonies within swarm aggregations. Genotypic frequencies differed significantly between males and females. This could not be explained by sex-biased dispersal but by sex-biased investment depending on colony breeding structure. Inbred colonies produced predominantly males, while outbred colonies produced predominantly females. This discrepancy could be caused by the pairing advantage of heterozygous females.

Where being green, profitable, and efficacious meet structural IPM: California, USA

Vernard Lewis

UC Berkeley, Berkeley, California, United States

The term pest control has evolved over the decades. Beginning in the early 1900's, replacement terms like pest eradication, integrated control, and systems control filled the academic and applied literature. More recently, the most widely accepted term is integrated pest management (IPM). Traditionally, the activities surrounding IPM where dominated by researchers, entomologists, agriculturists, and providers of natural enemies of pest populations. Today, stakeholder groups have grown and include urban homeowners, environmental groups, water quality, alternative and non-chemical suppliers, and well as traditional pest management service provides and manufacturers. Definitions that include urban stakeholders, assumed simple to define, have been proven demanding to achieve. California has a powerful economy, rated as high as seventh in the world and demands for protection for pests is great. However, additional responsibilities include being "green" imply being safe to the environment and non-target organisms. Additional regulatory oversight for new policies has placed a considerable demand on commercial service providers to be in compliance, yet all the while joggling budgets and profits. For today's presentation, using my entomological/research perspective, I will give specific examples on how the mandates of being green, efficacious, and profitable interplay with the IPM practices being offered to consumers in California. My hope is to help along the dialog among the world's urban and other stakeholder groups as we move towards pest management strategies that are effective, affordable, locally relevant, and take into consideration the many sensitive environments that occur globally.

Evolution and co-evolution of *Eurosta solidaginis* gall morphology with its host plant and natural enemies

Timothy Craig, Joanne Itami

University of Minnesota Duluth, Duluth, Minnesota, United States

Introduction: *Eurosta solidaginis* varies geographically with galls being more spherical, and having larger diameters in the prairie than in the forest biomes. In addition there is complex variation within biomes. *Eurosta* gall morphology is the result of the interaction of the insect genotype, its host plant, and the environment. The host plant, *Solidago altissima*, has diverged into different subspecies in the two biomes, and the fly populations into two host races.

Methods: Using common garden and reciprocal transplant experiments we measured the impact of host plant subspecies, and the geographic race of the fly on gall size and shape. We also determined whether populations of the parasitoid wasp, *Eurytoma gigantea*, and the inquiline beetle, *Mordellestina convicta*, were locally adapted.

Results: Gall diameter was strongly influenced by the host race of the fly and the environment, but not the plant subspecies. Gall shape was influenced by both the fly host race and the host subspecies but not the environment. *Eurytoma gigantea* showed evidence being locally adapted to the prairie galls each host race had a preference for their local host, and the prairie host race had longer ovipositors that are adaptive for reaching larvae in bigger galls. The inquiline did not show evidence of local adaptation, as both populations performed better on prairie galls.

Conclusion: The gall-maker, the host plant, and the parasitoid show evidence of having a strongly coevolved relationship.

Insect repellents and personal protection as components of integrated disease management

Daniel Strickman[1], Mustapha Debboun[2]

[1]US Department of Agriculture, Beltsville, Maryland, United States, [2]Academy of Health Sciences, US AMEDD Center & School, Houston, Texas, United States

Topical insect repellents seem like a logical choice for protection from arthropod-borne pathogens: they are safe, they are effective, and they target the objective precisely. Despite these apparent advantages, repellents have rarely been used as an important part of programs to protect the public from malaria, dengue, or other important diseases associated with arthropods. The challenges for efficient use of repellents include the difficulties of distribution, individual behavior, cosmetic qualities, and quality assurance of performance. These problems must be addressed in order to truly integrate the use of repellents into an efficient disease management system. At their best, repellents could make a major contribution toward efforts to break the chain of transmission at its weakest links. For non-zoonotic pathogens, the most effective strategy might be targeted application of repellents to those individuals either most susceptible to infection or most likely to serve as reservoirs of infection. For zoonotic pathogens, the thoroughness with which repellents are used should be in proportion to the number of bites experienced by the individual.

The PRONTI species selection method: Can this tool be used for risk assessments with biological control agents?

Jacqui Todd, Louise Malone, Padmaja Ramankutty, Emma Barraclough

HortResearch, Auckland, New Zealand

Introduction: The PRONTI (priority ranking of non-target invertebrates) species selection method has been developed for use in the problem formulation stage of environmental risk assessments of new environmental stimuli. The selection method is a computer-based tool that produces prioritised lists of species, ranked according to five commonly used selection criteria: (1) potential hazard; (2) potential exposure; (3) environmental impact of the species being affected by the new stimuli; (4) anthropocentric value; and (5) testability.

Methods: The selection method is driven by a basic hypothesis of the risk posed by the new stimuli to each invertebrate in the receiving ecosystem. Information on the biology of each species found in the receiving ecosystem is entered into a specially designed database and combined with information on the potential impacts of the new stimuli on each species. A "score" is then appointed to each piece of information, based on its usefulness for meeting each of the five selection criteria under the influence of the base hypothesis. The scores are then combined, using the model, to produce a final PRONTI score for each species. The flexibility of this system should allow it to be used for any stimuli in any agro-ecosystem. Can the benefits of biological control agents be included in the model?

Results: The PRONTI scores have been used to list the species from highest to lowest priority for biosafety testing with hazardous new stimuli.

Conclusions: Modifications that will allow the method to be used for biological control agents will be discussed.

Insects and technology

Arnold van Huis

Laboratory of Entomology, Wageningen University, Wageningen, Netherlands

Biomimicry uses designs and processes in nature to solve human problems. The iridescent blue *Morpho rhetenor* butterfly is visible over a distance of more than half a km, and is attributed to photonic structures formed by discrete multilayers of cuticle and air. The striking optical effect of such nanometre-scale architectures can be used in the paint and coating industry. The elastic properties of resilin, a protein in wings and legs of e.g. fleas, could be used to repair damaged arteries. Dragline silk from spiders is stronger than nylon and steel fibres and can be used to manufacture bulletproof vests, surgical thread, micro-conductors, and optical fibres. Termite mounds captures and manages wind so that it supports nest homeostasis. The complex network of tunnels keeps the heat, humidity and air quality at an optimum. This architecture can be used to design the eco-houses of the future. Google's PageRank algorithm follows the principle of ant trails. Swarm intelligence of social insects is the collective behaviour of independent agents, each responding to local stimuli without supervision. This feature of social insects is being used in robotics and nanotechnology, molecular biology and medicine, traffic and crowd control, and military tactics. The olfactory sensitivity of wasps or bees is at the level of parts per trillion. Wasps can be trained to detect certain compounds. This ability can be used to design cheap ultra-sensitive, flexible and portable odour detectors with wasps to find explosives, drugs, plant diseases, cancer, and tuberculosis.

Reflections and evidences on the present status of biological control of arthropod pests

Gennaro Viggiani

Dipartimento di Entomologia e Zoologia agraria; Filippo Silvestri - Università degli Studi di Napoli, Federico II, Portici, Italy

During the last two decades new tools and methodologies currently available, such as a few entomopathogenic agents and some natural products, suggested several changes in the original concept of biological control.

In the same period, several “chair-authors” started, first, to analyze the literature data on biological control projects concluding that most of them were unsuccessful, and then fearing biological and ecological risks. In particular, matters of concern were the conservation of biological diversity and consequently the accidental introduction of entomophagous species causes environmental risks. Matters of debate are also the methods used for evaluating the potential of biological control agents and their efficiency. In this context of general criticism, rarely based on precise facts, the increase of rigorous procedures and regulations for the importation of exotic entomophagous species do not favour the accomplishment of classical biological control projects against arthropod pests. Even the host specificity of an entomophagous species can avoid any ecological effect. But this “risk”, that is in the balance of nature, should not prevent the benefit derived from the introduction in new areas of predators and/or parasitoids. A classical project of biological control can not be evaluated in the same manner of inoculative and inundative releases for several reasons (long term and expanding area effect, heterogeneous environmental conditions, etc.). The most recent cases study of biological control carried out in Italy are discussed.

Leafhopper host plant associations for egg parasitoids (Hymenoptera: Mymaridae and Trichogrammatidae) in the vineyard agroecosystem of Italy

Gennaro Viggiani

Dipartimento di Entomologia e Zoologia Agraria, Università degli Studi di Napoli, Portici, Italy

During last five years a study was carried out in order to improve the knowledge on the functional biodiversity that can help the natural control of the grape vine leafhoppers. Using yellow sticky traps and samplings on *Vitis* spp., *Rubus ulmifolius*, *Salix* spp., *Ficus carica, Lonicera* spp. and *Ulmus minor* with parasitized eggs, several thousands of parasitoids were obtained and identified. The complex of parasitoids obtained from leaves and twigs was represented by *Anagrus atomus* (Linnaeus), *A. ustulatus* Haliday, *Stethynium triclavatum* Enock (Mymaridae), and *Pseudoligosita pallida* (Kryger) (Trichogrammatidae). The ratio between the *Anagrus* species changes in relation to the leafhopper host plant associations. The dominant species of *Anagrus* obtained from *Vitis* and *Rubus* in Northern, Central and Southern Italy was *A. ustulatus*. From *Ulmus* leafhoppers both species of *Anagrus* were identified, yet in this case the dominant egg parasitoid was the trichogrammatid *P. pallida.* Only *Anagrus*, mostly represented by *A. atomus,* have been obtained from *Ficocyba ficaria* (Horváth) which develops from late autumn to spring on *Lonicera* spp. and then on *Ficus carica*. An important source of *S. triclavatum*, egg parasitoid of *Empoasca* spp., has been found in *Salix* spp. On these plants the mymarid reproduces from spring to autumn on *Empoasca decedens* Paoli. Several phenological observations carried out in Southern Italy on *A. atomus* and *A. ustulatus* confirm that in this area both species can overwinter also as adults and continue to reproduce on developing hosts. In this habitat a wide complex of leafhopper host plant associations can provide in spring the antagonist biodiversity of potential pests that can spread in the vineyards.

Linking habitat use to range expansion rates in fragmented landscapes: a metapopulation approach

Robert Wilson[1], Zoe Davies[2], Chris Thomas[3]

[1]University of Exeter, Penryn, United Kingdom, [2]University of Sheffield, Sheffield, United Kingdom, [3]University of York, York, United Kingdom

Introduction: Insect geographic ranges are limited by temperature at high latitudes, where climate change is expected to lead to range expansions. However, documented expansions are largely restricted to habitat generalist and dispersive species. Therefore, techniques are required to identify the factors that limit range expansions by specialist species breeding in fragmented landscapes.

Methods: A metapopulation model (Incidence Function Model, IFM) was used to test effects of habitat use and landscape-scale habitat availability on patterns and rates of range expansion in the butterfly *Hesperia comma*. The model was applied to the species distribution between 1982 and 2002 in five habitat networks at its high latitude margin in the UK.

Results: Range expansion rates depended on the area and connectivity of suitable habitat, and were well-predicted by IFM modelling. Habitat availability for *H. comma* has increased associated with conservation management and climate change, but despite increased local population sizes the regional distribution of the species lags behind the distribution of suitable habitat. Landscapes lacking in habitat act as barriers to colonization, but long-distance dispersal events may lead to metapopulation state changes when formerly vacant networks are colonized.

Conclusions: Metapopulation models represent a promising approach for predicting rates of range expansion and for identifying landscapes where environmental change or conservation interventions could have the most significant effects on species distributions or persistence.

Passive ventilation in large termite mounds, and implications for human construction methods

Rupert Soar, Henk Versteeg, Weratunga Malalasekera, Haitham Abou-Houley

Loughborough University, Loughborough, Leicestershire, United Kingdom

The TERMES project [www.sandkings.co.uk] is in its final stage and brings together researchers in Entomology, Physiology, Construction and Mechanical Engineering. The project has sought to understand termite architecture (specifically in *Macrotermes michaelseni*) and the underlying function of mound ventilation and internal environmental regulation through structural homeostasis. The project has used 3D imaging and reconstruction techniques to capture both internal and external topology at millimetre scale resolution. Computational fluid dynamics modelling techniques have been applied to the model to explore mound skin permeability, the effects of highly localised perturbations, local and global convective flow within the structure and a simplified model of the internal reticulum to identify the functional components which make up the ventilation system. These will be described and their implication discussed.

Our ultimate objective is to seek novel passive methods which can inform modern construction practice in the face of energy concerns and recycle/re-use demands.

Individual variation in queen pheromone response is correlated with ovariole number in worker honey bees

Sarah Kocher, Christina Grozinger

North Carolina State University, Raleigh, NC, United States

Introduction: In honey bees (*Apis mellifera*), the reproductive queen produces a pheromonal signal that maintains worker sterility and is critical for colony social organization. A subset of this pheromone, a 5-component blend known as queen mandibular pheromone (QMP), produces many of the same effects as a live queen. QMP attracts workers from a short distance (retinue response), inhibits the rearing of new queens, inhibits worker ovary development, modulates age-related division of labor, and alters learning and memory. Despite the fact that queen pheromone plays such a critical role in honey bee social behavior, there is significant variation in QMP sensitivity both within and between colonies and subspecies.

Methods: This study examines the link between variation in pheromone response and ovariole number – a predictor of reproductive potential. The retinue response of individual bees from multiple colonies was scored over several days. Worker ovaries were then dissected and counted.

Results: We identified significant variation in QMP responsiveness among colonies, but also among individual workers within each colony. Individuals with a low pheromone response score had significantly more ovarioles than individuals with a high pheromone response score.

Conclusions: These results suggest that individuals with greater reproductive potential are less responsive to QMP, thus providing a link between pheromone response and reproductive potential in worker honey bees. Future studies will attempt to identify the molecular basis of this genetic variation and examine the evolutionary history of selection on this ecologically-relevant trait.

The impact of diet on immune function and disease resistance in *Spodoptera* caterpillars

Kenneth Wilson[1], Sonia Povey[1], Sheena Cotter[2], Kwang Pum Lee[3], Stephen J. Simpson[4]

[1]Lancaster University, Lancaster, United Kingdom, [2]Cambridge University, Cambridge, United Kingdom, [3]Seoul National University, Seoul, Republic of Korea, [4]University of Sydney, Sydney, Australia

Resisting pathogens is costly and can deplete resources that could otherwise be allocated to other functions, such as maintenance activities. Here, we examine the impact of dietary macronutrients (protein and carbohydrate) on immune function and resistance to bacterial and viral infections in *Spodoptera* caterpillars, and assess the capacity of the insects to alter their diets to offset the costs of mounting an immune response and resisting infection. We show that even in a species whose optimal diet is normally carbohydrate-biased, caterpillars that feed on protein-biased diets not only have elevated immune function (phenoloxidase activity, antibacterial activity, etc) but also exhibit enhanced resistance to both bacterial and baculovirus infections. Moreover, sub-lethally infected caterpillars exhibit an adaptive shift in their feeding behaviour, relative to uninfected individuals, so as to consume more of the dietary protein required for disease resistance.

Using *Tribolium castaneum* as a model to evaluate influence of landscape structure on behavior

Susan Romero[1], James Campbell[2], James Nechols[3]

[1]University of Kentucky, Department of Entomology, Lexington, KY 40546, United States, [2]USDA/ARS Grain Marketing and Production Research Center, Manhattan, KS 66502, United States, [3]Kansas State University, Department of Entomology, Manhattan, KS 66506, United States

Introduction: Landscape structure can influence the fine-scale movement behavior of dispersing animals that ultimately may influence ecological patterns and processes at broader scales. Theoretical and empirical ecological research has emphasized the need for understanding how animals perceive and respond to landscape structure and the importance of integrating both behavioral and landscape approaches when studying movement behavior.

Methods: Our research addresses questions concerning how insects respond to landscape structure by examining movement and oviposition behavior of a model insect, an important stored-product pest, red flour beetle (*Tribolium castaneum*), in experimental landscapes.

Results: Our data show that beetles modify movement behavior depending on landscape structure. Edge effects and inter-patch distances influenced landscape viscosity, or the degree to which landscape structure facilitates or impedes movement, resulting in significant differences in velocity and tortuosity (amount of turning) of movement pathways, as well as retention time in landscapes with different levels of habitat abundance and aggregation. Beetles responded to landscape structure differently depending on the activity in which they were engaged. Distribution of movement pathways was similar to that of the habitat, but distribution of oviposition sites were significantly more aggregated than pathways and habitat.

Conclusions: Our research demonstrates how detailed examination of patterns of movement and oviposition, coupled with measures of lacunarity (variation in gap sizes of a pattern on a landscape) can be useful in determining how an organism responds to various scales of heterogeneity and how this response may change according to the functional use of the landscape.

Tracking the field dispersal of the Colorado potato beetle using a portable harmonic radar

Gilles Boiteau[1], Charles Vincent[2], Bruce Colpitts[3]

[1]Agriculture and Agri-Food Canada, Fredericton, N.B., Canada, [2]Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu, Qc, Canada, [3]University of New Brunswick, Fredericton, N.B., Canada

Introduction: The dispersal ecology of this primary pest of potato, walking within and between host plants, remains poorly known because of the cryptic appearance of the adult with the soil and the time spent in the canopy. Harmonic radar technology should make it possible to locate the position of the pest in the field but must also be shown to have no effect on the movement itself.

Methods: In the field, a portable harmonic radar prototype was used to test its ability to detect walking CPB carrying electronic tags In the laboratory, the horizontal and vertical movement of individual CPB with and without electronic tags was compared using motion monitoring equipment and visual observations, respectively.

Results: Tagged adult CPB were tracked successfully on bare ground and within the crop canopy of potato fields. In the laboratory, the addition of a tag on the pronotum of adult Colorado potato beetles had no significant impact on the mean distance traveled by the beetles or on the mean speed of travel horizontally or vertically. However, tagged beetles tended to hesitate more than untagged beetles before a bout of walking activity.

Conclusions: Except for a possible underestimation of the frequency of dispersal over short time periods, small weight electronic tags provided representative tracks of CPB dispersal.

Spatial dynamics of omnivore-prey systems: predatory bugs as a model

Moshe Coll

Hebrew University, Rehovot, Israel

Theoretical studies suggest that feeding on plant materials should destabilize omnivore-prey systems, thus make omnivory rare in nature. This is predicted because the omnivore also competes with its prey for shared resources. These predictions do not, however, consider the spatial properties of omnivore-prey systems, particularly the disjunction often found in the distribution of prey and plant food sources. I will discuss the significance of spatial omnivore-prey dynamics in the light of several studies of anthocorid bugs. Work in Mediterranean forests suggests that *Anthocoris nemoralis* moves among tree species, tracking plant and prey foods. Likewise, *Orius* bugs congregate near pollen sources, often forcing their prey to inhabit sub-optimal sites on the plants. In strawberry system, the move out of preferred feeding sites may provide the prey with spatial refuge from its omnivorous predator, but may also lead to an increase in crop damage. Finally, field data indicate that *Orius* bugs respond to prey and pollen availability at different spatial scales. Taken together, results suggest that omnivore-prey interactions are weakened by changes in the spatial arrangement of plant-provided foods, the omnivore and its prey. This may enable omnivore-prey systems to persist in nature.

Incorporation of mitochondrial fragments in the nuclear genome (*Numts*) of the longhorned beetle *Monochamus galloprovincialis* (Coleoptera: Cerambycidae).

Fotini Koutroumpa[1], François Lieutier[1], Emmanuelle Magnoux[2], Géraldine Roux-Morabito[2]

[1]*University, Orleans, France,* [2]*INRA, Orleans, France*

Introduction: The longhorned beetle, *Monochamus galloprovincialis*, vector of the pinewood nematode in Portugal, presents a large distribution in Europe. In order to evaluate the genetic diversity within this xylophagous insect, a mitochondrial DNA study was conducted on European populations. Numerous ambiguous nucleotide sites were detected, requiring further investigations on their nature. Hypothesis of heteroplasmy and pseudogenes (*Numts*) were examined.

Material and methods: MtDNA was sequenced for part of the Cytochrome Oydase I gene (COI) and COII gene on 43 *M. galloprovincialis* populations. Separation of mtDNA and nuclear DNA was performed using alkaline lysis method and cloning. Populations of a sister species, *M. sutor*, was also sequenced for comparison.

Results: Final alignment of 792bp of the COI and 521bp of the COII genes revealed a high polymorphism within and between *M. galloprovincialis* populations. Half of the studied individuals (44.8%) showed ambiguities on multiple nucleotide sites. MtDNA isolation by alkaline lysis supports the hypothesis that the ambiguous sequences amplified were not of mtDNA nature and validates the presence of *Numts* in the nuclear genome of *M. galloprovincialis*.

Discussion: This is the first time that *Numts* are proved for a longhorned beetle. The incorporation mechanism of *Numts* in unknown for *M. galloprovincialis*, however, excess of ambiguous sites corresponding to synonymous mutations placed on third codon position as well as the absence of *Numts* in its sister species *M. sutor*, conducted to the hypothesis of a recent apparition of *Numts* in the nuclear genome of *M. galloprovincialis*.

Use of molecular markers to identify cryptic species or complexes of sibling species in invasive or potentially invasive conifer pest insects

Géraldine Roux-Morabito, Alain Roques, Marie-Anne Auger-Rozenberg

INRA, Orleans, France

Introduction: Molecular genetic approaches are powerful tools for studying evolutionary aspects of biological invasions, especially for the identification of cryptic species or divergent lineages which can hinder a clear biological characterization of invasive species. Phytophagous insects show several examples of complexes of sibling species as well as successful invasion histories. We will present two case studies of phytophagous invaders. The first case will consider species which have been extensively transported globally for decades along with the seed trade (*Megastigmus* spp. seed chalcids), and the second pine pitch weevil of unknown origin, *Hylobitelus xiaoi,* which is presently in outbreak and is expanding in southern China. We will present data showing tests of the efficiency of molecular techniques for assessing whether the insect species correspond to cryptic native species or invasive species.

Material and methods: We use a phylogeographic approach by sequencing mitochondrial DNA genes (COI and/or COII). Individuals from different localities and from different host species were sampled in both the invaded and the presumed native range of the species.

Results and discussion: The study revealed misidentifications in *Megastigmus* species which have been previously recorded either as invasive or native species. It validated the use of molecular tools to detect cryptic species in this genus. These results also highlighted the importance of studying genetics in native populations to confirm or invalidate species identification only based on morphological traits. It should allow both a clear identification of native lineages and the tracking of the source population for expansion in *Hylobitelus*.

Phylogeny of the Ichneumonidae

Andrew M. Bennett, David B. Wahl, Ian D. Gauld, Ashley P. Dowling, Michael J. Sharkey

[1]Canadian National Collection of Insects, Ottawa, Ontario, Canada, [2]American Entomological Institute, Gainesville, Florida, United States, [3]The Natural History Museum, London, United Kingdom, [4]University of Arkansas, Fayetteville, Arkansas, United States, [5]University of Kentucky, Lexington, Kentucky, United States

Introduction: The Ichneumonidae is the largest family in the Hymenoptera with over 23000 described species classified into 40 subfamilies. Among these subfamilies, several informal groupings have been proposed based on adult and larval morphological characters (e.g., the ophioniformes, pimpliformes and ichneumoniformes). Previous studies have addressed the monophyly of particular groupings, but no comprehensive analysis of all 40 subfamilies has been made.

Methods: Adult and larval morphological characters as well as life history traits and molecular sequence data were scored for exemplars from all subfamilies. The data were analyzed separately and in combined analyses. Different sequence alignment methods were also used.

Results: We present the most comprehensive analysis of the subfamilies of ichneumonids to date. Whereas some hypothesized relationships were upheld, other groupings did not have support in our analysis. Sequence alignment methods had a great effect on overall topology.

Conclusions: Additional sequence data and novel morphological character systems will help greatly to resolve areas of the ichneumonid phylogeny with ambiguous topologies.

A novel methodology for testing for niche partitioning in insect predator communities

Tobin Northfield, Gretchen Snyder, William Snyder

Washington State University, Pullman, WA, United States

Niche partitioning often leads to increased prey suppression with increased predator biodiversity by increasing the proportion of prey available to the predator community. However, it can be difficult to convincingly document that niche partitioning occurs, so we have developed a new methodology to test for niche partitioning by quantifying the niche breadth of predators. We used a hyperbolic decay model to estimate the number of aphids remaining on collard plants after 31 days, in a large scale field experiment wherein predator density was manipulated in cages with high or low predator diversity. The model was fit separately for each species assemblage and reaches a horizontal asymptote that predicts the number of prey remaining after being exposed to an infinite number of predators (the number of prey occupying predator-free niches). Comparing the asymptotes allowed us to test for an increase in functional niche space occupied by predators with increased predator diversity. In our study the functional niche space occupied by the diverse group of predators was significantly greater than the single species treatments, indicating that niche partitioning occurred. This methodology can be used in a wide range of insect communities to gain insight into the role that predator niche partitioning plays in driving biodiversity-biocontrol relationships.

Current and future prospects of microbial insecticides in agriculture

Ramon Georgis

Valent Biosciences Corp, Libertyville, IL, United States

Developing cost-effective programs that combine microbial insecticides with beneficial insects, reduced-risk insecticides, selective insecticides and semiochemicals will be critical for creating opportunities for profitable and sustainable IPM systems.

Advancements in formulation stability, production efficiency, quality control, field efficacy and application strategies of *Bacillus thuringiensis* (Bt) have allowed Bt products to become the most widely used microbial insecticides globally in the cultivation of vegetables, tree fruits and vines. Concerning the other microbial insecticides, although there are successes in certain markets, a substantial effort in basic and applied research, as well as in market positioning strategies, is needed to develop reliable products and ultimately, sustain profitable business.

Although the market for microbial insecticides is approximately US$268 million, its only represents approximately 1.5% of the total crop protection insecticide market and most of this is due to sales of Bt products (US$160 million). However, the market potential for the microbial insecticides will likely increase in the next few years due to the following:

1. The demand of the regulatory agencies and the general public for safer produce and for products with no detrimental effect to the environment.
2. High probabilities of insect resistance developing against reduced-risk insecticides.
3. An increase in the awareness of the growers, distributors and farm advisors about the benefits and the flexibility of including microbial insecticides in insect management programs.
4. The producers of microbial insecticides are positioning their products as partners and not as alternatives to chemical insecticides.

The annual growth rate of microbial insecticides from 1980 to 2004 has been ranging from 8.0% to 10.0% and is projected to be 10.0% in 2009. For the same period, the annual growth of chemical pesticides has been ranging from – 2.3% to 2.2% and is projected to be 0.75% in 2009.

MorphBank: A look into the state of the art of morphology-based systematics

Matthew Buffington

Systematic Entomology Lab, USDA/ARS, Washington DC, United States

The digital revolution has substantially changed the practice of systematic entomology. High-resolution digital images of both taxa and characters are commonplace on a scale never achieved before. How can this enormous amount of image data be store, organized, and easily retrieved? This presentation will focus on experience and methods using Morphbank, an open web repository of biological images available to the research community. The system not only allows for effective management of these images, but is also a powerful collaborative platform supporting research by scientists on opposite sides of the planet.

Expansion of the geographic range of the mountain pine beetle and one fungal symbiont genotype in Canada in response to increasing temperatures

Sangwon Lee[1], Richard Hamelin[2], Diana L. Six[3], Colette Breuil[1]

[1]University of British Columbia, Vancouver, Canada, [2]Laurentian Forestry Centre, Quebec, Canada, [3]University of Montana, Missoula, MT, United States

Introduction: The mountain pine beetle (MPB) is a serious forest pest in western North America. This beetle is associated with symbiotic fungi including two mycangial species, *Grosmannia clavigera* and *Ophiostoma montium*, which are important for host beetle development and reproduction. Due to above-average temperatures in the last decade, the beetle and its fungi have expanded their range northward and eastward in Canada. In this study, we looked at genetic diversity of *G. clavigera* collected from five sites in Canada and two sites in the US including sites within the newly expanded geographic range.

Methods: AFLP profiles from 170 fungal isolates were used to assess genetic variability within and among the populations sampled.

Results: Genetic variation was low in *G. clavigera*. There was higher heterozygosity and higher percentage of polymorphic loci in the Rocky Mountain (RM) populations than in the British Columbian (BC) populations. AFLP data indicated the presence of two genetically distinct groups (Group 1 and Group 2).

Conclusions: We found both Group 1 and 2 in the RM populations sampled, but only Group 1 in the BC populations. The presence of Group 1 in the newly expanded range of the beetle is likely due to expansions of beetles from BC northward as well as eastward into the RM region.

Host specificity, speciation, and coevolution in *Fergusonina* (Diptera: Fergusoninidae) - *Fergusobia* (Nematoda: Neotylenchidae) galling mutualists on Myrtaceae

Gary Taylor[1], Sonja Scheffer[2], Weimin Ye[3], Kerrie Davies[1], Robin Giblin-Davis[4]

[1]Australian Centre for Evolutionary Biology & Biodiversity, The University of Adelaide, Adelaide, South Australia 5005, Australia, [2]USDA Agricultural Research Service, Systematic Entomology Lab., 10300 Baltimore Ave, BARC-West, Beltsville, MD, 20705-0000, United States, [3]Nematode Assay Section, Agronomic Division, North Carolina Department of Agriculture & Consumer Services, 4300 Reedy Creek Road, Raleigh, NC 27607, United States, [4]Fort Lauderdale Research & Education Center, University of Florida, 3205 College Ave, Davie, FL 33314-7799, United States

Introduction: A unique tritrophic association between Fergusonina flies and Fergusobia nematodes forms galls on various myrtaceous hosts. Flies deposit juvenile nematodes into meristematic tissue at oviposition. Nematodes appear to induce gall development; both nematodes and developing flies coexist in the galls. Fertilised pre-parasitic nematodes invade mature female fly larvae and deposit eggs in the haemolymph. These hatch and move to the flies' ovarioles and are again deposited into fresh plant tissue when the adult flies emerge from the gall, disperse and oviposit. Transmission of nematodes between flies is vertical (mother to offspring), suggesting cospeciation between flies and nematodes.

Methods: Galls, flies and nematodes were collected from myrtaceaous plants from Australia and New Zealand. Molecular phylogenies for Fergusonina flies and Fergusobia nematodes were generated using multiple genes and standard techniques. These phylogenies were compared with each other, then with myrtaceous host phylogeny, gall form and fly morphology.

Results: Fly/nematode associations were collected from Angophora, Corymbia, Eucalyptus, Leptospermum, Melaleuca and Syzygium in Australia and Metrosideros in New Zealand. The associations are highly host-plant specific, and each species of fly is associated with a single species of nematode. There is good phylogenetic congruence of the terminal, but not the deeper nodes of the compared fly/nematode phylogenies. Deep nodes had low bootstrap support, and tree topology changed at these levels depending upon which taxa or genes were included in the dataset.

Conclusions: These results are consistent with a general model of cospeciation of flies and nematodes. Speciation by fly/nematode associates appears to be accompanied by periodic host plant shifts; there is strong evidence of evolutionary conservation of plant host genus.

Possible factors possibly acting as triggers for speciation of gall midges (Diptera: Cecidomyiidae)

Junichi Yukawa[1], Tomoko Ganaha[2], Nami Uechi[2], Misako Mishima[3], Shinsuke Sato[1], Makoto Tokuda[4]

[1]Kyushu University, Fukuoka, Japan, [2]Okinawa Prefectural Agricultural Research Center, Okinawa, Japan, [3]Kyushu University Museum, Fukuoka, Japan, [4]National Institute of Agrobiological Sciences, Tsukuba, Japan

Introduction: Most gall-inducing species of Cecidomyiidae (Diptera) are mono- or oligophagous and many examples of association of a gall-midge genus with a particular host-plant genus are known. Many gall midges may have diversified as a result of host-range expansion and host plant-shift within congeneric plant species. We tried to identify factors acting as triggers for speciation of gall midges.

Methods: Oviposition behavior of some gall midges was observed in the field and the development of galls on non-host plants was monitored. We also compared chromosomal numbers between galled and ungalled host plant individuals. In addition, we examined part of the mitochondrial DNA COI gene to determine host ranges of gall midges.

Results: Oviposition mistakes on congeneric non-host plants were occasionally observed in the field. Oviposition mistakes occurred under various ecological conditions when host and non-host plant organs were available for oviposition in the same season. Maturating of galls on non-host plants was rarely observed. We also found that some gall midges could not discriminate among ploidy levels of their host plant individuals, indicating that they cannot recognize slight genetic differences in host plants in the early stage of plant speciation. Host range expansion and host shift may provide gall midges with opportunities to become geographically or chronologically isolated in the course of plant speciation.

Conclusions: Oviposition mistakes and genetic changes in host plants leading to host range expansions and host shift are considered to be possible factors acting as triggers for speciation in gall midges.

Hot plants: heat reward for insect visitors to thermogenic flowers

Roger Seymour, Craig White

University of Adelaide, Adelaide, SA, Australia

Introduction: Over a thousand species of heat-producing flowers in the Neotropical forests are pollinated by large dynastine scarab beetles. Floral thermogenesis enhances scent production in all species, but temperature regulation often continues past the attractive phase and is always associated with insect residence.

Methods: Patterns of activity of beetles (*Cyclocephala colasi*) and thermogenesis of inflorescences of a large arum lily (*Philodendron solimoescence*) were observed in the field in French Guiana. These were related to laboratory measurements of metabolic rate (respirometry) and body temperatures (needle thermocouples and IR camera).

Results: Beetles were active during the night inside the floral chambers, where they mated and fed, and they rested the following day. The 24-hour cycle of respiration mirrored this, with bouts of endothermy at night (particularly in the early evening), and low rates during the day. Flying beetles had thoracic temperatures up to 9 ºC above ambient, but the temperature excess was less than 2 ºC inside the floral chamber. Floral chamber temperature during the night averaged 26.6 ºC while ambient air was 22.8 ºC. Beetles exposed to less than 27 ºC showed bouts of intense endothermy during which respiration could increase over 80-fold. Endothermy was rare at floral chamber temperature and above.

Conclusions: The energy costs of insect activity is so high that as little as 4 ºC elevation in floral chamber temperature can reduce the costs of activity 4-fold. Thus thermogenic flowers can provide a direct energy reward to insect visitors, and floral temperature regulation may be associated with it.

Habitat manipulation and supplementary food spray for enhanced pest management in organic cotton: implications to cotton IPM

Simplice Davo Vodouhe[1], Robert Kofi Mensah[2], Damien Sanfilippo[3]

[1]Organisation Béninoise pour la Promotion de l'Agriculture Biologique (OBEPAB, Cotonou, Benin, [2]Australian Cotton Research Institute, Narrabri, NSW, Australia, [3]Pesticide Action Network-UK (PAN-UK),, London, United Kingdom

Introduction: Many generalist predators have been recorded in cotton cropping systems in Benin in West Africa. Despite their abundance, the potential of these predators has not been fully exploited in cotton pest management due to lack of techniques to maximize their abundance and effectiveness. The study determined provision of supplementary food supplements in commercial cotton crops (surrounded by beneficial insect refuges on the predator to pest ratio conservation and utilization to and biological control cotton of pests. on cotton crops).

Method: The study was conducted ion a 2 ha commercial cotton field interplanted with sorghum at Kandi in the Republic of Benin during the 2006 cotton season. The food sprayFood spray was applied at 2.0 kg per hectare on these crops. The number of Ppests and predators were sampled and comparison made between food sprayed and unsprayed cotton crops. per metre on the cotton plots treated with the food spray was compared with crops that did not receive food sprays. In terms of seed cotton yield and gross margins, the food sprayed plot cotton crops that received food sprays were compared to with cotton cropsplots treated with neem solution and conventional insecticides. - treated plots located 400 metres away from the study site.

Results: The results showed that the food sprayed plot cotton plots interplanted with sorghum and treated with food spray recorded had significantly higher number of predatory insects (ladybirds, spiders, ants, bees, brown earwigs, glossy shield bugs etc) and lower number of pests such as *Helicoverpa armigera*, *Earias huegeli*, *Pectinophora scutigera*, *Crocidosema plebeiana*, *Anomis flava*, *Nezara viridula*, *Dysdercus sidae* per metre than the non-food sprayed treated plots. In terms of yield and gross margins, the average seed cotton yields harvested from plots treated with the food sprayed plot food spray was 805 kg/ha compared with 562 kg/ha in the neem and 1,145 kg/ha in the conventional insecticide treated cotton cropsplots. The gross margin was highest in the food sprayed plots (125,340FCFA/ha) followed by the conventional (89,450 FCFA/ha) and neem treated plots (80,248FCFA/ha).

Conclusion: The use of food sprays in cotton/sorghum interplant system can provide resources such as food and shelter, thereby conserve and increasing the abundance and effectiveness of natural enemies to manage pests profitably on commercial cotton fields.

Foraging patterns in fern-feeding arthropods occurring the Western ghats of Southern India

Alexander Jesudasan, Mini M. K.

Madras Christian College, Chennai, Tamil Nadu, India

Introduction: Though fern associated arthropods have been recorded in many parts of the world, their occurrence has been poorly documented from India. Hence, a study was initiated in the Western ghats of Southern India, which is one of the biodiverse hot spots of the world.

Methods: Surveys were conducted in fifteen places in the above cited ecological zone for diverse arthropods during September, 2006 – August, 2007. While the deformity to the foliage of pteridophytes by the herbivores was observed, the feeding damage by them was assessed using a portable leaf area meter.

Results: The study revealed the occurrence of thysanopterans [*Selenothrips rubrocinctus* (Giard)), *Heliothrips haemorrhoidalis* (Bouche), *Astrothrips* sp.], lepidopterans [*Callopistria* sp., *Herpetogramma* sp.], hemipterans [*Labioproctus polei* (Green), *Lepidosaphes* sp., *Coccus* sp., *Anchon ulniforme* Buckton, *Parayasa maculosa* Distant, *Telingana consobrina* (Distant)], coleopterans [*Chilochorus* sp.], orthopterans [*Orthacris maindronii* L., *Oxya fuscovittata* (Marsch) and *Chitura* sp.], a phasmid [*Carausius morosus*] and a mite [*Floracarus perrepae*], on sixteen ferns in the study area. The type and intensity of damage inflicted by the fern-feeding arthropods are discussed.

Conclusion: A comprehensive understanding of the herbivorous arthropods on some pteridophytes and their damage to the hosts existing in the western ghats of Southern India is reported.

Understanding insect biodiversity through insect faecology

Alexander Jesudasan, Vidhya S. A.

Madras Christian College, Chennai, Tamil Nadu, India

Introduction: A study on the biodiversity of four coleopteran stored product pests viz., *Oryzaephilus surinamensis* L. (Silvanidae), *Lasioderma serricorne* F. (Anobiidae), *Tribolium castaneum* Herbst (Tenebrionidae) and *Sitophilus oryzae* L. (Curculionidae) with reference to frass morphology and morphometry has been undertaken and reported.

Methods: Cultures of *Oryzaephilus surinamensis* on dates, rice and apricots(dry); *Lasioderma serricorne* on turmeric and fenugreek powder; *Tribolium castaneum* on Bengal gram flour, wheat flour, fenugreek powder and dates; and *Sitophilus oryzae* on rice were maintained in the laboratory. The frass deposited by each of them was collected and observed under a compound microscope and details of form, texture, colour, shape and size were recorded.

Results: Observations on the morphological characteristics of the frass of the insects revealed that differences existed in the frass egested by them and also in the frass deposited by individuals belonging to the same species depending on the developmental stage, sex and diet. Striking differences in the colour of the frass were noticed not only among the four insects, but also in the frass of the individuals of the same species reared on different stored products.

Conclusion: A study on the diversity of insect frass of the four coleopteran stored product pests based on the morphological characteristics has been presented.

First record of a *Conidiobolus* species (Ancylistaceae: Entomophthorales) infecting house fly, *Musca domestica* L. (Muscidae: Diptera) from India

C. M. Senthil Kumar

North East Institute of Science and Technology (CSIR), Substation, Lamphelpat, Manipur, India

Introduction: A new fungal pathogen infecting *Musca domestica* was discovered in an epizootic during 2006 – 2007 near cattle shed located inside the campus of NEIST substation, Manipur, India.

Methods: Morphological identification was based on the length and width of conidia, number of nuclei, presence/absence of special structures etc. Conidia and nuclei were stained in lactophenol cotton blue/lactophenol aceto-orcein and observed under phase contrast microscope.

Results: Infected flies were attached to the substrate especially on plant leaves by means of numerous rhizoids emerging out from the thorax. Unlike the symptoms of *Entomophthora muscae* (complex), the proboscis was not attached to the substrate but was extended. Wings and legs were also spread over the substrate. Mating of dead females by males (necrophilous) was observed. The conidia appeared larger than the *E. muscae* (complex) and the nuclei failed to stain in aceto-orcein. Primary conidia not surrounded by halo drop of cytoplasm and the papillae emerged from the spore outline and varied in shape. The size of the primary conidia ranged from 26-43µ × 213-35µ and that of the secondary conidia was in the range of 18-36µ × 14-30µ. Numerous smooth resting spores were observed. Based on these preliminary observations, the fungus appears to be an undescribed species of *Conidiobolus*.

Conclusions: This is the first record of *Conidiobolus* causing disease in house fly populations in India and further studies are underway to develop into a commercial biocontrol agent.

One hundred years of occupation: The Argentine ant in South Africa

Melodie McGeoch, Ndivhuwo Luruli

Centre for Invasion Biology, Dept. Conservation Ecology and Entomology, University of Stellenbosch, Stellenbosch, South Africa

Introduction: As is now generally appreciated for species range structures, the globally invasive Argentine ant is not evenly distributed within its range and its distribution and abundance is strongly associated with abiotic conditions. Here we examine in detail the range expansion and distribution of the Argentine ant in South Africa, one hundred years after its introduction.

Methods: Locality data were collated from literature, museum records and supplementary country-wide surveys. We examine trends in the temporal and spatial distribution of occupancy, and compare the distribution of the species with those predicted by bioclimatic models.

Results: Following the first records of the Argentine ant in South Africa in 1901, there was a sharp increase in the number of presence records in the mid 1950's and again in the mid 1980's. The extent of the range was reached fairly early and subsequent records have been largely space-filling. Minimum estimates of the rate of radial spread of the Argentine ant in South Africa are within the range of jump-dispersal spread rates recorded for the species globally. The extent of occurrence at present is estimated at 58 % of the countries surface area.

Conclusion: The agreement between observed and predicted distribution records of the species in South Africa was poor, a likely consequence of widespread human-mediated microclimate modification and the comparative paucity and narrow range of presence records for the species in natural areas.

Re-distribution of ex-South African strain of *Cotesia plutellae* Kurdjumov (Hymenoptera: Braconidae) in Africa for control of diamondback moth: Lessons from East Africa

Brigitte Nyambo[1], Gatama Gichini[1], John John Obiero[2], Bernhard Lohr[1], Glady Njumwa[1]

[1]icipe, Nairobi, East Africa, Kenya, [2]KARI, Muguga, Kenya

The ex-South African strain of *Cotesia plutellae* was field released in warm and semi-arid areas of Uganda and Kenya between 2003 and 2006, respectively, for control of diamondback moth (DBM) (*Plutella xylostella*).

In Central Uganda releases were done in November 2003. Post-release surveys 21 months later indicated that *Cotesia plutellae* was established and co-existed with *Oomyzus sokolowskii* and *Diadegma mollipla,* the indigenous DBM parasitoids. The level of parasitism due to *C. plutellae* was as high as 100% in some fields. In February 2006, the parasitoid was recorded for the first time in Western Kenya where parasitism rate increased from 5.9 to 36.6% by October 2007. During the October 2007 field survey, the parasitoid was also recovered further south close to the Tanzania border, an indication that it was still spreading and colonizing new areas.

In Kenya, first field release of *C. plutellae* ex-South African strain was done in June 2005 in semi-arid areas of Eastern Province. However, despite repeated releases on similar sites, establishment and its impact remains unsatisfactory. Contrary to expectations, *Diadegma semiclausum*, an efficient parasitoid for cool highlands, released earlier in Kenya highlands, colonized the areas and became the most frequently found parasitoid of DBM. Despite additional releases of *C. plutellae* done in other areas of Eastern Province in June 2006, its establishment and spread remains unsatisfactory. Lessons learned and implications to wider use of the *C. plutellae* ex-South African strain are discussed.

Plant mediated multitrophic interactions between aboveground and belowground herbivores

Roxina Soler

Netherlands Institute of Ecology (NIOO-KNAW), Heteren, Netherlands

Introduction: The study of interactions between spatially separated organisms is scaling up from simple interactions between organisms directly associated to the plant roots and shoot to a more complex approach involving higher trophic levels. The multitrophic approach linking food webs from the soil and the aboveground domains aims to address the complexity of populations of plants, herbivores and carnivores more realistically, to identify and further understand the forces that regulate populations of plants and insects in terrestrial communities.

Results and Conclusions: I will present a number of case studies that explored interactions between root herbivores, foliar herbivores and their parasitoids. Remarkably, the results of these studies show evidence that the presence of herbivores feeding on a plant in one (sub) domain can have negative effects on the herbivores in the opposite domain by reducing herbivore's performance, and simultaneously can provide advantages for the herbivore by interfering with the plant mediated attraction of parasitoids. Soil organisms, whose presence passes habitually unnoticed, can interfere in the interactions of plants, herbivores and their parasitoids, generating complex processes that still are far to be unravel.

Neural circuits controlling feeding behavior and metabolism in *Drosophila*

Michael Pankratz

University of Bonn, Bonn, Germany

Feeding behavior is regulated by external sensory inputs and internal metabolic status. We are interested in studying the genes and neural circuits that coordinate this universal behavior in *Drosophila*. The current focus is on a small assembly of neurons in the subesophageal ganglion that expresses the neuropeptide gene hugin, which has homology to mammalian neuromedian U and insect PBAN (pheromone biosynthesis activiting neuropeptide). We have begun a genetic and anatomical dissection of the hugin neurons with respect to their possible function in gustation and metabolism, and with their connection to other central and neuroendocrine circuits.

The status of the genus *Hylaeus* F., supposed ancestral bees of the old authors

Holger H. Dathe

Deutsches Entomologisches Institut, ZALF, Müncheberg, Germany, Germany

The Colletidae is considered to be a basal group of bees. The species are easily distinguishable from all other Apidae by a short, broad glossa, which was interpreted as a spheciform character. Whilst many Colletidae are densely hairy and actually look like bees, the small, black, practically hairless *Hylaeus* species resemble some Crabronidae; they possess no scopa and transport larval food in the oesophagus. They nest like *Pemphredon* in narrow cavities in plant stems. For this reason they were long regarded as the most ancient taxon of extant bees („Urbienen").

Phylogenetic analyses have supported the monophyly of the Hylaeinae, but no support could be found for its basal position. The supposedly basal characters are apparently the result of convergence driven by functional pressure. The broad tongue is a tool used to cover the interior of the brood cells with a silk secretion, whilst pubescence and external apparatus for food collection were probably lost secondarily. Unfortunately there are few exact studies on habits at species level, and cladistic studies are nearly completely lacking.

The genus *Hylaeus*, the largest in the family with worldwide distribution, is considered difficult, but when examined closely it is highly differentiated. Conspicuous characters such as scent gland fields on the 6th sternite of the male, that emit a characteristic lemon scent, have so far not been evaluated. The contribution provides an overview on the state of our knowledge and the diversity in significant characters, as well as providing hints on phylogenetic character evaluation preferably in Palaearctic species.

The spread and distribution in Europe of *Harmonia axyridis*, a non-native coccinellid.

Peter M.J. Brown[1], Michael E.N. Majerus[3], Helen E. Roy[2], David B. Roy[2]

[1]Anglia Ruskin University, Cambridge, United Kingdom, [2]NERC Centre for Ecology and Hydrology, Monks Wood, United Kingdom, [3]University of Cambridge, Cambridge, United Kingdom

Native to Asia, *Harmonia axyridis* (Pallas) (Coleoptera: Coccinellidae) is considered an invasive alien coccinellid in Europe and North America, where it was widely introduced as a biological control agent of aphids and coccids. There is strong evidence that *H. axyridis* will have a negative impact on the native insect fauna of Europe. The species was sold by various biological control companies from 1995 in France, Belgium and the Netherlands, and was also intentionally released in at least nine other European countries. It has spread very rapidly, particularly since 2002, and is now regarded as established in thirteen European countries. The established range extends from Denmark in the north to southern France in the south, and from Czech Republic in the east to Great Britain in the west. In this paper we map the spread and distribution of *H. axyridis* in Europe. We report first records of the species in seven countries; Spain, Sweden, Scotland, N. Ireland, Denmark, Czech Republic and Italy; and first evidence of *H. axyridis* establishment in the latter three countries. Despite releases of *H. axyridis* in Portugal, Spain and Greece, there is little evidence of establishment in southern Europe. It is predicted that the spread and increase within Europe will continue and that *H. axyridis* will become one of the most widely distributed coccinellids in the continent. We report on vectors for the spread of the species, particularly transportation via human activity. We also briefly examine the occurrence of the species in Africa and North and South America.

Multitrophic level interactions in changing landscapes

Teja Tscharntke

Agroecology, University, Goettingen, Germany

Understanding multitrophic level interactions and their relation to ecosystem services, needs a perspective from human-dominated landscapes, because most species experience their surroundings at spatial scales beyond the plot level, and spillover across natural and managed ecosystems is common. Management is often focused on few species and local processes, but in the dynamic, agricultural landscapes, only a diversity of insurance species may guarantee resilience, i.e. the capacity to reorganize after disturbance. Structurally complex landscapes enhance local diversity in land-use systems, which may compensate for local high-intensity management. Organisms with high dispersal abilities and little habitat specialisation appear to drive these patterns and processes, because of their recolonisation ability and larger resources experienced. In simple landscapes, local allocation of habitat, i.e. changes in landscape configuration, is more important than in complex landscapes, which are in total at risk. Examples from plant-insect, predator-prey and host-parasitoid interactions will illustrate how interacting species experience their surrounding landscape at different spatial scales, which influences food web structure and multitrophic interactions.

Complementary resource use in species-rich predator and parasitoid assemblages

Teja Tscharntke

Agroecology, University, Goettingen, Germany

Suppression of prey and host species may be more effective in species-rich enemy assemblages, but empirical evidence is mixed. Experimental manipulation of rich enemy complexes is often difficult or even impossible, so understanding patterns and processes relies on well-designed field studies in most cases. Here, I present the outcome form our case studies of the natural enemies of gallmakers, cereal aphids, bees and wasps, testing the idea of complementarity via resource partitioning and discussing its relative importance. The findings will be also discussed in the context of the insurance hypothesis, i.e. whether only a wealth of enemy (insurance) species provides the capacity to reorganize after spatio-temporal disturbance at small and large scales.

Coffee pollination on a landscape scale

Teja Tscharntke

Agroecology, University, Goettingen, Germany

The destruction and fragmentation of tropical forest negatively affects pollinators, causing a decline in successful pollination in fragmented sites. Rainforest serve as a source habitat for pollinators foraging in the agricultural landscape, so the distance of non-forest areas like coffee agroecosystems to forest fragments or continuous forest influences pollinator diversity and ecosystem services such as enhanced coffee pollination and yield. Coffee intensification changed traditional shade coffee to open sun coffee and reduced the area of neighbouring forests, which resulted in dramatic losses of biodiversity and associated ecological functions. Increased diversity of bees may enhance magnitude and stability of fruit set, yield and net revenues of farmers. When coffee shrubs flower synchronously, the landscape-wide density of coffee bees may be limited, resulting in a dilution effect and reduced yields. Local and landscape management for coffee bees require a more detailed understanding of landscape composition and configuration allowing spillover of bees across the noncrop-crop interface.

Landscape perspectives on land-use change and insect outbreaks

Teja Tscharntke

Agroecology, University, Goettingen, Germany

Spatiotemporal changes in insect densities require a landscape management perspective, because the species pool in the surrounding landscape and the distance of crop from natural habitat is important for the conservation of enemy diversity and, in particular, the conservation of poorly-dispersing and specialized enemies. Hence, structurally complex landscapes with high habitat connectivity may enhance the probability of pest regulation. In contrast, generalist and highly vagile enemies may even profit from the high primary productivity of crops at a landscape scale and their abundance may partly compensate for losses in enemy diversity. Enemy distribution in agricultural landscapes is determined by beta diversity among patches, while enemy communities in managed systems are more similar across space and time than those in natural systems, emphasizing the importance of natural habitat for a spillover of diverse enemies. Complex landscapes characterized by highly connected crop-noncrop mosaics may be best for long-term conservation biological control and sustainable crop production, but experimental evidence for detailed recommendations is still needed.

Integrated pest management Pest Information Platform for Extension and Education (*ipm*PIPE)

Dennis Kopp, Kitty Cardwell

USDA/CSREES, Washington, DC, United States

Introduction: The *ipm*PIPE is a web-based information system platform which provides the capability for real time early-warning, tracking and monitoring of invasive or migrating pests. This system also provides decision making tools and IPM options for pest and disease risk reduction and crop protection.

Methods: This information system was first developed and implemented for soybean rust in 2004. Developed by private and public sector agricultural scientists, supported by grower organizations and private industry, the *ipm*PIPE charted the movement of soybean rust, informed soybean producers regarding the disease spread and identified best management options. The *ipm*PIPE has expanded beyond soybean rust reducing crop loss risk and improving pest and disease management in numerous other crops across Mexico, the US and Canada.

Results: Since 2005, *ipm*PIPE provided soybean growers with maps and information about the spread of soybean rust, describing effective management options reducing many unnecessary fungicide treatments. In `05 and `06, PIPE saved soybean producers an estimated $299 million. By 2007, 73% of soybean grower decisions to spray for rust were based on *ipm*PIPE data. At $18 per acre for a fungicide application, it is estimated that US soybean producers using PIPE saved **$836.63 million** in saved crops and production expenses.

Conclusions: The *ipm*PIPE is a coordinated effort involving agricultural scientists in the private and public sector and representatives from grower organizations. These scientists reduce the risk of crop loss by monitoring, tracking, and delivering expert advice to growers, providing real time decision-making support for management of invasive or migrating pests.

A phylogeny of the leafhopper genus *Flexamia* (Hemiptera: Cicadellidae) constructed with morphological and molecular characters

Therese Catanach[1], Chris Dietrich[2], Robert Whitcomb[3], Jim Woolley[1]

[1]Texas A&M University, Department of Entomology, College Station, TX, United States, [2]Illinois Natural History Survey, Center for Biodiversity, Champaign, IL, United States, [3]Deceased, n/a, United States

Flexamia (Hemiptera: Cicadellidae) is a broadly distributed North America leafhopper found mainly in grasslands. While various phylogenies have been published, no single study has included both morphological and molecular data. Data were analyzed using parsimony in both PAUP and TNT. Based on morphological data and two mitochondrial genes, 16S and NADH dehydrogenase 1, the monophyly of *Flexamia* was supported. Some species groups proposed by Whitcomb and Hicks were found to be polyphyletic while others are well supported. Overall, constructed phylogenies partially agree with previous phylogenies although there are some major differences.

The evolution of lady beetles (Coleoptera: Coccinellidae): Reconstructing phylogeny based on molecular data

Jose Giorgi, Joseph McHugh, Adam Slipinski, Kelly Miller, Lori Shapiro, Michael Whiting

University of Georgia, Athens, GA, United States; CSIRO Entomology, Canberra, ACT, Australia; University of New Mexico, Albuquerque, New Mexico, United States; Pennsylvania State University, University Park, Pennsylvania, United States; Brigham Young University, Provo, Utah, United States

Introduction: Lady beetles are conspicuous and charismatic elements of most insectan faunas. With nearly 6,000 described species, Coccinellidae represents one the most diverse families within Cucujoidea. Coccinellid evolution has produced a spectacular variety of forms and adaptations, some of which are beneficial to humans; however, the phylogeny of the group has never been investigated in a rigorous manner. This study examines the phylogenetic relationships of the main coccinellid lineages in order to provide the first robust evolutionary framework for the family and to form the basis for a meaningful and stable classification.

Methods: This dataset, with 96 ingroup species and 6 genes (12S, 16S, 18S, 28S, COI, COII), is the largest ever utilized in a phylogenetic study of Coccinellidae. Species of Erotylidae, Discolomatidae, Latridiidae, and Endomychidae were used as outgroups. Sequences were aligned using Muscle. Parsimony analysis was accomplished using NONA as implemented by WinClada.

Results: Coccinellidae was supported as monophyletic. Four of the six currently recognized subfamilies, Sticholotidinae, Chilocorinae, Coccidulinae, and Scymninae were recovered as paraphyletic.

Conclusion: Coccinellidae appears to be a natural group, however, the current subfamilial classification is unsatisfactory and requires major modification in order to reflect the evolution of the group.

The role of a maternal gift in the larval development of a dung beetle

Marcus Byrne[1], Bronwen Watkins[1], Megan Yates[2], Gus Bowyers[1], Marlien Maritz[1], Jeremy Midgely[2]

[1]University of Witwatersrand, Johannesburg, South Africa, [2]University of Capetown, Capetown, South Africa

One aspect of brood ball construction in scarabaeine dung beetles has been either overlooked or mentioned only in passing; the production a faecal "gift" by the mother. Once she has constructed a ball inside the nest, the female lays a large egg into a cavity within the dung, and in many species cements the egg into place by what appears to be her own faeces. The attachment of the egg varies from a simple faecal smear in *Euoniticellus intermedius*, to an elaborate faecal pillar in other species. The role of the maternal gift has never been investigated, but is assumed to be a microbial inoculation of the larval food store with symbionts which will assist in breakdown of the dung creating an "external rumen" for the larva. Brood balls of *E. intermedius* were manipulated by removal of the maternal gift and sterilisation by heat or antimicrobials, to determine if the gift was simply a provision of small food particles for the newly hatched larva or microbial injection of symbionts essential for larval development. Results from sterility trials were supported by stable isotope analysis to estimate how many trophic levels separate larval and adult dung beetles from their food source and considered together, suggest a new role for the maternal gift as a "packed lunch" for the newly hatched larva.

Simultaneous disruption of a leafroller complex using a common pheromone dispenser

Ashraf El-Sayed, Jill Mclaren, Vanessa Mitchell, Lee-Anne Manning, Max Suckling

HortResearch, Lincoln, New Zealand

Introduction: Three leafrollers, *Epiphyas postvittana*, *Ctenopseustis obliquana* and *Planotortrix octo* are widespread in New Zealand, and economic pests of NZ's export horticulture industries. Mating disruption has been successfully used in the past against these pests. However, two pheromone dispensers are needed to provide control of the complex. This research was undertaken to develop a common pheromone dispenser for mating disruption of these three species simultaneously, thus reducing the labour required for application of the separate pheromone dispensers and enable widespread adoption of the technology.

Methods: Several laboratory and field experiments were conducted to investigate the interaction in the pheromonal communication systems among the three leafrollers. Accordingly, several blends were formulated and tested for mating disruption of these leafrollers in the lab and in a small field plot experiment. Based on the results obtained in these previous experiments, a pheromone blend was chosen and formulated in a twist-tie dispenser and tested in area-wide mating disruption trials.

Results: Cross-talk experiments indicated that the three leafrollers can detect the pheromone of each other and there were various degrees of antagonism between the pheromone of the three species when combined in a single lure. The combination of carefully selected blends showed various degrees of mating disruption, with blends that contained all pheromone components of the three species showing the optimum mating disruption effect on the three species.

Conclusions: A common pheromone dispenser has been developed that provides simultaneous and efficient mating disruption of the three leafrollers. Because this generic pheromone dispenser was not attractive to any of these leafrollers, this indicates that mating disruption was achieved via habituation or adaptation of olfactory system.

What is special about the Argentine ant, and what is not? – A comparison with other invasive ants

Jes S. Pedersen

Department of Biology, University of Copenhagen, Copenhagen, Denmark

Introduction: Some ants have realised the old truth that in union there is strength. They have abandoned boundaries between colonies so that a free exchange of individuals within a network of nests makes the entire population function as single social unit. Such unicolonial organisation is probably responsible for the invasiveness of these ants as they form extensive and ecologically dominating supercolonies when introduced outside their native range. In recent years the Argentine ant *Linepithema humile* has been studied intensively and stands currently as a model species for such invasive ants. Here I ask the question to what extent the various characteristics of this species can be generalised to other invasive ants.

Methods: Data from genetic, behavioural, and chemical analyses were used to compare the Argentine ant to two species that represent different histories of invasion and time associated with man: the pharaoh ant *Monomorium pharaonis* and the invasive garden ant *Lasius neglectus*. Closely related non-invasive species were also included.

Results: The comparative studies revealed that the three invasive species share a number of traits likely to increase their ecological success when introduced, and differences may be attributed to their specific history. Paradoxically, the most important preadaptation to become invasive seems to be local mating and a very limited dispersal of new queens. Furthermore, ecological release may be important for the success of introductions.

Conclusions: These findings confirm the Argentine ant as a good model for invasive ants and potentially makes it possible to predict new invasive ant species.

The history of sleeping sickness control in Africa

Ian Maudlin, Susan Welburn

[1]Centre for Infectious Diseases, Royal (Dick) School of Veterinary Studies, College of Medicine and Veterinary Medicine, The University of Edinburgh, United Kingdom, [2]Centre for Infectious Diseases, Royal (Dick) School of Veterinary Studies, College of Medicine and Veterinary Medicine, The University of Edinburgh, United Kingdom

Attitudes towards sleeping sickness have changed from the colonial view - *the* disease that must be controlled at all costs - to its present position as one of the 'neglected' diseases. This change in perception does not truly reflect a change in the threat posed by sleeping sickness to the peoples of the endemic area but rather reflects changes in economic drivers of African development. Agriculture, particularly rubber and cotton, was the backbone of colonial African economies and huge resources were put into the control of sleeping sickness that threatened rural labour. Africa, in common with other developing parts of the world, is now subject to very different economic drivers, reflected in rapid urbanization. Control of endemic diseases in Africa is no longer a matter left to sovereign states, but is subject to external economic forces. Sleeping sickness, because of the habit of its vector – the tsetse fly - exclusively affects the rural poor and no longer attracts the sort of resources now devoted to diseases of urban/peri-urban Africa (e.g. HIV, malaria, TB). Sleeping sickness nonetheless remains a disease that is fatal if left untreated and, as we have seen recently, is undiminished in its ability to cause serious epidemics of disease. In response to these shifts in economic priorities, tsetse researchers have provided cheap and safe tools that enable the poor livestock keeper in sub-Saharan Africa to deal with both human and animal trypanosomiasis within the community.

Exocrine glands of leaf beetle larvae: Protective structures against attacking predators and pathogens

Juergen Gross[1], Henrike Schmidtberg[1], Kerstin Schumacher[2], Andreas Vilcinskas[1]

[1]Justus-Liebig-University, Giessen, Germany, [2]Julius Kuehn Institute – Federal Research Centre for Cultivated Plants, Kleinmachnow, Germany

Introduction: The exocrine glandular secretions of leaf beetle larvae of the taxon Chrysomelinae are well-known defensive devices used against generalistic predators. Recently it was shown that larvae of some species produce fluid exocrine secretions containing deterrent and antimicrobial compounds. As leaf beetles share with other eukaryotes an innate immune system mediating endogenous defense against pathogens, the ecological role of antimicrobial compounds from secretions was investigated.

Methods: Morphological structures of larval glands were studied by scanning electron microscopy. The chemical composition of glandular volatiles collected from the larval headspace was analysed by GC-MS. Antimicrobial properties were investigated by inhibition zone tests and *in vivo* experiments using several entomopathogenic microorganisms (bacteria and fungi)

Results: We identified different volatiles as major components of enveloping perfume clouds. They are emitted by specialized openings of larval glandular reservoirs and inhibit *in vitro* the growth of bacteria as well as the germination of fungi. The suggested role of these components as fumigants in exogenous antimicrobial defense was confirmed *in vivo* by their removal from glandular reservoirs. This resulted in an enhanced susceptibility of the larvae to infections with the fungal entomopathogens *Beauveria bassiana* and *Metarhizium anisopliae.*

Conclusions: We conclude that exocrine glands of leaf beetle larvae are defensive devices which act not only against predators but also against pathogens. Hence, antimicrobial defense in leaf beetles can be expanded beyond innate immunity to including external disinfection of their microenvironment. For the first time we report the contribution of fumigants to antimicrobial defense in animals.

Multitrophic interactions between the apple proliferation phytoplasma, its psyllid vectors, and their host plants

Juergen Gross[1], Christoph Mayer[2], Andreas Vilcinskas[1]

[1]Justus-Liebig-University, Giessen, Germany, [2]Julius Kuehn Institute – Federal Research Centre for Cultivated Plants, Dossenheim, Germany

Introduction: In recent years it was discovered that the univoltine psyllid species *Cacopsylla melanoneura* (Foerster) and *C. picta* (Foerster) (Hemiptera: Psyllidae) are the vectors for *Candidatus* Phytoplasma mali, a small bacterium which causes major economic yield losses in apple orchards by inducing shoot proliferation and tasteless dwarf fruits (apple proliferation disease). In the presented study we investigated the interactions between the psyllids, their different host plants for reproduction and overwintering, as well as the influence of the transmitted phytoplasma on both plant chemistry and vector behaviour.

Methods: Behavioural responses on olfactory cues were tested using dynamic Y-shaped olfactometers. Plant volatiles were collected from their headspace and analysed by GC-MS. Infection of plants and insects by the phytoplasma were detected by PCR using apple proliferation phytoplasma specific primer pairs.

Results: The overwintering and reproduction host plants of both psyllids species were determined and the distribution of the apple proliferation phytoplasma in the phloem of these plants was investigated. Only in apple trees the phytoplasma could be detected. Further, we show that phytoplasma altered the odour of infected apple trees as well as the attractiveness of emitted plant volatiles to their vector *C. picta*.

Conclusions: The psyllid vectors use several plants for reproduction and overwintering, but only the apple plants could act as reservoir for the uptake of the apple proliferation phytoplasma. Finally, we conclude that the apple proliferation phytoplasma manipulates the odor of infected apple as well as the behaviour of vector insects to promote its propagation.

Lethal and sublethal effects of methoxyfenozide on Colorado potato beetle *Leptinotarsa decemlineata* (Say) (Coleoptera: Chrysomelidae)

Roghaiyeh Karimzadeh, Mir Jalil Hejazi

University of Tabriz, Tabriz, Islamic Republic of Iran

Introduction: One of the major management challenges posed by CPB is its ability to develop resistance against insecticides; and new insecticides are needed to aid in CPB management programs. Methoxyfenozide is a biorational insecticide and has been shown to have sublethal effects on some insects. In this study the lethal and sublethal effects of this insecticide was assessed on the CPB.

Methods: To assess the lethal effects on 1st instars, the range of concentrations tested was 48-120 mg ai/L. Potato leaves used for feeding the larvae were dipped in the insecticide solutions. The treatments were kept at 25±1°C, 60±5 RH and a photoperiod of 16:8 (L: D) h. Mortalities were recorded 72 h after treatment. To evaluate the sublethal effects of methoxyfenozide, two concentrations equivalent to LC_7 and LC_1 were used. First instars were fed on treated leaves for 48 or 96h and later on, untreated leaves; and were monitored until adult stage. Fecundity of the adults was then evaluated.

Results: LC_{50} for the 1st instars was 80.6 mg ai/L. Sublethal doses of methoxyfenozide prolonged the larval developmental time and caused mortality in later instars. The number of larvae developing into pupae and adults was significantly lower in methoxyfenozide treatments compared with control. The number of eggs per female was also significantly decreased.

Conclusion: It was concluded that the combination of lethal and sublethal effects of methoxyfenozide is considerable; and if this insecticide performs equally well in the field, it might be a suitable candidate for integrated management of the CPB.

Insect community structure and invasive insect species: Potential impacts of a rapidly changing climate

Nigel Andrew

University of New England, Armidale, NSW, Australia

The relative importance of climate, host plant evolutionary history (phylogeny), and host plant traits on structuring insect herbivore assemblages is fundamental to understanding how insects will respond to a rapidly changing climate. The use of Climate Change Response Groups, may also deliver powerful predictive tools for understanding the impacts of climate change on herbivore-plant interactions worldwide. However, what happens when an invasive species enters the community and begins to significantly change the interactions among species and trophic levels? This presentation will assess the current status of our understanding of insect communities in relation to the potential impacts of climate change and assess the influence that invasive specie may have on community structure.

The impact of *Bombus terrestris* invasions on natural ecosystems

Amots Dafni, Peter G. Kevan, Caroline C. Gross

[1]Haifa University, Institute of Evolution, Department of Evolutionary and Environmental Biology, Haifa, Israel, [2]Guelph University, Department of Environmental Biology, Guelph, Canada, [3]University of New England, Ecosystem Management, Armidale, Australia

Bombus terrestris has been reared artificially and supplied commercially from the 1980s especially for pollination of tomatoes in greenhouses. Very early after its introduction, it was recognized that this species is invasive (especially in Tasmania, Japan, and Israel) and may disturb local ecosystems. *B. terrestris* has various characteristics that suggest its capacity to be a successful pollinator: high adaptability to artificial conditions, the ability to produce large colonies, high pollination efficiency in various crops, better quality of seed/fruit production as a result of pollination by this bee, year-round availability and activity under greenhouse conditions and a high pollination efficiency in open air crops.

The invasive characteristics of *B. terrestris* are: high migration ability, early seasonal emergence, high adaptability under adverse climatic conditions in various habitats, generalist or polylectic foraging using a wide variety of flowers for resources, wide foraging, a thermoregulatory metabolism that enables it to withstand low temperatures, no natural enemies to check population growth in areas outside its natural range, and it may develop two reproductive cycles in a year (bivoltine) in a newly colonized area. In addition, commercial bees produce more gynes and are better competitors than the local conspecific populations and may replace them in the likely event of an escape.

The documented evidence on invasion impact of *B. terrestris* on natural ecosystems includes: negative interactions with local bee fauna, competition for nest sites with, and genetic contamination of, local *Bombus* spp, spread of parasites and pathogens and negative interactions with plant reproductive capacity.

We will discuss the possible measures that must be taken to minimize the *B. terrestris* invasion on local as well as on global levels.

When pollination syndromes break down: Principles and a case study of *Cyclamen persicum*

Amots Dafni

Institute of Evolution, Department of Evolutionary and Environmntal Biology,Haifa University, Haifa, Israel

Introduction: Pollination syndrome breakdown – an abrupt case in which the flowers show clear suit of adaptations to a certain pollinator but are actually pollinated by an agent of another "pollination guild", e.g. a typical bird flower which is pollinated by a bee. The plants don't show any adaptive changes towards the promotion of new pollinator. That to differ from "pollination shift" in which a flower adapted to a certain pollinator is replaced by (or share) another pollinator as a result of local selective forces on floral traits.

Theoretically one may consider several cases in which pollination syndromes could break down:

1. Extinction of the original pollinator and a replacement by a" surrogate" pollinator which is not includes at the original "pollination guild".
2. Invasion of a new pollinator to a new territory and an exclusion of the local original pollinator.
3. Invasion of a plant to a new territory and an adoption of local pollinator which can operate the flower and to cause pollination.
4. A genetic change of floral trait which cause a switch from one pollination guild to another one.

Literature survey reveals very rare events of such cases.

Results: *Cyclamen persicum* is, morphologically, a typical buzz pollination flower (pendulous flowers, radially symmetrical, reflexed petals and introrsely poricidal anthers). Buzz pollination in *C. persicum* is extremely rare and the most frequent pollinators are various unspecialized species of thrips and syrphids and also a primitive moth *Micropterix elegans.*

Conclusions: Based on the lack of buzz pollination in *Cyclamen* spp. along the Mediterranean and our results, we assume that the original pollinator what extinct and the other assemblage of unrelated and unspecialized pollinators invade into this vacant pollination niche. This low efficiency situation is compensate, long stigma receptivity and prolonged pollen viability and the actual result is a high seed production. Pollination syndromes break down, from its own definition, could be found in specialized flowers which are relative rare while most of the flowers are generalistic. So this phenomenon may be a priori rare.

Isolation and characterization of *Bacillus thuringiensis* and their toxicity against different ISSR- PCR based biotypes of *Helicoverpa armigera*

Senthilkumar Nachimuthu

Department of Biotechnology, Mizoram University, Aizawl - 796 009, Mizoram, India

Introduction: The search for new virulent strain of *Bacillus thuringiensis* (Berliner) has gained much significance for biological control purposes. Biotypes are distinct lineages of an organism that differ in some aspect of their biology and have implications for the design and implementation of pest control strategies. Inter Simple Sequence Repeats (ISSR) amplification utilizes anchored SSR primers that are complementary to genomic micro satellites and have been used for genetic characterization of insects.

Methods: In the present study, eight geographical isolates of *Bt* were isolated and their protein concentrations were determined. We characterized the biotype status of *Helicoverpa armigera* (Hubner) from S. India and tested the efficacy of *Bt* against different biotypes of *H. armigera*. ISSR-PCR was utilized for revealing polymorphisms between the biotypes of *H. armigera.*

Results: The genetic variation resulted in identification of two biotypes. The Coimbatore and Bangalore larvae were found to be genetically related, whereas the Hyderabad larva was very distantly related. *Bt* samples were tested for their toxicity against *H. armigera* and was found to vary significantly between the different biotypes of *H. armigera*. *Bt* samples numbered 5 and 8 produced higher mortality and the mean mortality was 70% in *H. armigera* larva and both had high protein concentration. The susceptibility of the biotypes varied and the Hyderabad biotype was found to be less susceptible than the other biotypes.

Conclusions: The results disclosed the usefulness of ISSR in differentiating the biotype variation among the genotypes and the differential toxicity of *Bt* against different *Helicoverpa* biotypes.

Scratchpads: getting biodiversity online, redefining publication

Vincent Smith, David Roberts, Simon Rycroft

Natural History Museum, London, United Kingdom

Introduction: Taxonomists have been slow to adopt the web as a medium for building research communities. Yet, web-based communities hold great potential for accelerating the pace of taxonomic research.

Implementation: We have developed an intuitive web application (Scratchpads) that collaboratively enables researchers to build, share, manage and publish their data online. Our architecture is based on the Drupal content management system and provides a scalable, flexible resource that allows distributed communities of taxonomists to collaborate. Sites are hosted at the Natural History Museum London, and offered free to any scientist that completes an online registration form. Information supported by the Scratchpads includes bibliographies, image galleries, specimen records, documents, custom data sets and maps. Data are classified and aggregated around a taxonomy supplied by the user. This is supplemented with information from high quality web accessible databases (currently Genbank, GBIF, Biodiversity Heritage Library, Yahoo! Images and Google Scholar) to automatically construct rich web pages about any taxon documented within a site.

Results: In the first year of operation, the Scratchpads have attracted 466 registered users from more than 30 countries, across 53 separate sites. Collectively these users have produced more than 110,000 web pages, and attract an average of 6,000 visits with 50,000 page views per month.

Conclusion: Ongoing work is linking the Scratchpads to the Encyclopedia of Life project, and the EDIT Cybertaxonomy platform. The template of our architecture may serve as a model to other research communities developing knowledge bases outside biological taxonomic research. Further details from http://scratchpads.eu.

EGF signaling and the origin of dorsal-ventral polarity in insects

Jeremy Lynch, Axel Drechsler, Siegfried Roth

University of Cologne, Cologne, Germany

The establishment of the anterior-posterior (AP) and dorsal-ventral (DV) axes is a critical step in the development of bilaterally symmetric animals, and often depends on maternal cues. Among the insects, this process is only well understood in *Drosophila*, where both axes depend on signaling provided by the tgf-alfa like ligand Gurken, whose mRNA is localized around the oocyte nucleus, and whose protein activates the EGF-receptor in the overlying somatic follicle cells. We have sought to test whether this system operates in insects with different modes of oogenesis and embryonic development by cloning and testing the function of tgf-alfa like ligands and EGF receptors from a variety of insects: the beetle *Tribolium,* wasp *Nasonia*, bug *Oncopeltus*, and the cricket *Gryllus*. In *Tribolium* pRNAi against the ligand and receptor leads to defects in oocyte nucleus migration and major disruptions of DV axis patterning, including apparent duplication of the DV axis, and in other cases the expression of DV markers perpendicular to the DV axis of the egg. In all insects tested, tgf-alfa RNAi leads to defects in oocyte encapsultion by the follicle cells. We have also found a conserved association of high EGF signal and the position of the oocyte nucleus in late oogenesis. In summary, EGF signaling from the germline to the soma appears a mechanism of providing spatial cues for proper oocyte and egg patterning broadly conserved among the insects, but whose deployment and downstream output is variable due to different modes of oo- and embryogenesis.

Morphological description of the last instar larva of *Solenopsis saevissima* Forel (Hymenoptera: Formicidae)

Eduardo Fox, Daniel Solis, Carlos Jesus, Odair Bueno

CEIS / UNESP, Rio Claro, SP, Brazil

Introduction: Larval descriptions are suposed to aid in taxonomy and systematics of hymenopterans, but are generally neglected by specialists in the field. Herein we present the description of the last larval instar of *Solenopsis saevissima*, a poorly studied species.

Methods: Whole nests were obtained from Estiva, Minas Gerais, Brazil, from which immatures were fixed in Dietrich's and conserved in 80% alcohol. The last instar larvae were sorted based on morphological differences as in *Solenopsis invicta*. All samples were slide-mounted and observed under an optical microscope or under a scanning electronic microscope.

Results: Body dolichoderoid about 300-um long with evenly-distributed deeply bifid, bifid and simple setae; ten spiracles. Head setae: 6-8 occipital bifid; five simple frontal on the frons; five simple genal, and one bifid and one simple above antennae; antenna a row of three setaceous sensilla, with a setacious sensila under it. Two sensilla near base of each mandible. Clypeus rectangular with four setae lining the roughly rectangular depressed mesad labrum, which is heavily scuptured at lower surface with rounded and spike-like papillae. Peg-like galeae with two setaceous sensilla; maxillary palpus with three basiconic sensilla and a setacious sensilum. Mandibules robust with two prominent apical teeth and one or two subapical short teeth followed by a blade. Labium elliptical; labial palpus an elevation with three basiconic and one setacious sensillum.

Conclusions: We hope the provided description adds to the knowledge of this species and facilitate species diagnosys in this complicated ant group. We are currently describing the other immature stages.

Different identification protocols yield incongruous species identification to Brazilian Fire Ants (Hymenoptera: Formicidae: *Solenopsis*)

Eduardo Fox[1], Cintia Martins[1], Adriana Pianaro[2], Daniel Solis[1], Anita Marsaioli[2], Odair Bueno[1]

[1]CEIS / UNESP, Rio Claro, SP, Brazil, [2]IQ / UNICAMP, Campinas, SP, Brazil

Introduction: Fire ants are of particularly difficult systematics, and to assess taxonomically. Many species are polymorphic and prone to considerable morphological variation, rendering most characters used for their identification poorly reliable. Also, some of them have been demonstrated to hybridize and there are cryptical species. Some identification methods have been proposed by different authors in order to facilitate species diagnosis in the group, and should provide similar results. Herein, we demonstrate some of these methods yielding clearly conflicting species identification with Brazilian specimens.

Methodology: Entire nests and samples were collected from the field. Some ants and ant larvae of each sample were morphologically analysed for classical characters, while others were surveyed through the mitochondrial DNA technique proposed by Shoemaker et al. Moreover, the alkaloid composition of their venom was determined through GC-MS, being compared to species records in the literature.

Results: One nest was morphologically identified as *Solenopsis invicta*, and was confirmed by the other techniques. However, one sample from other nest was identified as *Solenopsis saevissima* through adult and larval morphology, while being appointed as *S. invicta* through DNA and presenting venom alkaloid composition equal to *Solenopsis aurea*. Another sample was morphologically identified as *Solenopsis richteri*, while being appointed as *S. invicta* through DNA analysis and of unprecedented alkaloid composition.

Conclusions: We think our results clearly demonstrate the techniques do not fit. We suspect South American species have been poorly sampled in past studies, and also that identification by non-specialists might have misguided the design of the molecular approaches.

Community and ecosystem consequences of plant genetic differentiation along an elevational gradient

Joe Bailey, Jennifer Schweitzer

University of Tennessee, Knoxville, TN, United States

While many physical environmental factors vary along gradients of elevation and latitude, variation in temperature is commonly implicated as a mechanism driving variability in biodiversity and ecosystem function. However, many of the patterns of biodiversity and ecosystem function we find along elevational or latitudinal gradients may be an indirect consequence of natural selection acting on a focal species rather than a direct consequence of the physical environmental factors varying with elevation or latitude, however this hypothesis remains untested. In support of this hypothesis, in a common garden of clones taken from a variety of localities along an elevational gradient, we found significant genetic variance for plant performance and fitness, morphology, phytochemistry, arthropod community composition, species richness, total abundance, trophic interactions, soil nitrate, and total soil nitrogen at the genotype and locality level. Generally, locality averages for the phenotypes measured were correlated with the elevation of the site from which the trees were initially collected, suggesting that phenotypic differentiation was related to underlying physical factors related to elevation. Average leaf area appeared to be an important trait affecting biodiversity and ecosystem function along this elevational gradient. We believe this represents a critical new hypothesis describing patterns of biodiversity and ecosystem function across the landscape, particularly in relation to elevational and latitudinal gradients. These results provide evidence that there were cascading coevolutionary and ecosystem level consequences of population level genetic differentiation in *Populus* and are important for understanding the whole system consequences of climate change.

Revegetation for pest management - designing the 'right' biodiversity for sustainable production in Southern Australia

Glenys M. Wood, Helen E. Degraaf, Richard V. Glatz

Entomology Unit, South Australian Research and Development Institute, Box 397 GPO Adelaide, Australia

Introduction: The utility of endemic vegetation as a refuge for beneficial insects in agricultural systems has been the focus of much investigation over the preceding decade. Here we present work aiming to refine the approach to assessing and predicting the effect of endemic plants. We have developed an *in vitro* screening assay to predict plants that will reduce pest pressure and identified key parasitoids for manipulation using native vegetation.

Methods: The Northern Adelaide Plains provides a model where exotic weeds host *Frankliniella occidentalis* (Western flower thrips; WFT) a vector of Tomato Spotted Wilt Virus, the major cause of vegetable crop loss in the region. We utilised mechanical vacuum, sticky traps and flower funnels for field sampling of various plants. Petri-dish arenas were used to develop a screening system to identify vegetation not supporting WFT development. Key parasitoid species were identified by field sampling and subsequent culturing with potential hosts.

Results: Sampling showed endemic plants supported diverse parasitoids. Among these were a small number of potential biological control agents including parasitoids of WFT, an Agromyzid leaf-miner and the Rutherglen Bug (Lygaeidae). In vitro leaf assays showed a range of endemic plant species supported less WFT reproduction than control capsicum plants.

Conclusions: We developed a reproducible system to identify plants not supporting WFT, for recommendation as low-risk revegetation plants. Analysis of beneficial insects should focus on key parasitoid species rather than total parasitoid diversity. Results suggest integrated plant refuges can create a buffer to rapidly support colonisation of useful insects.

Mass trapping of the male moths (*Metisa plana* Wlk, Lepidoptera: Psychidae) for control of bagworms on mature oil palms in a smallholder plantation in Malaysia

Norman Kamarudin, Siti Nurulhidayah Ahmad, Othman Arshad, Mohd Basri Wahid

Malaysian Palm Oil Board, Bangi, Selangor, Malaysia

Introduction: The bagworm, *Metisa plana* Wlk (Lepidoptera: Psychidae) is an important pest for oil palms in Malaysia. A serious infestation will cause yield decline of around 30-40% over two years after attack. Pheromone trapping is an easy method for smallholders. Success of mass trapping depend on the efficient removal of male adults, hence preventing its copulation with females which can result in a decline in the population.

Methods: Sticky vane traps were baited with four receptive females of *M. plana*. The traps were hung on wooden poles (6' and 12'). Three trapping transects were set in the trapping plot. Ten traps (alternate for different heights) were placed in each transect. Captures were recorded up to 14 days. Percentage of hatchings were recorded to determine the effects of trapping on mating and reproduction success. Yield of the palms were compared between the trapping and control plots.

Results: The population of live larvae (30/frond) and percentage of egg hatching (14-28%) in the trapping plot was always lower compared to the control plot (respectively, at 48/frond and 30-49%). Trapping plot has significantly higher yield (14 kg/bunch) compared to control (10 kg/bunch). Hence, mass trapping reduced the chances of mating and egg hatching, frond damage and subsequently improving yields

Conclusions: The use of the female pheromone of *M. plana* for mass trapping the male moths to reduce the next generation of bagworm larvae has shown potential. The damage in the trapping plot remained lower than the control plot, contributing to higher yield.

Comparative effectiveness of two release rates of the egg parasitoid *Trichogramma chilonis* Ishii (Hymenoptera: Trichogrammatidae) to control a sugarcane borer in Reunion.

Marlène Marquier[1], Clarisse Clain[1], Elisabeth Tabone[2], Régis Goebel[3], Estelle Roux[1]

[1]Département de Mise au Point des Méthodes de Lutte, FDGDON-Réunion, 97460 Saint-Paul, Reunion, [2]Unité de lutte biologique, INRA – Centre de Sophia Antipolis, 06560 Valbonne, France, [3]Unité de Recherche Systèmes cultures annuelles, CIRAD, 34398 Montpellier, France

Introduction: *Trichogramma chilonis* Ishii (Hymenoptera: Trichogrammatidae) is an egg parasitoid of *Chilo sacchariphagus* Bojer (Lepidoptera: Crambidae), a stem borer attacking sugarcane stalks during the growth period. This research aimed at improving the cost / benefit ratio of a release method established in 2002 and 2004 trials. We evaluated two strategies with either reduced a) release points or b) release rate.

Methods: *T. chilonis* was released at two rates in nine sugarcane plots in Reunion. Response to release rate was measured by the percentage of stem attacked 2, 4 and 6 month after the first release. Releases were made with a density of 100 release points in six plots, three plots with a release rate of 16/ 7d and three with 10 /10d. Three more plots were tested with 50 release point at 16/7d release rate.

Results: All nine release sites had significantly lower level of damage, on average half that of the control plots. The damage reduction was not significantly different in fields with 50 and 100 release points. Likewise the release rate did not affect damage reduction.

Conclusion: These results help define augmentative release parameters for successful and cost effective use of *T. chilonis* as a biological control agent of sugarcane stem borer in field conditions. Combining both optimizations will bring a sustainable control strategy to Reunion sugarcane growers.

Chemical ecology of parasitic honeybee workers

Vincent Dietemann[1], Peter Neumann[2], Stephan Härtel[3], Jochen Pflugfelder[4], Robin Crewe[1]

[1]Zoology and Entomology Department, University of Pretoria, Pretoria, South Africa, [2]Swiss Bee Research Centre, Agroscope Liebefeld-Posieux, Bern, Switzerland, [3]Institut für Biologie, Molekulare Ökologie, Martin-Luther-Universität Halle-Wittenberg, Halle (Saale), Germany, [4]Institut für Bienenkunde, (Polytechnische Gesellschaf), J. W. Goethe-Universität Frankfurt a. Main, Oberursel, Germany

Introduction: Workers of the Cape honeybee, *Apis mellifera capensis*, were brought into contact with and invaded colonies of the neighbouring subspecies *A. m. scutellata*. Once they enter a host colony, *A. m. capensis* workers produce female offspring thelytokously, thus replicating themselves while using the colony's resources, eventually destroying their host. We used the unique clonal lineage that constitutes the parasitic population to determine the pheromonal mechanisms that mediate social parasitism between the two honeybee subspecies. Since the mandibular gland pheromone is tightly linked with reproductive dominance in workers, we tested the hypothesis that the parasitic lineage has been selected on the basis of pheromonal dominance.

Methods: We performed pheromonal contest bioassays by exposing individual workers to workers or queens of different origins (hosts and parasites). After four to seven days, we extracted their mandibular gland pheromones and analysed their composition by gas-chromatography.

Results: The parasitic lineage of *A. m. capensis* won the pheromonal contests against workers in all cases and the onset of their reproductive activity was not hindered by the presence of host queens.

Conclusions: The difference in composition of mandibular pheromones of queens between the two subspecies of honeybees is likely to be the key that gives one of them the ability to parasitise the other. We suggest that the parasitic lineage was selected for the speed with which it is able to produce inhibitory mandibular signals, a trait associated with its ability to take over reproduction in host colonies and to out compete other parasitic strains.

Low tide is high time! Timing of adult eclosion in *Clunio marinus*

Tobias Kaiser[1], Dietrich Neumann[2], David G. Heckel[1]

[1]Max-Planck-Institute for Chemical Ecology, Jena, Germany, [2]University of Cologne, Cologne, Germany

Introduction: In adaptation to its intertidal environment the chironomid *Clunio marinus* ecloses only on the days of spring tide (lunar rhythm) and only during the time of low tide (circadian rhythm). For each population the circadian eclosion time is adapted to the local time of low tide. Crossing experiments show that these adaptive differences are genetically determined. The differences might lie in the circadian clock itself, in the eclosion hormonal cascade – or in the still unknown coupling mechanism between these two. The molecular basis of lunar entrainment is also unknown. cOpsins, light receptive proteins discovered in insects only recently, are promising candidates to be moonlight receptors.

Methods: Microsatellites, AFLP fingerprints and intron length variation are being used to map the loci that control circadian eclosion time. Additionally, possible points of circadian regulation and thus candidate genes are examined by (1) testing clock genes for differential expression and (2) testing for differential release of eclosion triggering neuropeptides through antibody staining. Two cOpsins have been cloned. Their expression patterns across artificial daily and lunar cycles have been measured using qRT-PCR.

Results: A preliminary genetic map shows that QTL mapping is feasible and crosses between populations with different rhythms for QTL mapping are in progress. In a moonlight-receptive population, one cOpsin shows a striking expression pattern that appears to anticipate full moon.

Conclusions: Mapping of these and other clock-related genes will enable testing of specific hypotheses on the genetic variation that underlies the physiological and behavioural adaptations by which different populations of *Clunio marinus* respond appropriately to their local environments.

Morphometry of the salivary glands in pollen-feeding butterflies of the genus *Heliconius*

Stefan Eberhard, Harald Krenn

Department of Evolutionary Biology, University of Vienna, Vienna, Austria

Introduction: *Heliconius*-butterflies actively collect pollen-grains with their proboscides. The pollen is admixed with saliva forming a pollen-lump outside on the proboscis. During pollen-treatment amino acids are extracted. The utilization of pollen was a key-innovation in the evolution of these neotropical butterflies. In this study two pollen-feeding species, two related non-pollen-feeders, and one outgroup-species were used for a biometrical comparison of the salivary glands. Since high quantities of saliva are expected to be necessary for pollen-feeding it is hypothesised that the salivary glands of pollen-feeding butterflies differ from those of related non-pollen-feeding species.

Methods: Several paramters of dissected salivary glands were measured using a drawing tablet connected with a computer. Additionally, the individual body lengths were measured and the volume of the secretory part of the salivary glands was calculated. A multivariate data analysis was performed using log-transformed data for allometric reasons to reveal differences of the salivary gland morphology between pollen-feeders, non-pollen-feeders, and the outgroup-species.

Results: The salivary glands of pollen-feeders are larger than those of the non pollen-feeding groups. The multivariate data analysis of the salivary glands and body lengths indicated differences between pollen-feeders, non-pollen-feeders, and the outgroup species especially concerning the salivary gland volumes.

Conclusions: The salivary glands are larger in pollen feeding *Heliconius*-butterflies. Despite their similar anatomy the greater secretory region enables *Heliconius*-butterflies to release bigger amounts of saliva. Salivary gland morphology is regarded to be an adaptation to pollen-feeding and might be a crucial innovation for the evolution of this unique feeding-behaviour.

The effects of anthropogenic activities on the termite-fungus mutualism in fungus-growing termites

Paul Eggleton

Natural History Museum, London, United Kingdom

Introduction: Fungus-growing termites (Termtidae: Macrotermitinae) have a unique mutualism with the white-rot fungus, *Termitomyces.* This mututalism has allowed the termite:fungus symbiont complex to become one of the most effective decomposer systems in the world. Here, I describe what is known about the effect of human disturbance on that system.

Methods: Data from standardised transect surveys from all tropical regions are presented and analysed.

Results:.Tropical rain forests have the highest species-level and phylogenetic diversities of Macrotermitinae. Human disturbance results in a general decline in diversity of the Macrotermitinae but not necessarily in their ecological or economic impact. In Africa and Asia, areas cleared from forest for intensive sylviculture and agriculture often have major problems from macrotermitine crop pests that feed on roots and leaves, particularly of saplings. The major leaf litter removing and decomposing invertebrates in such systems are often Macrotermitinae, particularly of the genus *Macrotermes*.

Conclusions: The ability of many fungus-growing termites to control their internal nest environment very precisely may contribute to their survival in heavily disturbed environments.

Termites – the sophisticated cockroaches

Paul Eggleton

The Natural History Museum, London, United Kingdom

Introduction: The position of termites among the Dictyoptera has long been disputed. I present molecular evidence to show conclusively that termites are cockroaches. However, termites have diverged from cockroach traits in many ways, particularly through the greater phenotypic plasticity that eusociality has provided.

Methods: I will present two phylogenetic datasets, one for Dictyoptera (five genes) and a larger one for termites (three genes) as well as data on gut structure and function.

Results:.Termites are eusocial cockroaches. However, termite eusociality has allowed for an extraordinary range of behavioural, anatomical and physiological traits to evolve. One good example is trophic ecology - a wider variety of feeding substrates can be consumed by termites than by other closely related cockroaches. This has been made possible through the development of specialised castes that have freed workers to evolve gut structures not possible, for intrinsic design-cost reasons, in other cockroaches. These changes are not just observed between *Cryptocercus* and other termites, but also found in other parts of the tree: the general trend being from mid-gut detritivory to hind-gut fermenting. I will discuss the evolutionary and ecological consequences of these changes.

Conclusions: Eusociality has allowed termites to become a very sophisticated sort of cockroach.

Phylogenetic evidence for steps in the early social evolution of termites

Paul Eggleton

The Natural History Museum, London, United Kingdom

Introduction: all termites are fully social: all have a sterile caste within a colony led by a king and a queen. Even the earliest branching termites (*Mastotermes*, *Stolotermes*, *Archotermopsis*) have true soldiers, even though some may not have true workers. We therefore have to look to the closest relatives of termites to find phylogenetically well-supported hypotheses of early termite evolution particularly for the origin of eusociality. A well corroborated phylogenetic tree now exists for the Dictyoptera (mantids, cockroaches and termites) and that tree will be used as a basis for discussing how eusociality evolved in termites.

Methods: A robust phylogenetic tree was constructed using a Bayesian method and five gene markers. The tree was used to examine the plausibility of existing hypotheses concerning the early social evolution of termites.

Results: The tree clearly corroborates a hypothesis relating termites to wood-feeding cockroaches, particularly to *Cryptocercus*, the sister group of termites. This hypothesis emphasises parental care in cockroaches that have highly-specialised gut biotas and therefore need extended offspring:parent contact to allow inter-generational passage of that biota.

Conclusions: The finding that termites are derived cockroaches has greatly helped to clarify the steps to eusociality in termites.

Evolution of neotenic lineages in Lycidae (Coleoptera: Elateroidea): from body softness to larviform females.

Ladislav Bocak[1], Milada Bocakova[2], Alfried P. Vogler[3]

[1]Palacky University, Fac. Sci., Olomouc, Czech Republic, [2]Palacky University, Fac. Educ., Olomouc, Czech Republic, [3]Imperial College, Dept. Biol., London, United Kingdom

Introduction: Neoteny is a radical way of generating evolutionary novelty. Often controlled by the environment in facultative neotenics, retention of larval features is obligatory in many species of Lycidae (net-winged beetles). They are studied here as an example of how developmental shifts and ecology interact to produce macroevolutionary impacts.

Method: We conducted an evolutionary analysis of Lycidae based on DNA sequences from nuclear (18S and 28S rRNA) and mitochondrial (*rrnL*, *cox1*, *cob* and *nad5*) genes from a representative set of lineages (73 species), including 17 neotenic taxa. Almost all higher taxa of Lycidae were included in analyses.

Results: Phylogenetic analyses universally supported three independent origins of neotenics in Lycidae without reversals to fully metamorphosed forms. The south-east Asian Lyropaeinae and Ateliinae were in basal positions indicating evolutionary antiquity, unlike the Neotropical leptolycines nested within Calopterini and presumably much younger. Neotenics exhibit typical K-selected traits including slow development, large body size, high investment in offspring and low dispersal. Although neotenic lineages are ancient, their representatives are rare and all affected lineages are species poor.

Conclusions: Our findings are contradicting earlier suggestions of recent evolution from dispersive non-neotenics or reversal from neotenic to winged forms. We propose the series of morphological modifications from body softness to winglessness and to the evolution of lineages with completely larviform females.

Outcome of enemy-enemy interactions: Role of behavior, life-history and scale

Christer Bjorkman

Department of Ecology, Swedish University of Agricultural Sciences, Uppsala, Sweden

Introduction: It has lately become evident that it is important to consider the combined, total effect of sets of natural enemies when evaluating the role of top-down forces in ecological systems.

Methods: Field and laboratory studies were used to explore the outcome of enemy-enemy interactions on willows (*Salix* spp.). Two species of mirid bugs (Miridae) and an anthocorid bug (Anthocoridae) were studied. The two mirids are characterized by their habit of staying at a site and eat all prey before moving ('find-and-stay') whereas the anthocorid typically feeds on one or a few prey and then moves along ('run-and-eat'). The bugs are all predators of leaf beetles (Chrysomelidae), an important pest in willow plantations used for producing biofuel.

Results: At the scale of individual plantations, we found (1) a negative relationship between the density of two mirid bug species and (2) a tendency for a positive relationship between the density of the most common mirid bug and the anthocorid bug. At the scale of willow saplings, we found (a) an additive effect when combining two mirid bug individuals or when combining one mirid and one anthocorid bug, but (b) a negative, synergistic effect when combining two anthocorid bugs.

Conclusions: Enemy-enemy interactions are likely to be negative when (a) enemies with active and similar behavior compete over prey or (b) enemies compete over a strongly limited resource. The interactions are neutral when (a) enemies with less active, but similar behavior compete over prey or (b) enemies with different behaviors compete over prey.

Locusts versus grasshoppers: presence of adipokinetic peptides and functional aspects

Gerd Gade

University of Cape Town, Rondebosch, South Africa

Introduction: The corpora cardiaca of insects synthesise the adipokinetic peptides which are involved in regulating the level of circulating metabolites (lipids, carbohydrates, proline) by activating phosphorylases or lipases in fat body cells.

Aim and Results: Here the isolation and primary structure elucidation of such octa- or decapeptides of the adipokinetic hormone family of peptides in various members of the caeliferan Orthoptera are presented. Moreover, the physiological actions of such AKH peptides are contrasted in true locusts where lipid-mobilisation is controlled by them during long-distance flight and in those grasshoppers which are unable to fly or fly relatively poorly. The South African pest species *Locustana pardalina* serves as a test case for the group of locusts. Whereas all investigated species of locusts and grasshoppers contain AKH peptides (between 2 and 3 per species), pronounced overt changes of haemolymph lipids are only measured in locusts and not grasshopper species investigated. Flight in *L. pardalina* results in a decrease in the haemolymph carbohydrate concentration first and subsequently in an increase in the concentration of lipids during longer flight periods.

On the relationships between biodiversity and habitat fragmentation across spatial scales

Joan Ll. Pretus[1], Guillem Chust[2,] Nuria Roura-Pascual

[1]Universitat de Barcelona, Barcelona, Catalonia, Spain, [2]AZTI Tecnalia, Sukarrieta, Basque Country, Spain

Introduction: We synthesize our recent results and current research on the effects of habitat fragmentation on several insect assemblages at different spatial scales. In all cases sampling effort was designed to capture a gradient of natural habitat loss, and samples were taken on remaining fragments of climax vegetation. Studied biomes comprise two Mediterranean zones (Menorca Island and Mediterranean Pyrenees, Spain), one Euro-Siberian (Central Pyrenees, France) and one Tropical locality (Seasonally dry tropical forest in Guerrero, Mexico). Sampling design comprised small (250 cm^3) soil cores (Collembola), 10x10 m quadrats at constant effort (Diptera, Homoptera), transects for gall wasps (Cynipidae, Hymenoptera), and light traps (Lepidoptera).

Methods: Landscape parameters were extracted at increasing scales from land cover types produced through supervised classification from satellite images. Local microhabitat factors and spatial coordinates were taken into account as covariates. Insect data were regressed to landscape parameters to model its composition, species diversity (total richness, endemic richness, extrapolated richness through Collector's curves, alfa- and beta-diversity), and life history. Variance partitioning at different scales unveiled the mixture of spatial influences affecting insect assemblage parameters.

Results: Scales of response ranged from 60 m in Homoptera to a few kilometers in several other groups. When trophic level is considered, predators and parasites respond with more precision and to a lower scale than saprophagous and phytophagous. The number of endemics in Collembola respond to two spatial scales, 150 m and 1710 m, with 71,6% of the richness variance incorporated into a linear model.These findings allow for high resolution maps of potential richness distribution for target groups, at useful but yet unsolved scales. Ongoing research is centered in defining intrapatch quality of remaining natural fragments and its effects on moth diversity.

Metabolic strategies and adipokinetic hormones of two stinkbug taxa

Heather G. Marco, Gerd Gade

University of Cape Town, Rondebosch, South Africa

Introduction: In insects studied to date, metabolism is regulated by small neuropeptide hormones belonging to the adipokinetic hormone (AKH)/red pigment-concentrating hormone (RPCH) peptide family. In the sister group, crustaceans, AKH/RPCH affects the movement of epithelial and retinal pigment. In decapod crustaceans, RPCH is conserved, whereas insects contain a variety of AKH structures. Recently, we discovered RPCH in the corpora cardiaca (CC) of the stinkbug *Nezara viridula* (Superfamily: Pentatomoidae; Family: Pentatomidae), where it acts as an AKH. In the current study, we perform comparative investigations on metabolic regulation in *N. viridula* and the related inflated stinkbug *Encosternum delegorguei* (Family: Tessaratomidae); the latter occurs in the Limpopo Province of RSA where it is a sought-after food item for local tribes.

Methods: CCs were dissected from stinkbug heads; peptides were extracted and purified via RP-HPLC, structurally characterised by mass spectrometry and used in *in vivo* bioassays to monitor their effect on circulating levels of lipids and carbohydrates in stinkbugs. Additionally, metabolites were monitored before and after flight episodes, and the activation of glycogen phosphorylase in the fatbody of bugs in response to CC extract or RPCH were determined.

Results: *E. delegorguei* produces two AKH peptides, viz. RPCH and Schgr-AKH-II. Homologous bioassays reveal that both stinkbugs react to injection of CC extracts and conspecific peptides by increasing lipid levels in the haemolymph; carbohydrates are not affected. Flight of two min (*N. viridula*) and 3 min (*E. delegorguei*) resulted in small increases in lipids and a small decrease in carbohydrates.

Conclusion: Two related stinkbugs show a similar metabolic strategy and both contain RPCH as an active AKH. A second AKH occurs in the tessaratomid.

Evolution of cleptoparasitism, eusocial behavior and shifts in diversification rates in apid bees (Hymenoptera: Apidae).

Sophie Cardinal[1], Jakub Straka[2], Bryan Danforth[1]

[1]Cornell University, Ithaca, NY, United States, [2]Charles University in Prague, Faculty of Science, Prague, Prague, Czech Republic

Apidae is the most speciose family of bees with over 5600 species. Its monophyly has been well established, but relationships among the tribes within Apidae are unclear. Among the most challenging phylogenetic questions within the apid bees are the phylogenetic affinities of the cleptoparasitic groups. To address this problem, we performed a phylogenetic study of the family Apidae based on molecular (DNA sequence) data and morphology from both adults and larvae. The study includes representatives from all apid tribes and every presumed independent origin of cleptoparasitism. Five nuclear protein-coding genes and two nuclear ribosomal genes were sequenced for 190 taxa and 220 morphological characters were coded. We then used the phylogeny to investigate origins of cleptoparasitism and patterns of host-parasite relationships within the family. Results indicate that there have been fewer independent origins of cleptoparasitism in the Apidae than was previously hypothesized based on morphological data alone. We used a relaxed fossil calibrated molecular clock model to investigate the antiquity of eusocial and cleptoparasitic behavior within apid bees as well as major shifts in diversification rates. This study represents the first comprehensive tribal level phylogeny of the family Apidae based on molecular and combined molecular plus morphological data.

Rynaxypyr® (Chlorantraniliprole): A novel DuPont insecticide with low toxicity for beneficial arthropods providing excellent tools (DuPont™ Coragen® and Altacor®) for uses in integrated pest management (IPM)

Axel Dinter

DuPont de Nemours (Deutschland) GmbH, Bad Homburg v.d.H., Germany

DuPont™ Rynaxypyr® insecticide (chlorantraniliprole) is a new anthranilic diamide insecticide with a novel and very specific mode of action activating insect ryanodine receptors causing impaired regulation, paralysis and ultimately death of sensitive species at rates of 10 to 60 g per ha. Anthranilic diamide insecticides exhibit > 500-hold differential selectivity toward sensitive insect, over mammalian, receptors. In worst-case Tier 1 glass plate tests the two indicator species, *Aphidius rhopalosiphi* (DeStephani-Perez) (Hymenoptera: Braconidae) and *Typhlodromus pyri* Scheuten (Acari: Phytoseiidae), were not sensitive to either formulated product, DuPont™ Coragen® or Altacor® insecticides, at up to 750 g Rynaxypyr® per ha, the maximum rates tested indicating low toxicity for non-target arthropods. Low risk for non-target arthropods was confirmed in a wide range of tests with several other beneficial arthropods (e.g. predatory mites, chrysopids, anthocorids, coccinellids and syrphids) under worst-case laboratory and field conditions. Overall, Rynaxypyr® and the formulations, Coragen® and Altacor®, were demonstrated to be safe to numerous beneficial non-target arthropod species including honeybees or to have rather low and transient short-term impact. The DuPont™ Rynaxypyr® insecticide formulations will be excellent tools in integrated pest management (IPM) programmes to conserve naturally occurring beneficial arthropods in the field as well as protect predators and parasitic wasps released for greenhouse pest control.

Attraction and repellence of grubs in soil systems as part of pest control strategies: the cockchafer *Melolontha melolontha* example

Rob van Tol, Gerrie Wiegers, Willem Jan de Kogel

Plant Research International, Wageningen-UR, Wageningen, Netherlands

Introduction: Despite the presence/availability of several natural enemies to control pests in soil systems (entomopathogenic nematodes, fungi and predators) the overall control results are still variable and poor for most soil pests. Lack of knowledge about the existing interactions in soil may explain this poor and variable control. Understanding these interactions may provide us with new tools for growers how and when to apply natural enemies in a more efficient way leading to higher and more reliable control of soil pests. For the white grub - plant roots - natural enemies interaction it is our goal to select for attractive plant species to lure the grubs and study the efficacy of these plants with natural enemies in a lure-and-kill system. The involvement and identification of semiochemicals in attracting or repelling white grubs and/or natural enemies to host-plant roots and pest in the soil is part of this study as well. Integrating aboveground attraction/repellence of the adult beetle to pheromone and plants as part of a system approach to control this pest insect is a further goal in this project.

Methods: A specific olfactometer for studying these grubs has been developed and different plant species were tested on attraction or repellence for the grubs in single and dual plant choice experiments.

Results: We demonstrate that for the white grub *M. melolontha* several plant species are highly attractive in an olfactometer where the grubs are unable to contact the roots. Two plant species were clearly preferred over several other plant species tested. Further we found two plant species that repelled 100% of the responding grubs from a distance.

Conclusions: White grubs appear to use sensory receptors for detection and selection of plant species from a distance. The grubs can detect several plant species without contacting the roots and are strongly attracted or repelled by some of the tested plant species. The strong preference and repellence may be used in a push-pull or attract-and-kill system with effective natural enemies.

Generalization and odor learning by honeybees

Geraldine Wright

Biology, Newcastle University, Newcastle upon Tyne, United Kingdom

Sensory biases in the responses of signal receivers to novel stimuli can be produced when an animal learns to associate two different outcomes, such as reward and punishment, with perceptually similar stimuli in the same modality. While such biases are well-described from experiments using visual and auditory stimuli, we know little about the development of learned sensory biases towards odors. Here, I describe a series of experiments showing that honeybees can acquire sensory biases towards both simple and complex odors as a result of differential learning of two perceptually similar olfactory stimuli. These experiments also demonstrate that the strength of a sensory bias depends upon the relative value of the positive and negative reinforcers. The implications for the use of odor signals by bees during foraging and nestmate recognition, and their significance with respect to our understanding of bee “cognition” will be explored.

How do long-range insect migrants influence their flight direction?

Jason Chapman

Rothamsted Research, Harpenden, United Kingdom

Behavioural adaptations of long-range insect migrants are often disregarded by many researchers, as migrant windborne insects are generally considered to be “passive” or “accidental” dispersers at the mercy of the wind. This simplistic approach has come about because of the difficulty associated with studying insects actively engaged in migration, which often utilise fast winds by flying hundreds of metres above the ground. In this talk I describe how two new research tools, vertical-looking entomological radar (VLR) and computerised flight simulators, are providing evidence that a wide range of insect taxa have evolved specialised behaviours to influence their direction of movement. Data from our VLR studies demonstrate that these behaviours include simple path straightening mechanisms in green lacewings *Chrysoperla carnea*, and selection of favourable airstreams in noctuid moths. Flight simulator studies of the Painted Lady butterfly *Vanessa cardui* indicate that this species uses a sun compass without time-compensation to direct its migratory flights in seasonally-advantageous directions. Finally, VLR data from migrant Silver Y moths *Autographa gamma* demonstrate that the high-flying moths use a compass to select favourable winds for their southerly return migrations, and also to compensate for lateral wind-drift away from their preferred migratory direction. Our data demonstrate that a wide range of species have evolved complex behavioural adaptations that significantly increase their chances of successfully exploiting seasonal resources.

Pestilence arising from cooperation: symbiotic associations among plant enemies

Matthew Ayres

Dartmouth College, Hanover, NH, United States

We propose that mutualisms among plant enemies have the general ecological effect of promoting plant pestilence. The theory, which we have dubbed "*Pestis symbiotica*", is comprised of six postulates: (1) symbioses are common among plant enemies; (2) symbioses tend to be mutualisms and commensalisms; (3) plant pestilence is typically the result of extreme population fluctuations in plant enemies; (4) population fluctuations are wrought by complex endogenous dynamics and/or variable exogenous effects; (5) commensalisms, and especially mutualisms, tend to destabilize population dynamics by contributing to complex endogenous dynamics and amplifying exogenous effects; (6) symbioses among plant enemies promote pestilence in evolutionary time by favoring the retention of virulence in microsymbionts and selecting for increased aggressiveness in macrosymbionts. If these postulates hold, it follows that many cases of plant pestilence are an emergent property of symbiotic associations among plant enemies, and that understanding this class of plant pestilence involves understanding community interactions among plant enemies. In support of *Pestis symbiotica*, 37-42% of the taxa that appear on plant pest quarantine lists for Europe (EPPO) and the United States (APHIS) have symbiotic associations with other plant enemies. *Pestis symbiotica* may also be relevant to animal pestilence and human disease. A general implications is that food web theory requires expansion to accommodate positive interactions, which are generally not trophic interactions. Finally, *Pestis symbiotica* runs counter to a prevailing theme of symbiology: the emergence of cooperation among previously independent biological entities. Ironically, the theory predicts that symbionts as ecological units tend to become "red in tooth and claw".

Bee diversity in coffee agroecosystems in Costa Rica

Hien Ngo, Laurence Packer

York University, Toronto, Ontario, Canada

Introduction: The intensification of coffee agroecosystems affects animal groups in different ways. The effect of shade trees on bee diversity in coffee agroecosystems was examined.

Methods: Bees were collected with Malaise traps in: i) shaded coffee farms, ii) unshaded coffee farms and iii) non-agricultural sites during 2005 and 2006 in Costa Rica. Bee diversity, evenness, species richness and abundance were compared among three site types. In addition, similarity indices were used to compare community complementarity.

Results: The diversity of bees across all site types did not differ from each other ($F_{2, 14} = 1.72$, $p=0.224$). Unshaded coffee farms had greater species richness and abundance but lower evenness than the other two site types. Results of the same analyses for different bee guilds will be presented. Similarity indices based on presence/absence (Jaccard) and abundance (Morisita-Horn) both show that non-agricultural sites are different in composition than agricultural sites types. *Lasioglossum* subgenus *Dialictus* made up 49% of the bee individuals collected. *Dialictus* has never been reported to be commonly found in coffee agroecosystems and this may be due to biases of different sampling methods. These findings have important implications for pollinator conservation and coffee agriculture.

Conclusions: Shade trees do affect the patterns of bee diversity in coffee agroecosystems. Sampling methods exhibit strong biases which can affect conservation strategies by misrepresenting biodiversity. The possible role of *Dialictus* and other often ignored bees in coffee pollination requires further investigation.

Integrated pest eradication: technologies for incursion response against invasive species

David M. Suckling

HortResearch, Lincoln, Canterbury, New Zealand

Introduction: Eradication of any insect from an area is normally only undertaken after justification from an economic and/or environmental impact analysis. Further key considerations include the ability to fully delimit and characterise the target population, as well as the availability of suitable technologies that can be used in the landscape where the pest has been detected. While standard IPM tools such as insecticides may be available, their suitability for use in an eradication programme may be constrained in urban or natural ecosystems. The types of tools available depend on the pest biology, and certain orders of insects have a wider arsenal available than others. For example, there are attractants identified for many Lepidoptera, while the same applies for certain Coleoptera, Diptera and Hymenoptera, and to a lesser extent for Hemiptera and other groups. In many cases pest management programmes have provided the basis for "Integrated Pest Eradication" when pests are detected in new regions.

Conclusions: More socially-acceptable tactics are urgently needed to reduce the almost inevitable establishment and range expansion of invasive species. Research challenges include the discovery of new and more powerful attractants and their development into mass trapping, lure and kill, mating disruption or other tactics which are broadly more acceptable than broadcast insecticides. In addition, the sterile insect technique, biopesticides, and other methods will be used increasingly, but need research along with key aspects of pest biology and ecology. Recent experience with successful and unsuccessful eradications of various species will be used to illustrate progress in this area.

Obscure mealybug pheromone is the kairomone of an introduced parasitoid in New Zealand

Vaughn A. Bell, David M. Suckling, James T.S. Walker, J.G. Millar, Lee-Anne Manning, Ashraf El-Sayed

HortResearch, Lincoln, Canterbury, New Zealand

Introduction: The obscure mealybug (*Pseudococcus viburni*) is a serious cosmopolitan pest of apples and many other crops. New options for managing this species in New Zealand include the release in 2001 of the host-specific parasitoid, *Pseudaphycus maculipennis* and the recent identification of a synthetic sex pheromone.

Methods: Pheromone-baited sticky traps with a range of loadings of *Pseudococcus viburni* pheromone were tested in orchards to determine optimal doses for monitoring mealybugs as part of anIPM program.

Results: This study evaluated the efficacy of the mealybug pheromone in the field and serendipidously discovered that the parasitoid was also attracted to traps baited with the pheromone of its host. The presence of female *P. maculipennis* in baited (but not control) traps suggests recognition of the host female sex pheromone as a kairomone. Male *P. viburni* were trapped in 11 Hawke's Bay orchards. Traps also recovered the parasitoid *P. maculipennis* from eight Hawke's Bay orchards where releases had been made.

Conclusions: The finding of kairomonal activity in the parasitoid has readily enabled monitoring the fate post-introduction of a biological control agent. The phenology of the two species as revealed by the trap data showed a mealybug generation without evident parasitoid catch in the middle of winter. Future applications of mealybug sex pheromones for managing the pest and parasitoid will be discussed.

Soil invertebrate-plant feedbacks and community change in a California coastal prairie

Daniel Gruner[1], Donald Strong[2]

[1]University of Maryland, College Park, MD, United States, [2]University of California, Davis, CA, United States

The yellow bush lupine (Fabaceae: *Lupinus arboreus*) is a dominant, nitrogen-fixing woody shrub in California coastal prairie. It is attacked by a suite of aboveground foliar- and seed-feeding herbivores which can defoliate plants and strongly reduce seedset. Belowground, the primary herbivore is a stem- and root-boring lepidopteran (Hepialidae: *Hepialus californicus*). By severing vascular cambia, these ghost moth caterpillars also can reduce reproduction, but often girdle and kill mature bushes, releasing limited space, light and available nitrogen to native and invasive plant colonists and facilitating change in plant community structure. In field and laboratory experiments, soil-dwelling entomopathogenic nematodes ('EPN', *Heterorhabditis marelatus*) can control *Hepialus* and provide protection to lupines via a trophic cascade. However, longer duration, spatially explicit studies demonstrate that the strength of these interactions varies temporally and spatially, and caterpillar outbreaks and lupine devastation can occur even within a background of robust EPN populations. Limited locomotion – both by nematodes and insect hosts in soil – impair EPN recruitment to high local host densities and reinforce the inherent patchiness of naturally-occurring EPN populations. Spatial autocorrelation functions showed that characteristic patch sizes of EPN were larger than the scale of individual lupine rhizospheres, but that these dynamic 'clouds' swelled into grasslands during the wet season and retreated to lupine rhizospheres following dry Mediterranean summers. Summer desiccation risk drove EPN into moisture refugia, both within lupine rhizospheres and into deep (>80 cm) soils lacking host insects. Monthly samples of soil columns from grassland and lupine rhizospheres over one year confirm that lupine canopies facilitate EPN populations with higher soil moisture and by harboring greater diversity and abundance of arthropod larvae in the soil. These features create greater opportunity under lupine canopies for individual movement, host-finding behavior, and survival of IJs, and promote recycling of additional EPN generations through alternative arthropod hosts. Research from the *Heterorhabditis – Hepialus – Lupinus* system provides clear examples of how subterranean interactions can instigate potent ramifications for the structure and diversity of aboveground plant and animal communities.

Interactions among invasive ants, herbivores, and plants

Lori Lach[1], Andrew V. Suarez[2]

[1]Murdoch University, Murdoch, WA, Australia, [2]University of Illinois, Urbana, IL, United States

Because ants play so many roles in ecological communities, invasion by non-native ants can have many direct and indirect consequences. For example, invasive ants can positively or negatively affect herbivore populations, which can then have cascading effects on the plant community. Outside of agricultural settings, however, few experiments have examined interactions among invasive ants, herbivores, and plants. We studied the effects of invasive ants via ant exclusion experiments on two plants on a small Mauritian islet. The native shrub, *Scaevola taccada,* hosts sap-sucking scale insects, and the invasive tree, *Leucaena leucocephala*, also hosts scale insects, but offers extrafloral nectaries as well. *Technomyrmex albipes* was the most common ant visitor to both plants. Honeydew-producing hemipterans declined rapidly on branches of *S. taccada* to which ants had been excluded, and these branches had 22-30% and 32-45% greater growth and fruit production, respectively, compared to ant-allowed branches on the same plants. On *L. leucocephala*, ant exclusion resulted in 22% and 35% lower vegetative growth and seed production, respectively, most likely because ant presence lowered the prevalence of psyllids. However, the beneficial effect of the ants was diminished when scale insects were present on the tree. Stable isotope analysis confirmed that the ants behaved more as herbivores on the native *S. taccada*, and as predators on the invasive *L. leucocephala* tree. Our findings illustrate the context-dependency of invasive ant effects on plants. Negative effects on native plants and positive effects on invasive plants are means through which ants may be especially insidious invaders.

Social parasitism in the allodapines: new insights from a unique tribe of bees

Jaclyn Smith[1], Theresa Wossler[2]

[1]Flinders University, Adelaide, South Australia, Australia, [2]University of Stellenbosch, Matieland, South Africa

Introduction: Allodapine bees are unique among bees, with most species rearing their highly dependent brood progressively in an undivided communal tunnel without the presence of cell partitions. Social parasitism within these bees has received little attention in the past, but recent research on allodapine social parasites indicates that these bees have much to contribute to our general understanding of social parasitism. Behavioural work on allodapine social parasites has shown that they are able to invade host colonies with surprising ease. These results are largely unexpected since the costs associated with parasitism should result in the selection of nest defence with it expected that the host colonies should be able to refuse entry to a parasite.

Methods: We investigated whether allodapine social parasites are manipulating their cuticular hydrocarbon profiles to avoid detection and gain entry into host colonies. Two species of allodapine bees, *Exoneura robusta* (host) and *Inquilina schwarzi* (social parasite) were collected in Australia and their hydrocarbons were extracted. The cuticular hydrocarbon profiles of both species were analysed in South Africa, using gas-chromatography mass-spectroscopy (GC-MS).

Results: Multivariate statistical analyses have indicated some interesting differences between the hydrocarbon profile of the host and parasite species within the parasitised nests, but also differences between parasitised and unparasitised nests.

Conclusions: The results from the GC-MS analyses, together with previous behavioural observations on these two species have provided a unique insight into the fascinating phenomena of social parasitism.

Understanding the evolution of social parasitism: Implications from phylogenetic analyses of allodapine bees.

Jaclyn Smith, Michael Schwarz

Flinders University, Adelaide, South Australia, Australia

Introduction: Much research has focused on the social parasites of ants, wasps and honeybees, however, very little research has focused on social parasitism within allodapine bees. This group of bees have much to contribute to understanding the evolution of social parasitism, as social parasitism has evolved many times in the allodapines, resulting in this tribe having a higher proportion of socially parasitic species than any other social insect group. The allodapines can therefore provide a unique insight into the processes that were involved in the evolution of a parasitic strategy.

Methods: Allodapine social parasites, from Australia, Madagascar, Africa and Asia (19 species in total), were analysed with molecular tools to explore the host-parasite relationships. Bayesian analyses were used to determine phylogenetic relationships and divergence dates were estimated with Sanderson's Penalised Likelihood Method (R8s).

Results: Eight independent origins of social parasitism were found. These origins have varying divergence ages, ranging from relatively recent, to very ancient, and each of these origins demonstrated variable phylogenetic relationships between the parasites and their hosts. In most cases, social parasites were phylogenetically allied to their hosts. However, where taxonomic sampling was dense, there was no evidence for a sister-group relationship between hosts and parasites and therefore no evidence for sympatric speciation origins for social parasites.

Conclusions: No firm evidence for sympatric origins of social parasitism are apparent, though host and parasite lineages were usually phylogenetically allied. There is good evidence for cospeciation between hosts and parasites suggesting that the two become very closely linked.

The impact of phosphate fertilizer as a pest management tactic in four cowpea varieties

Joseph Asiwe, Frank Kola Ewete, Sagary K Nokoe, Louis E.N. Jackai

[1]ARC-Grain Crops Institute, Potchefstroom, South Africa, [2]Department of Crop Protection and Environmental Biology, University of Ibadan, Ibadan, Nigeria, [3]University for Development Studies, Ghana., Accra, Ghana, [4]2 GWC-Agricultural Experiment Station, College of Agricultural, Environmental and Natural Sciences, Tuskegee University, Tuskegee, Alabama 36088, USA, Alabama, United States Minor Outlying Islands

Introduction: Insect pests constitute serious threat to cowpea production in sub-Saharan Africa. In some severe situations, total yield loss results. Chemical control is the most effective and quick method. However, it is not a sustainable method for cowpea insect management. Investigation of other control options such as cultural practices that are environment friendly is critically important.

Methods: This paper reports the effects of four levels of phosphorus fertilizer application (0, 15, 30 and 45 kg P_2O_5 ha^{-1}) on insect population, damage and grain yield of four cowpea varieties (IT91K-180, IT95M-118, TVu 1890 and Vita 7) planted at research farm of International Institute of Tropical Agriculture (IITA), Nigeria. Data collected included insect counts, pod evaluation index, and damage by insects (*Aphis craccivora, Megaluro sjostedti*, *Maruca vitrata* and pod-sucking bugs).

Results: Results indicated that infestation by *A. craccivora* in cowpea plots fertilized at 30 kg P_2O_5 ha^{-1} was significantly ($P < 0.05$) lower in the first than second season. Damage by *M. sjostedti* was significantly ($P < 0.05$) lower at 30 and 45 kg P_2O_5 ha^{-1} during second season. Pod evaluation index (*Ipe*) was significantly higher in cowpea plots treated with 30 and 45 kg P_2O_5 ha^{-1}. Counts of pod-sucking bugs were not significantly different among P-levels and test varieties.

Conclusions: Insect damage was minimal at 30 and 45 kg P_2O_5 ha^{-1} and consequently higher grain yields were obtained. These P-levels are recommended, and can be used in conjunction with other cultural interventions for integrated insect pests management in cowpea.

The phylogeographic population structure of Argentine ants in South Africa: genetic evidence for multiple introductions

Bettine van Vuuren, Thomas Lado, Steven Chown

DST-NRF Centre of Excellence for Invasion Biology, University of Stellenbosch, Stellenbosch, South Africa

Introduction: Much is known about the genetic structure of the Argentine ant across its native and introduced ranges. However, very little is known about the genetic composition of the species across South Africa.

Methods: Segments from two mitochondrial DNA genes (COI and cytb) as well as six microsatellite loci were used to investigate the phylogeographic population structure of ants sampled across South Africa.

Results: Alignment of COI sequences indicated four variable sites resulting in five haplotypes, two of which are identical to those from other parts of the world. COI haplotypes are separated by (at most) only 0.4% uncorrected sequence divergence or 3 mutational changes. As is documented for introduced Argentine ants across the world, the majority of South African specimens (93%) are characterized by a single haplotype. In contrast to the COI results, genotyping of Argentine ants revealed moderate levels of genetic diversity (H_e = 0.51 ± 0.22). Microsatellite analyses further indicated significant sub-structure across South Africa (R_{ST} = 0.14; $p<0.05$). This result was confirmed by non-metric multidimensional scaling of pairwise genetic distances. A comparison of Argentine ant cytb haplotypes from South Africa and across the world indicated multiple source populations for introduction into South Africa.

Conclusions: Limited mitochondrial genetic variability characterizes Argentine ants from South Africa. In contrast, moderate levels of variation were found for microsatellite loci. Significant substructure further characterized nuclear loci with evidence for introductions from multiple source populations

Western corn rootworm and European corn borer important pests of maize in Croatia

Marija Ivezic[1], Emilija Raspudic[1], Mirjana Brmez[1], Ivana Majic[1], Andrija Brkic[2]

[1]*Josip Juraj Strossmayer University of Osijek, Faculty of Agriculture in Osijek, Osijek, Croatia,* [2]*Agricultural Insitute Osijek, Osijek, Croatia*

Introduction: Western corn rootworm (WCR) (*Diabrotica virgifer virgifera* LeConte) and European corn borer (ECB) (*Ostrinia nubilalis* Hübner) are considered to be the most harmful pests of maize in Croatia. Research was done with the aim to evaluate combined attack of both pests in Croatia.

Methods: The research was carried out at the Agricultural Insitute Osijek, in years from 2003 to 2007 on 7 Croatian commercial maize hybrids. WCR population was monitored by pheromone traps. Root injury was assessed during July according to the Iowa Node Injury Scale (0-3). In order to determine ECB larvae and total damages per plant were dissected in September.

Results: Node-injury ratings ranged from 0.58 to 1.61. From 2003 to 2006, rating of all hybrids except one, planted in monoculture for 7 years, were assessed over 1. Hybrid OSSK 617 showed greater tolerance to the WCR larvae. Since the maize was grown in monoculture only for two years, considerably less damage was determined in 2007 when node-injury ratings ranged from 0.38 to 0.73. ECB attack in 2003 and 2004, was more than 81%, in 2005 and 2006 damage was more then 41% and it was considerably lower. In 2007, nearly 100% maize stalks were infested with ECB larvae. Stalk damage was positively correlated with the intensity of ECB attack.

Conclusions: The obtained results indicate that Western corn rootworm and European corn borer are severe pests of maize in Croatia and in order to avoid economic damages integrated pest management is recommended.

The characteristics of ant subfamilies (Hymenoptera: Formicidae) wing venation and their significance for paleontological investigations

Ksenia Perfilieva

Lomonosov Moscow State University, Biologycal Faculty, Moscow, Russian Federation

Introduction: Ants are among the most common and dominant groups of insect in various Cenozoic. While, winged ants or only the wings form a large part of preserved fragments, which are very difficult in identifying, since the venation of wings is not used as taxonomic characteristics for recent ants. Differences in wing venation of recent ant subfamilies have not practically been investigated yet.

Methods: Investigations has been made on the 17 recent ant subfamilies of Formicidae. Differences in wing venation of subfamilies were analyzed by geometric morphometrics methods.

Results: We present the principals of wings description for recent and fossil ants, which will permit more precisely to describe a forewing venation of ants. For that we proposed scheme of forewing venation types, which consist of 16 types. The different subfamilies may have the same types of forewing venation. Nevertheless, recent subfamilies have different composition and ratio of venation types. Differences in features of venation of the same type that in turn indicate the differences between various subfamilies are very important for paleontological research. Usually the features of venation (relative length, slope of veins) are conditioned by various ways of wing evolution in different subfamilies. With the help of geometric morphometrics methods, we show that subfamilies (Pseudomyrmecinae, Dolichoderinae, Myrmicinae, Myrmeciinae, Poneromorpha, etc.) has peculiar venation traits, such as the shape of cells, location, slope of definite veins and other.

Conclusions: Subfamilies of Formicidae (Pseudomyrmecinae, Dolichoderinae, Myrmicinae, Myrmeciinae, Poneromorpha, etc.) has peculiar venation traits, which allows identifying recent and fossil ants wings.

Yield losses due to natural infestation of tomato by *Liriomyza* spp., Central Sudan

[1]Faiza. E. Salah, [2]E. M. Elamin, [1]E. M. A. Eltoum, [3]D. Bordat

[1]Dept. Crop Protection, Gezira University, Medani, Sudan. P.O. Box 20; [2]Agricultural Research Corporation, Medani; [3]CIRAD, Montpellier, France

The leafminer (LM), *Liriomyza* spp. (Diptera: Agromyzidae) is known to attack tomato crops in the Gezira all year around. The effect of such infestation was not tackled researches in the Sudan. This study was done at the Experimental Farm of the Faculty of Agricultural Sciences, University of Gezira on the tomato variety Peto 86 (season 1996/97) and the breeding line Wad El-Obaid (season 1997/98). One experiment was conducted for each. Two treatments (i.e. insecticide-treated and untreated) were laid out in a RCB design with six replicates. The untreated plots were left to the LMs natural infestation, while the treated plots were protected by the IGR Trigard 75% WP. Highly significant differences ($P<0.01$) in percentage of leaf infestation were correlated with the highly significant differences in yield between treated and untreated plots. Differences in leaf infestation of *ca*. 48% in plots of the tomato variety Peto 86 resulted in a yield loss of approximately 44%, compared to 43% loss in yield of Wad El-Obaid, where the percentage of leaf infestation was *ca*. 56%. Therefore, it is recommended that tomato crop should be treated with insecticides to reduce the effect of the LMs.

Monitoring the operational impact of insecticide usage for malaria control on *Anopheles funestus* from Mozambique

Michael Coleman[1], Sonia Casimiro[2], Janet Hemingway[3], Brian Sharp[1]

[1]Medical Research Council, South Africa, Durban, South Africa, [2]National Institute of Health, Maputo, Mozambique, [3]Liverpool School of Tropical Medicine, Liverool, United Kingdom

Introduction: Indoor residual spraying (IRS) has again increased for malaria control in Africa. DDT was re-introduced into Mozambique's IRS programme in 2005 and has become the main insecticide used for malaria vector control. Use of DDT in Mozambique is evidence-based, taking account of the susceptibility of Anopheles funestus and Anopheles arabiensis to all available insecticide choices and operational costs of spraying. To maintain integrity of control operations, monitoring the susceptibility status of both major vectors needs to be embedded within routine operations of the control programme.

Method: Sentinel sites were monitored for insecticide resistance using WHO bioassays and biochemical assays. Assays were conducted on 1-3 day old F1 offspring of field collected adult females to determine levels of insecticide resistance and gene resistance frequency in vector population.

Results: Lambda cyhalothrin replaced DDT for malaria control in Mozambique in 1993. However, resistance appeared quickly to this insecticide and, in 2000, the pyrethroid was phased out and the carbamate, bendiocarb, introduced. Low level resistance was detected by biochemical assay to bendiocarb in 1999 in both *An. funestus* and *An. arabiensis*.

Surveys conducted between 2002-2006, detected bendiocarb resistance in *An. funestus,* populations using WHO bioassays and resistance levels increased over this period. The pyrethroid resistance is linked to elevated levels of monooxygenase activity and the carbamate resistance is predominantly due to an altered acetylcholinesterase. Pyrethroid resistance declined after lambda cyhalothrin was withdrawn. This process of monitoring resistance is incorporated into an integrated malaria decision support system, improving the malaria control programme's ability to make informed decisions and policy.

Monitoring the operational impact of insecticide usage for malaria control on *Anopheles funestus* from Mozambique

Michael Coleman[1], Sonia Casimiro[2], Janet Hemingway[3], Brian Sharp[1]

[1]Medical Research Council, South Africa, Durban, South Africa, [2]National Institute of Health, Maputo, Mozambique, [3]Liverpool School of Tropical Medicine, Liverool, United Kingdom

Introduction: Indoor residual spraying (IRS) has again increased for malaria control in Africa. DDT was re-introduced into Mozambique's IRS programme in 2005 and has become the main insecticide used for malaria vector control. Use of DDT in Mozambique is evidence-based, taking account of the susceptibility of Anopheles funestus and Anopheles arabiensis to all available insecticide choices and operational costs of spraying. To maintain integrity of control operations, monitoring the susceptibility status of both major vectors needs to be embedded within routine operations of the control programme.

Method: Sentinel sites were monitored for insecticide resistance using WHO bioassays and biochemical assays. Assays were conducted on 1-3 day old F1 offspring of field collected adult females to determine levels of insecticide resistance and gene resistance frequency in vector population.

Results: Lambda cyhalothrin replaced DDT for malaria control in Mozambique in 1993. However, resistance appeared quickly to this insecticide and, in 2000, the pyrethroid was phased out and the carbamate, bendiocarb, introduced. Low level resistance was detected by biochemical assay to bendiocarb in 1999 in both *An. funestus* and *An. arabiensis*.
Surveys conducted between 2002-2006, detected bendiocarb resistance in *An. funestus,* populations using WHO bioassays and resistance levels increased over this period. The pyrethroid resistance is linked to elevated levels of monooxygenase activity and the carbamate resistance is predominantly due to an altered acetylcholinesterase. Pyrethroid resistance declined after lambda cyhalothrin was withdrawn. This process of monitoring resistance is incorporated into an integrated malaria decision support system, improving the malaria control programme's ability to make informed decisions and policy.

Effects of soil type on incidence of *Agrotis ipsilon* (Hfn.) on potato, in Sudan

[1]Faiza E. Salah, [2]A. M. Zein Elabdien, [2]S. El –Tom, [2]A. Azrag

[1]Dept. Crop Protection, Gezira University, Medani, Sudan. P.O. Box 20; [2]Dept. Crop Protection, University of Khartoum, Sudan

The potato in the Sudan is growth in different soil types. The black cutworm (BCW), *Agrotis ipsilon* (Hfn), is one of the major pests of this crop. The present work objective was to study the effect of light soil (Karari site, Northwest of Omdurman) and heavy vertisol (Shambat site, Khartoum North) on the incidence of this pest.

The results revealed that potato grown in light soil exhibited higher BCW damage (29.7) than that grown in the heavy vertisol (16.13). The mean (%) BCW damage in the marketable tubers of the three tested potato varieties Alpha, Ajax and Formosa was 20.4, 32.6 and 36.1% for the light soils and 12.3, 14.2 and 21.9% for the heavy soils, respectively. Differences in BCW damage were highly significant between varieties and the soil types. Thus, it is advisable to grow potato in heavy soils.

From DDT to integrated pest management of Colorado potato beetle (*Leptinotarsa decemlineata* Say.) in Poland

Stefan Pruszynski, Danuta Sosnowska

Institute of Plant Protection, Poznan, Poland

Colorado potato beetle (CPB) (*Leptinotarsa decemlineata*) is an insect of high importance for Polish agriculture and Polish plant protection, as a result of intensive potato production and the role of this crop in the Polish economy. The area under potato in Poland amounted until quite lately to 2.7 mln ha, and presently amounts to about 0.7 mln ha. The pest is controlled by repeated insecticide applications to a yearly total of 1.0 mln ha, which is the greatest amount of insecticide used in Poland.

The first CPB was found in Poland in 1945 and a great invasion of this pest took place in 1950. The first compounds recommended were arsenates and in the following years the main pesticides were from chlorinated hydrocarbon group withdrawn from the use in beginning of the seventies. Those pesticides were replaced by organophoshorous insecticides, carbamates, synthetic pyrethroids and recently chitin synthesis inhibitors, neonicotinoid insecticides and phenylpyrazole.

The programme of scientific work started after CPB appearance and consisted the following subjects: biology and ecology of CPB, influence of appearance and control of CPB on the biocenosis of fields, methods of control, biochemical factors influencing the life cycle of these pest and forecasts and prognosis of appearance of pest. The possibility of using biological methods was also started.

Pioneering studies carried out at the beginning on the entomopatogenic fungi, mainly of the genus *Beauveria.* In 1959 trials of introduction in to Poland of natural enemies of CPB were undertaken and predatory bugs: *Perillus bioculatus* and *Podisus maculiventris*, (Pentatomidae, Heteroptera) were introduced. In 1967, an unsuccessful trial introduction of *Doryphorophaga doryphorae* (Tahinidae, Diptera) was undertaken. Research conducted on parasitic nematodes, protozoans, entomopathogenic fungi and registration of bioproduct Novodor contining a new strain of *Bacillus thuringiensis* should also be mentioned here.

During 1996/1997 joint Polish, Czech and USA research project on evaluation of the possibility of elaboration of biological and integrated CPB control was carried out. From that research we conclude that three treatments with either of the biopesticides Mycotrol (*Beauveria bassiana*) and Novodor prove level of control of *L. decemlineata* similar to two treatments with chemical pyrethroid. Economical aspects of CPB recommendation should be also discussed.

A forensic conflict: What happened to *Sarcophaga cruentata*?

Jacobus Hendrik Kolver, Theunis Christiaan Van der Linde

University of the Free State, Bloemfontein, South Africa

Introduction: Recent casework raised the question whether burning has an influence on the decomposition of and insect succession on bodies. Prof. T. C. van der Linde conducted a trial and found that *Sarcophaga cruentata* (Diptera: Sarcophagidae) was the most dominant decomposer due to the fact that burning resulted in sufficient desiccation of the carcasses to completely skip the initial phases of decomposition. The current study was undertaken to provide a more complete database of the influence of burning on insect succession and the decomposition process.

Methods: Three pig carcasses were doused with different volumes of petrol and burnt to different degrees (Slight = 1.5L. Medium =5L, Heavily = 10L). The decomposition of and insect succession onto these carcasses was compared to a control carcass.

Results: In the current study it was found that *Chrysomya albiceps, Chrysomya marginalis* and *Chrysomya chloropyga* (Diptera: Calliphoridae) were the dominant decomposers. Representative samples of larvae collected during decomposition revealed that *C. albiceps* larvae preferred to feed underneath the carcasses, with *C. marginalis* larvae feeding mostly inside and on top of the carcasses. *Sarcophaga cruentata* was only present in very low numbers and only a small number of larvae were found feeding on the carcasses. This conflictive finding raised the question: What happened to *S. cruentata*?

Conclusions: The correct question is: What happened to the other decomposers during Van der Linde's trial? Baseline research is vital, because the accuracy of determining the PMI is based on the knowledge base of the research scientist.

A forensic anomaly: Decomposition in the fast lane

Jacobus Hendrik Kolver, Theunis Christiaan Van der Linde

University of the Free State, Bloemfontein, South Africa

Introduction: Recent casework raised the question whether burning has an influence on the decomposition of and insect succession onto bodies. During a criminal investigation, the major contribution made by a forensic entomologist is an estimate of the postmortem interval (PMI), requiring the entomologist to analyse the species of insects present and the weather conditions that allow these species to be active. The accuracy of determining the PMI is therefore based on the knowledge base of the research scientist.

Methods: Three pig carcasses were doused with different volumes of petrol and burnt to different degrees (Slight = 1.5L. Medium =5L, Heavily = 10L). The decomposition of and insect succession onto these carcasses was compared to a control carcass.

Results: Burnt carcasses decomposed faster than a control carcass during summer conditions in previous trials, with a control carcass reaching the skeletonised stage within 11 to 14 days. During one trial peculiar results were obtained, with all four carcasses reaching the skeletonised stage within 3½ days. During January and February 2006 the average relative humidity was 68.7% and 75.8%, respectively. Average total rainfall during January was 147.6mm and for February 147.2mm. Average temperatures for January and February were 22.8°C and 21.5°C, respectively.

Conclusions: The anomaly was attributed to environmental conditions, since the decomposers remained the same as in other trials.

The ecology of insect-pathogen interactions and the implications for microbial control of locusts and grasshoppers

Matthew Thomas, Simon Blanford, Justine Klass

Penn State, University Park, PA, United States

Recent years have seen an upsurge in locust and grasshopper populations in many parts of the world. Environmentally sustainable approaches to locust and grasshopper control may be possible through the use of biopesticides based on entomopathogenic fungi. Unfortunately, the performance of these biopesticides is highly variable. Here we demonstrate that environmental temperature and host thermoregulatory behavior critically determine host resistance and pathogen virulence and hence, the pattern and extent of locust mortality after biopesticide applications. We quantify these effects through a combination of lab and field studies and use the information to develop a temperature-dependent model that enables us to predict the field performance of *Metarhizium anisopliae* var. *acridum*, the key fungal pathogen used in locust biopesticides. We demonstrate how the model can assist in the development of improved application strategies to optimize the performance of the biopesticide. More generally, we show how quantifying the effects of local environmental factors can enhance our understanding of the ecology and evolution of host-pathogen interactions.

Costly butterfly anti-aphrodisiac: direct and indirect arrestment of egg parasitoids

Nina Fatouros[1], Martinus Huigens[1], Joop van Loon[1], Marcel Dicke[1], Monika Hilker[2]

[1]Wageningen University, Department of Entomology, Wageningen, Netherlands, [2]Free University of Berlin, Berlin, Germany

Introduction: To locate tiny eggs of herbivorous host insects, egg parasitoids employ chemical cues either from the plant induced by host egg deposition or from the adult host stage[1]. The large cabbage white *Pieris brassicae* and its egg parasitoid *Trichogramma brassicae* were used to investigate, which chemical cues the wasps use to locate the butterfly eggs.

Methods: Bioassays were conducted in an olfactometer, an arena and a small Petri-dish. Female butterfly accessory gland secretion was analyzed by GC-MS.

Results: (1) Mated female butterflies were the most attractive to the wasps. During mating, *P. brassicae* females receive with the male ejaculate the anti-aphrodisiac benzyl cyanide (BC) that reduces the females' attractiveness for males[2]. Female wasps responded only to virgin female butterflies when they were treated with the anti-aphrodisiac showing that they spy on the pheromone. Once the wasps located mated host females, they mount them and hitch-hike to oviposition sites to parasitize freshly laid host eggs[3]. (2) *P. brassicae* egg depositions were shown to induce phytochemical changes in Brussels sprout plants arresting *T. brassicae* wasps[4]. The elicitor inducing this plant defence response was identified as BC present in butterfly gland secretion associated with eggs. When applied onto leaves, BC alone induced phytochemical changes that arrested the egg parasitoid. Thus, the male-transferred butterfly anti-aphrodisiac in egg secretions elicits oviposition-induced plant cues luring egg parasitoids[5].

Conclusions: Our results suggest that the anti-aphrodisiac pheromone incurs fitness costs for the butterfly both by mediating phoretic behaviour and plant defence traits.

The potential for novel malaria control interventions using fungal entomopathogen sprays

Matthew Thomas[1], Penny Hancock[2], Charles Godfray[3], Andrew Read[1]

[1]Penn State, University Park, PA, United States, [2]Imperial College, Silwood Park, United Kingdom, [3]Oxford University, Oxford, United Kingdom

Biopesticide sprays containing spores of infectious fungi are being evaluated as a novel method of controlling mosquito vectors of human diseases. Unlike chemical insecticides, fungal entomopathogens do not kill mosquitoes instantly. They can nonetheless be very effective at reducing disease transmission because malaria and other pathogens require time to mature in the vector, and thus mosquitoes do not transmit the disease until relatively late in their life. Different strains of fungi vary in virulence (the mean time to death) as well as the temporal pattern of mortality they induce. To compare the epidemiological impact of these different strains and to aid in the design of vector control programmes, we developed a model of a malaria-transmitting mosquito population that explicitly includes mosquito age and the duration of both fungal and malaria infections. The model shows how the density of infectious mosquitoes is influenced by the choice of fungal strain, and how the optimum choice may depend on parasite maturation time, a variable that is strongly affected by local environmental conditions. The effect of biopesticide coverage and the reduction in biopesticide efficacy with time after spraying is also explored. Overall, the results indicate that fungal biopesticides have the potential to cause considerable reductions in the density of malaria-transmitting mosquitoes while potentially imposing minimal selection pressure for evolution of resistance.

Identification and field evaluation of host plant volatiles attractive to sorghum chafer, *Pachnoda interrupta*

Wolde-Hawariat Yitbarek[1], Bengtsson Jonas[2], Seyoum Emiru[1], Jembere Bekele[1], Negash Merid[1], Hansson Bill.S[3], Hillbur Ylva[2]

[1]Addis ababa University, Addis Ababa, Ethiopia, [2]Swedish University of Agricultural Sciences, Alnarp, Sweden, [3]Max Planck Institute for Chemical Ecology, Jena, Germany

Introduction: Sorghum chafer is an economically important pest of sorghum in Ethiopia. The aim of the study is to develop host derived kairomones.

Methods: Headspace volatiles were collected from sorghum, *Sorghum bicolor* (Poaceae) and *Abutilon figarianum* (Malvaceae). The response of *Pachnoda interrupta* antennae, to these volatile compounds were recorded by coupled gas chromatography electroantennographic-detection (GC-EAD). Compounds were identified using coupled gas chromatography-mass spectrometry (GC-MS) and comparison with authentic samples. The attractivity of the identified compounds was tested under field condition.

Results: Antennally active compounds includes (*Z*)-3-hexen-1-ol, tridecane, 1-octen-3-ol and 1-octanol from sorghum and (*Z*)-3-hexen-1-ol, tetradecane, methyl salicylate and methyl anthranilate from abutilon. The identified compounds performed well in the field when they are tested as a blend than when they are applied individually. Moreover, the addition of compound(s) such as eugenol and methyl salicylate to sorghum blend and the addition of eugenol to abutilon blend have increased the trap catch more significantly indicating that these compounds could be part of the host components used by the insect in locating its hosts.

Conclusions: This study suggests that synthetic sorghum or *Abutilon* blends with the addition of eugenol /and methyl salicylate, can be used as a tool for monitoring or control by themselves or can be incorporated in IPM package of sorghum chafer control.

Changes on the species diversity of craneflies (Diptera: Limoniidae) by improvement cutting of Yambaru, a subtropical forest of Japan

Masahiro Sueyoshi, Hideaki Goto, Hiroki Sato

Kyushu Research Center, Forestry and Forest Products Research Institute, Kumamoto, Japan

Species richness and abundance of limoniid craneflies captured by emergence traps for logs were compared among forest stands of different ages after improvement cutting of natural forests (ICNF) and among different quantity and quality of decaying woods in Japanese subtropical forests. The objective of this study is to investigate the effects of ICNF on species diversity of saprophagous forest insects in the Yambaru, which is northern mountain area of the Okinawa Island, Ryukyus, Japan. Limoniids are one of major forest insects in species richness and abundance, inhabiting rotten woods at their immature stages.

From February 2006 to February 2007, we set 12 plots (10m*10m) in the eight stands aged 1-23 years after ICNF, one stand of 50 year-old ater clear-cutting, and one stand without cutting records. All decaying woods (fallen trees and branches) (> 3cm in diameter and > 50cm in length) in the plots were measured and their volumes were calculated. These decaying woods were classified into six categories by diameter and stages of decay, and then packed separately by a category in the emergence traps. Number of species and individuals of limoniids emerged from the decaying woods were counted. Humidity of each plot was recorded at summer and winter seasons.

Species richness and abundance of limoniids increase by ICNF and they decline along with succession of forests after ICNF. Supplement of rotten woods in middle size and the late stage of decay and high humidity at the stands conserve species diversity of limoniids in the Yambaru.

Genes and pheromones: The molecular basis of social parasitism in insect societies

Robin Moritz[2], Theresa Wossler[1]

[1]Stellenbosch University, Stellenbosch, South Africa, [2]Martin-Luther-Universitat, Halle-Wittenberg, Germany

Social parasitism is a fascinating phenomenon within the social insects where one species exploits the social resources of another species or conspecific. Many of these social parasites are unable to survive without their hosts. This relationship is obviously beneficial to the parasite, but is often detrimental to the host colony. The goal of the session will be to close the gap between organismal approaches dealing with parasitism and the molecular mechanisms driving the transition from sociality to parasitism. Social parasites are found throughout the social insect taxa and have been studied with various ant, bee and wasp species, with the intriguing host-parasite relationships in these species being used to explore many areas such as, behavioural interactions between species, colony recognition processes.

Genes and pheromones: The molecular basis of social parasitism in insect societies

Robin Moritz[2], Theresa Wossler[1]

[1]Stellenbosch University, Stellenbosch, South Africa, [2]Martin-Luther-Universitat, Halle-Wittenberg, Germany

Social parasitism is a fascinating phenomenon within the social insects where one species exploits the social resources of another species or conspecific. Many of these social parasites are unable to survive without their hosts. This relationship is obviously beneficial to the parasite, but is often detrimental to the host colony. The goal of the session will be to close the gap between organismal approaches dealing with parasitism and the molecular mechanisms driving the transition from sociality to parasitism. Social parasites are found throughout the social insect taxa and have been studied with various ant, bee and wasp species, with the intriguing host-parasite relationships in these species being used to explore many areas such as, behavioural interactions between species, colony recognition processes.

Sitotroga cerealella (Olivier) interactions with *Rhyzopertha dominica* F. and *Sitophilus* spp. on threshed and unthreshed sorghum columns

Brighton M. Mvumi[1], Tanya E. Stathers[2], Pete Golob[2], Denash P. Giga[1]

[1]University of Zimbabwe, Harare, Zimbabwe, [2]Natural Resources Institute, Chatham Maritime, Kent, United Kingdom, [3]formerly with University of Zimbabwe, Harare, Zimbabwe

Sitotroga cerealella is an important pest of stored grains in the tropics. While its biology has been well-researched in small laboratory experiments, comparatively little is known about its interactions with other key storage pests which share a similar ecological niche.

This study examined the spatial and temporal interactions of *S. cerealella* with *Rhyzopertha dominica* and *Sitophilus* spp. in columns of sorghum. Investigations were conducted, under controlled temperature and relative humidity, to determine the interactions between *S. cerealella* and *S. oryzae* on threshed grain and between *S. cerealella* and *R. dominica* on unthreshed grain over a 21-week storage period. A sampling procedure was developed to provide information on the comparative vertical dispersal pattern and populations changes of the insects in the grain after being introduced at the top of the grain columns.

In threshed sorghum, both *S. cerealella* and *S. oryzae* were concentrated in the top 30-35cm in single populations but the *S. cerealella* population was generally lower. In mixed populations, *S. oryzae* was the dominant species. In unthreshed sorghum, *S. cerealella* was more prolific than *R. dominica* at all depths as single species but was adversely affected by *R. dominica* in mixed populations although it still remained more abundant. The density of threshed grain prevented *S. cerealella* from performing its normal biological functions which require inter-granular space as was available in the unthreshed grain. The results are discussed in relation to the ecology of these storage pests and the implications for pest management strategies.

Social regulation of plasticity in the circadian clock of the honeybee (*Apis mellifera*)

Yair Shemesh, Mira Cohen, Guy Bloch

The Hebrew University of Jerusalem, Jerusalem, Israel

In honeybees (*Apis mellifera*) natural plasticity in circadian rhythms is associated with the division of labor that organizes their colonies. “Nurse” bees (typically < 2 weeks old) care for brood around-the-clock whereas bees older than 3 weeks of age typically forage for flowers with strong circadian rhythms. We found that nurses care for brood around-the-clock even under a light/dark illumination regime. Brain oscillations in the abundance of the putative clock genes *Period* and *Cryptochrom-m* were attenuated or totally suppressed in nurses as compared to foragers, irrespective of the illumination regime. However, nurses showed circadian rhythms in locomotor activity and molecular oscillations in brain clock gene expression shortly after transfer from the hive to constant laboratory conditions. The onset of their activity occurred at the subjective morning, suggesting that some clock components were entrained even while in the hive and active around-the-clock. These results suggest that the hive environment induces reorganization of the molecular clockwork. To test this hypothesis, we studied activity and brain clock gene expression in young bees that were confined to a broodless area on the honeycomb in a light/ dark illuminated observation hive. These bees experienced the hive environment and could interact with other bees, but not with the brood. By contrast to same-age nurses from these colonies, the confined bees showed molecular oscillations in clock gene expression and were more active during the day. These findings are consistent with the hypothesis that interactions with the brood modulate plasticity in the molecular clockwork of the honeybee.

Assessing the risk of introduction of *Bactrocera invadens* (Diptera: Tephritidae) into sub-Saharan Africa

Abraham Addo-Bediako

University of Limpopo, Polokwane, South Africa

Introduction: Trade is increasing significantly in Africa, and as trade increases, the risk of introduction of exotic pests would also increase. The entry of exotic species into a country can have devastating effect on Agriculture and export programmes. The fruit fly, *Bactrocera invadens* was recently recorded for the first time in Kenya, and has subsequently been reported in many countries in Africa.

Methods: The risk associated with the likelihood of introduction and establishment of *Bactrocera invadens* from infested areas to non infested areas within sub-Saharan Africa was assessed using both qualitative and quantitative risk assessment. The pathways considered for the analysis included movement of infested fruits from infested to non infested areas including hitchhikers, natural spread and vendors. The likelihood for establishment in various areas in the region was examined and patterns of spread described, in relation to the prevailing climatic conditions and host availability.

Results: The preliminary results using qualitative assessment indicated a high risk of introduction and establishment of the fruit fly due to the absence of effective mitigation measures to control illegal movement of fruits in certain parts of the region, the high reproductive potential of the pest, availability of suitable hosts, and favourable climatic conditions in most parts of the region.

Conclusion: It is important for countries to implement acceptable quarantine measures to reduce the risk of introduction.

The functional organization of size-related division of labor in bumblebees – from circadian rhythms and phototaxis to gene expression

Guy Bloch

The Hebrew University of Jerusalem, Jerusalem, Israel

Size, division of labor, and diurnal activity rhythms are correlated in colonies of the bumblebee *Bombus terrestris*. Large workers typically forage outside the nest with strong diurnal rhythms and low activity at night, whereas small bees typically care for (nurse) brood around the clock with weak or no diurnal rhythms. In laboratory conditions under constant darkness or a light: dark illumination regime, we found that activity rhythms were weaker, less stable, and developed at a later age in small (nurse-size) bees compared to their larger (forager-size) sisters. The brain expression of the "clock genes" *Period* and *Cryptochrome* appeared to oscillate with a stronger amplitude in foragers compared to nurses collected from free-flying colonies. More cells immunostained with antiserum against the clock neuropeptide Pigment Dispersing Factor in the brain of large, forager-size bees as compared to small nestmates. Taken together these findings reveal naturally-occurring attenuation or suppression in the circadian clock of small bees that is determined during pre-adult development. We also found stronger positive phototaxis in foragers relative to nurses. In one of two colonies, foragers had higher brain mRNA levels of *PKG*, a gene previously implicated in phototaxis in honeybees. This deficiency in clock function and phototaxis in small bees, however, does not result in pathology but rather appears to be functionally significant because it facilitates around-the-clock brood care activity in the nest, and therefore apparently improves divisions of labor and colony efficiency. These findings suggest that the social biology of bees influences traits of the circadian clock and phototaxis.

Assessing the risk posed by the invasion of *Harmonia axyridis* on European ladybirds. 1. Likelihood of encounter

Marc Kenis[1], Renate Zindel[1], Rene Eschen[1], Michael Majerus[2], Remy Ware[2]

[1]CABI Europe-Switzerland, 2800 Delemont, Switzerland, [2]Department of Genetics, University of Cambridge, Cambridge, CB2 3EH, United Kingdom

Introduction: The risk posed by the invasion of the harlequin ladybird, *Harmonia axyridis*, on native ladybirds in Europe can be considered as the product of the likelihood that a given ladybird species encounters *H. axyridis* in the field, and the consequence of this encounter, through direct predation, or competition for food. In this presentation we will focus on the likelihood of encounter, whereas the consequences of encounter will be the topic of the following presentation.

Methods: Ladybird larvae and adults were collected in various habitats and ecosystems recently invaded by *H. axyridis* in Switzerland. Niche overlap indices, cluster analyses and canonical component analyses were used to assess which species most often encounter *H. axyridis* in the field. Data were compared to published data found in the literature.

Results: *Harmonia axyridis* was found in nearly all habitats surveyed. However, niche overlap was greater with arboreal aphidophagous species found on broadleaved trees than with ladybirds found mainly or exclusively in grasslands or on conifer. The European species that will most likely encounter *H. axyridis* during their lifetime are *Calvia quatuordecimguttata*, *Adalia bipunctata*, *Adalia decempunctata* and *Oenopia conglobata*.

Conclusion: These results, once combined with data on the consequence of encounter, will allow us to list the species that will most likely suffer from the invasion of *H. axyridis* and to develop adequate management and conservation strategies.

Assessing the risk posed by the invasion of *Harmonia axyridis* on European ladybirds. 1. Likelihood of encounter

Marc Kenis[1], Renate Zindel[1], Rene Eschen[1], Michael Majerus[2], Remy Ware[2]

[1]CABI Europe-Switzerland, 2800 Delemont, Switzerland, [2]2Department of Genetics, University of Cambridge, Cambridge, CB2 3EH, United Kingdom

Introduction: The risk posed by the invasion of the harlequin ladybird, *Harmonia axyridis*, on native ladybirds in Europe can be considered as the product of the likelihood that a given ladybird species encounters *H. axyridis* in the field, and the consequence of this encounter, through direct predation, or competition for food. In this presentation we will focus on the likelihood of encounter, whereas the consequences of encounter will be the topic of the following presentation.

Methods: Ladybird larvae and adults were collected in various habitats and ecosystems recently invaded by *H. axyridis* in Switzerland. Niche overlap indices, cluster analyses and canonical component analyses were used to assess which species most often encounter *H. axyridis* in the field. Data were compared to published data found in the literature.

Results: *Harmonia axyridis* was found in nearly all habitats surveyed. However, niche overlap was greater with arboreal aphidophagous species found on broadleaved trees than with ladybirds found mainly or exclusively in grasslands or on conifer. The European species that will most likely encounter *H. axyridis* during their lifetime are *Calvia quatuordecimguttata*, *Adalia bipunctata*, *Adalia decempunctata* and *Oenopia conglobata*.

Conclusion: These results, once combined with data on the consequence of encounter, will allow us to list the species that will most likely suffer from the invasion of *H. axyridis* and to develop adequate management and conservation strategies.

HYMAToL: Assembling the Hymenoptera tree of life

HYMAToL Team, Michael Sharkey

Department of Entomology, University of Kentucky, Lexington, Kentucky 40546-0091, United States

Introduction: For almost five years a large international team of systematists have been working towards developing a robust phylogenetic hypothesis for the Hymenoptera at the superfamilial level. This talk will summarize the results obtained.

Methods: A number of separate analyses were conducted by various labs. These include standard morphological data and sequence information from 28S (domains 1-10), 18S, EF1α, and CO1, as well as data from numerous protein coding genes for a restricted number of exemplar taxa. Here we include all data in a total evidence analysis. Some of the later talks in this symposium will investigate and summarize results of analyses of the component datasets.

Results: Preliminary results corroborate many of the groupings that have recently been proposed by various authors based on single genes or intuitive analyses of diverse morphological data.

Conclusions: Although our concatenated analysis is not complete at the time of writing this abstract we expect that the data will support a monophyletic Proctotrupomorpha, and the classical symphytan position as a basal hymenopteran grade is also expected to be substantiated. The most interesting conclusions will center on the relationships among the remaining non-proctotrupomorpha Apocrita, especially the Evaniomorpha. Monophyly of this group and relationships among the included superfamilies remain problematic. It is hoped that further progress will be made with the concatenation of the component datasets.

HYMAToL: Assembling the Hymenoptera tree of life

HYMAToL Team, Michael Sharkey

Department of Entomology, University of Kentucky, Lexington, Kentucky 40546-0091, United States

Introduction: For almost five years a large international team of systematists have been working towards developing a robust phylogenetic hypothesis for the Hymenoptera at the superfamilial level. This talk will summarize the results obtained.

Methods: A number of separate analyses were conducted by various labs. These include standard morphological data and sequence information from 28S (domains 1-10), 18S, EF1α, and CO1, as well as data from numerous protein coding genes for a restricted number of exemplar taxa. Here we include all data in a total evidence analysis. Some of the later talks in this symposium will investigate and summarize results of analyses of the component datasets.

Results: Preliminary results corroborate many of the groupings that have recently been proposed by various authors based on single genes or intuitive analyses of diverse morphological data.

Conclusions: Although our concatenated analysis is not complete at the time of writing this abstract we expect that the data will support a monophyletic Proctotrupomorpha, and the classical symphytan position as a basal hymenopteran grade is also expected to be substantiated. The most interesting conclusions will center on the relationships among the remaining non-proctotrupomorpha Apocrita, especially the Evaniomorpha. Monophyly of this group and relationships among the included superfamilies remain problematic. It is hoped that further progress will be made with the concatenation of the component datasets.

Herbivory-boosted primary metabolism: A mechanism to alleviate fitness costs of plant vaccination

Andre Kessler[1], Rayko Halitschke[1], Jason Hamilton[2]

[1]Cornell University, Ithaca, NY, United States, [2]Ithaca College, Ithaca, NY, United States

Introduction: Herbivory is thought to be detrimental to plant fitness and the paradigm of an herbivore-induced metabolic shift in plants is emerging: photosynthetic processes are typically down-regulated, while resource allocation to defenses is increased in herbivore-attacked plants. This metabolic shift contributes to the fitness costs of induced plant responses. However, herbivore attack does not always decrease host plant fitness. In the native tobacco plant *Nicotiana attenuata* damage by leaf-chewing tobacco hornworms (*Manduca sexta*) but not cell content-feeding mirid bugs (*Tupiocoris notatus*) reduces plant fitness although both herbivores induce a similar plant defense response.

Methods: We used CO_2 gas exchange and chlorophyll fluorescence measurements to analyze herbivore-induced changes in photosynthetic activity of tobacco plants in response to both herbivore species—a hypothesized plant mechanism to alleviate the fitness costs of herbivore attack.

Results: We report a mirid-induced increase in photosynthetic activity as a compensatory plant response, which likely provides the resources to alleviate fitness costs of induced defenses and tissue loss. By applying isolated salivary secretions we demonstrate that component(s) of the mirid salivary secretions specifically elicit an increase in photosynthetic activity.

Conclusion: In contrast to earlier studies we suggest that the photosynthetic activity in herbivore-damaged leaves is not solely regulated by a simple feedback loop sensing the source/sink status of the leaf changed by tissue loss. It rather represents an herbivore elicitor-specifically induced mechanism of the plant to compensate for tissue loss and resources allocation to defense production.

The effects of six novel insecticides and an acaricide on *Galendromus occidentalis* Nesbitt, Acarina, Phytoseiidae

Noubar J. Bostanian[1], Howard Thistlewood[2], John M. Hardman[3], Gaetan Racette[1]

[1]Hortic. Dev.Res.Centre, St. Jean-sur-Richelieu, Qc., Canada, [2]Pacific Agri_food Res. Centre, Summerland,BC, Canada, [3]Atlantic Food and Hortic. Centre, Kentville, NS, Canada

Introduction: Biological control of phytophagous mites in orchards requires that pesticides used to manage other arthropod pests or diseases in orchards are innocuous to predacious mites as these are essential to keep phytophagous mites at non-injurious population levels. This study evaluates seven new pesticides currently used in western Canadian orchards.

Materials and Methods: *Galendromus occidentalis* collected from the Okanagan valley BC was reared in growth chambers in Quebec and used for toxicological tests in the laboratory. Leaf discs were treated with formulated pesticides at different concentrations and the pesticides were evaluated for toxicity to adults, fecundity, egg viability and repellency. Probit analyses were done to establish LC_{50} values and compare them with label rates.

Results: Acetamiprid and imidacloprid were toxic to the adults. Spinosad, thiamethoxam, thiacloprid, methoxyfenoxide and spirodiclofen were harmless. Significantly fewer eggs were laid by females exposed to acetamiprid and imidacloprid residues. The effect on fecundity was intermediate for thiamethoxam and spirodiclofen. None of the compounds were ovicidal. However, imidacloprid was toxicity to the larvae, as was spirodiclofen. Intrepid acetamiprid and thiacoprid were repellent to *G. occidentalis*.

Coclusion: The safest of the seven compounds evaluated were, in order, thiamethoxam, spinosad, and thiacloprid. Imidacloprid and acetamiprid showed adverse effects in at least three of the four parameters measured. The label rate for acetamiprid is 0.1 167g/ Land is 5.6 fold the LC_{50} (0.02 g/ L). The field rate for imidacloprid is 0.1600g/L and it is 10.2 fold the LC_{50} value of 0.0156g/L.

The effects of six novel insecticides and an acaricide on *Galendromus occidentalis* Nesbitt, Acarina, Phytoseiidae

Noubar J. Bostanian[1], Howard Thistlewood[2], John M. Hardman[3], Gaetan Racette[1]

[1]Hortic. Dev.Res.Centre, St. Jean-sur-Richelieu, Qc., Canada, [2]Pacific Agri_food Res. Centre, Summerland,BC, Canada, [3]Atlantic Food and Hortic. Centre, Kentville, NS, Canada, [4]Hortic.Dev. Res. Centre, St. Jean-sur-Richelieu, Qc., Canada

Introduction: Biological control of phytophagous mites in orchards requires that pesticides used to manage other arthropod pests or diseases in orchards are innocuous to predacious mites as these are essential to keep phytophagous mites at non-injurious population levels. This study evaluates seven new pesticides currently used in western Canadian orchards.

Materials and Methods: *Galendromus occidentalis* collected from the Okanagan valley BC was reared in growth chambers in Quebec and used for toxicological tests in the laboratory. Leaf discs were treated with formulated pesticides at different concentrations and the pesticides were evaluated for toxicity to adults, fecundity, egg viability and repellency. Probit analyses were done to establish LC_{50} values and compare them with label rates.

Results: Acetamiprid and imidacloprid were toxic to the adults. Spinosad, thiamethoxam, thiacloprid, methoxyfenoxide and spirodiclofen were harmless. Significantly fewer eggs were laid by females exposed to acetamiprid and imidacloprid residues. The effect on fecundity was intermediate for thiamethoxam and spirodiclofen. None of the compounds were ovicidal. However, imidacloprid was toxicity to the larvae, as was spirodiclofen. Intrepid acetamiprid and thiacoprid were repellent to *G. occidentalis*.

Coclusion: The safest of the seven compounds evaluated were, in order, thiamethoxam, spinosad, and thiacloprid. Imidacloprid and acetamiprid showed adverse effects in at least three of the four parameters measured. The label rate for acetamiprid is 0.1 167g/ Land is 5.6 fold the LC_{50} (0.02 g/ L). The field rate for imidacloprid is 0.1600g/L and it is 10.2 fold the LC_{50} value of 0.0156g/L.

Present and future of GM corn in Romania

Ioan Rosca, Rada Istrate, Constantin Popov

[1]*University of Agricultural Sciences and Veterinary Medicine; Bucharest, Bucharest, Romania,*
[2]*Agricultural Research and Development Institute Fundulea, Fundulea, Romania*

Introduction: The maize, cultivated on three million ha in Romania, is one of the most important crops, and the crop technology involves complex protection measures versus pests.

Methods: The main problems for corn in Romania are weeds and pests, after corn weevil (*Tanymecus dilaticollis*) and Western Corn Rootworm (*Diabrotica virgifera*) the most important lepidopterous pests are *Ostrinia nubilalis* and *Helicoverpa armigera* which affected more than 0.3 million of ha.. Possible impact of Roundup Ready® or Bt corn on the trophic chains in agrocenosis is of concern to farmers who cannot any longer afford expensive mechanical or chemical control of weeds and pests, to policy makers who recommend expansion of maize fields, and to organisations and societies interested in environment conservation. Our objective was to evaluate potential impact of Roundup maize on the epigeic fauna and on the useful fauna on the corn plants.

Results: Data obtained regarding resemblance of whole insect fauna from the corn variants investigated represented by value of Sörensen index (71.43, 79.25, 86.66 in 2000 and 91,3 in 2004), confirmed the hypothesis that genetically modified corn (Bt or RR), has no impact on the insect fauna in corn field. In conclusion it is possible to affirm that the cultivation of genetically modified corn (Bt or RR), has no influence on the epigeic fauna or plant-dwelling predators. Structure of predatory Heteroptera species seems to be an indicator for biodiversity in corn fields, because being predaceous, their number and species composition could reflect changes in whole corn agro ecosystem.

Present and future of GM corn in Romania

Ioan Rosca, Rada Istrate, Constantin Popov

[1]*University of Agricultural Sciences and Veterinary Medicine; Bucharest, Bucharest, Romania,*
[2]*University of Agricultural Sciences and Veterinary Medicine; Bucharest, Bucharest, Romania,*
[3]*Agricultural Research and Development Institute Fundulea, Fundulea, Romania*

Introduction: The maize, cultivated on three million ha in Romania, is one of the most important crops, and the crop technology involves complex protection measures versus pests.

Methods: The main problems for corn in Romania are weeds and pests, after corn weevil (*Tanymecus dilaticollis*) and Western Corn Rootworm (*Diabrotica virgifera*) the most important lepidopterous pests are *Ostrinia nubilalis* and *Helicoverpa armigera* which affected more than 0.3 million of ha.. Possible impact of Roundup Ready® or Bt corn on the trophic chains in agrocenosis is of concern to farmers who cannot any longer afford expensive mechanical or chemical control of weeds and pests, to policy makers who recommend expansion of maize fields, and to organisations and societies interested in environment conservation. Our objective was to evaluate potential impact of Roundup maize on the epigeic fauna and on the useful fauna on the corn plants.

Results: Data obtained regarding resemblance of whole insect fauna from the corn variants investigated represented by value of Sörensen index (71.43, 79.25, 86.66 in 2000 and 91,3 in 2004), confirmed the hypothesis that genetically modified corn (Bt or RR), has no impact on the insect fauna in corn field. In conclusion it is possible to affirm that the cultivation of genetically modified corn (Bt or RR), has no influence on the epigeic fauna or plant-dwelling predators. Structure of predatory Heteroptera species seems to be an indicator for biodiversity in corn fields, because being predaceous, their number and species composition could reflect changes in whole corn agro ecosystem.

Landscape effects of insect resistant GM crops

Nicholas Storer[1], Galen Dively[2], Rod Herman[1]

[1]Dow AgroSciences LLC, Indianapolis, IN, United States, [2]University of Maryland, College Park, MD, United States

Putative effects of incorporating GM crops into agricultural landscapes have long been proposed. Here we examine the evidence for such effects within dynamic and heterogeneous agroecosystems, based on widespread commercial deployment insect resistant *Bt* crops for over 10 years. While there is good evidence for changes in the population sizes of several target pest populations and for the increasing importance of some secondary pests, there is no evidence of landscape-level effects on non-target species. These findings were anticipated by laboratory and field characterization of the high specificity of action of the *Bacillus thuringiensis* proteins currently deployed, and the equivalence of the GM crops to their non-transformed conventional counterparts. Indirect effects of the insect resistant GM crops on the agricultural ecosystems due to multitrophic exposure, loss of prey, or reduction of prey quality, are generally negligible compared with the direct effects of other more dramatic environmental manipulations that are standard agricultural practices.

Insulin-signaling regulates static allometry in *Drosophila*

Alexander Shingleton

Michigan State University, East Lansing, United States

The regulation of static allometry, the relationship between final body size and organ size, is a fundamental developmental process that determines the shape of an animal. Nevertheless, the mechanisms that underlie this regulation remain virtually unknown. Here we elucidate the developmental regulation of static allometry in *Drosophila.*

Most organs scale isometrically with body size in *Drosophila*. However, the male genitals scale hypoallometrically with body size, and are approximately the same absolute size irrespective of body size. Variation in developmental nutrition is a major regulator of body and organ size in *Drosophila*, and we show that the hypoallometry of the genitals reflects their relative insensitivity to reduced developmental nutrition compared to other organs. The insulin-signaling pathway regulates growth with respect to nutrition in all animals, and suppression of the pathway's activity has a less of an effect on the size of the genitals than on other organs. Thus, variation among organs in their sensitivity to changes in insulin-signaling, and hence developmental nutrition, appears to underlie variation in their scaling relationships with each other and with body size. We present data indicating that it is the organ-specific expression or activity of insulin-signaling genes that regulates insulin sensitivity, and show that altering the expression of these genes in a single organ is sufficient to alter that organ's allometric relationships. These data implicate the insulin-signaling pathway – which plays major roles in longevity, diabetes and the regulation of cell, organ, and body size – as a key regulator of allometry and organismal shape.

Soil-applied imidacloprid is translocated to nectar and kills nectar-feeding beneficial insects in landscapes

Vera Krischik

University of Minnesota, St. Paul, MN, United States

Currently, few published studies quantify the concentration of imidacloprid in nectar and its affects on behavior and survival of nectar feeding beneficial insects. Since imidacloprid is widely used in greenhouse on plants later installed in landscapes and on ornamentals and crops, the potential non-target effects of imidacloprid on beneficial insects, such as lady beetles, lacewings, parasitoids, and bees is important. Soil-applied imidaclopird (Marathon 1%G) was imidacloprid translocated to nectar and altered behavior and survival of beneficial insects, such as pink lady beetle, *Coleomegilla maculata* (DeGeer), (Smith and Krischik 1999), green lacewing, *Chrysoperla carnea* (Stephens), (Rogers et al. 2007), and *Anagyrus pseudococci* (Girault) parasitoid (Krischik et al. 2007). Residue analysis of nectar from *Asclepias curassavica* (L.) treated with 1X or 2X label rate of soil -applied imidacloprid (Marathon 1%G) showed imidacloprid levels in flower nectar as 2 ppb in controls, 15 ppb in 1X, and 27 ppb in 2X treated plants, which is similar to levels found in another species, *Fagopyrum esculentum* (Moench) (0 control, 16 ppb 1X, and 29 ppb 2X) (Krischik et al. 2007). Residue analysis detected imidaclopird in nectar at the last sample date 63 d after application. A second application 7 mo later resulted in 0 ppb in controls, 53 ppb in 1X, and 110 ppb in 2X treated plants. The hydroxy and olefin metabolites were also found in nectar. Higher levels of residue may be due to imidacloprid persistence in nectar, since it can persist in tree leaves 1 to 2 years after application.

Segmentation in the honeybee (*Apis mellifera*)

Peter Dearden, Megan Wilson

University of Otago, Dunedin, New Zealand

Insect segmentation is a well-studied developmental pathway in flies and segmentation genes have been studied in a few other insects. We employ a systems-biology approach to understand how this complex developmental cascade evolves. Using the Honeybee, with its recently sequenced genome, as our model, we have investigated long-term evolution of this pathway. In this talk I will present our recent studies of *giant* and *even-skipped* function and regulation, using RNA interference and transgenic *Drosophila* to identify differences in the control of segmentation from the fly paradigm, and to discover how those differences may have evolved.

Microbial control of rhinoceros beetle, *Oryctes rhinoceros* (Coleoptera: Scarabeidae) on oil palm in Malaysia

Ramle Mslim[1], Norman Kamarudin[1], Mohd Basri Wahid[1], Trevor A. Jackson[2], Idris A. Ghani[3]

[1]Malaysian Palm Oil Board, PO Box 10620, 50720 Kuala Lumpur, Malaysia, [2]AgResearch, Gerald Street, PO Box 60, Lincoln, New Zealand, [3]National University of Malasysia, Faculty of Science and Technology, UKM 43600 Bangi Selangor, Malaysia

Introduction: *Oryctes rhinoceros* is a major pest of oil palm causing significant yield losses to the plantations. Two types of microbes, the fungus *Metarhizium anisopliae* (Ma) and the *O. rhinoceros* virus (OrV) were used to control the beetle in several plantations in Malaysia.

Methods: The Ma was applied by (i) direct spraying of spore solutions, (ii) broadcasting of granule made from mycelium and (iii) by inoculation trap to disseminate the spores into the beetle breeding sites. The OrV was introduced by releasing the inoculated young adults into the field.

Results: Application of fungal spore solutions reduced the beetle population, especially the immature stages. This technique, when applied onto the breeding sites significantly reduced the third instars larvae, pre-pupa and pupae of the beetle. Application of the granule of the Ma was much easier than the spore solution. The granule was supplemented with the nutrient for fungal growth, which gave longer effect in the field. The use of inoculation trap for dissemination of fungal spores is simple. The attracted adults get infected in the trap and carry the spores and contaminating their habitat. High trap density was required to ensure the effectiveness of this technique in controlling the beetle. The release of OrV gradually reduced the adult population, followed by the reduction of the palm damage. The released virus spread all over the field after a year of introduction.

Conclusions: The Ma is targeted for reducing the immature stage and the OrV is for the adult stage of the rhinoceros beetle. Application of both microbes reduced the population of the beetle.

The role of haemoglobin in diving insects

Philip Matthews

The University of Adelaide, Adelaide, South Australia, Australia

Introduction: Aquatic backswimmers (Hemiptera: Notonectidae) use haemoglobin and a small bubble of air held on the abdomen to supply them with oxygen while underwater. Unusually for an aquatic insect, they have a pelagic habit, entering a protracted phase of near-neutral buoyancy during every dive. To determine haemoglobin's role in buoyancy regulation and supplying oxygen for respiration, the oxygen partial pressure (PO_2) and volume of the backswimmer's air bubble, as well as the insect's buoyancy, were measured.

Methods: Fibre optic oxygen probes were placed in the air bubbles of submerged backswimmers (*Anisops deanei*) to measure changes in PO_2 during a dive. These data were analysed to determine the haemoglobin's oxygen-binding properties. Changes in buoyancy were measured by securing backswimmers to a submerged rod suspended from an electronic balance. Air-bubble volume was determined indirectly from buoyancy measurements and by collecting air bubbles from free-diving insects.

Results: Following an initial linear decline, the PO_2 of the backswimmer's bubble temporarily plateaus as oxygen is released from the haemoglobin. This serves to stabilise the volume and buoyancy of the air bubble while supplying the insect's respiration. The oxygen-binding properties of backswimmer haemoglobin in critical in establishing this plateau by unloading over 50 % its oxygen across a very narrow (4.14 – 3.30 kPa) range of oxygen partial pressures.

Conclusions: Haemoglobin is fundamental to the backswimmer's ability to occupy its pelagic niche. The haemoglobin's oxygen-binding properties ensure that the PO_2 and volume of the air bubble are stabilised at a level where the insect is neutrally buoyant.

The biological control of codling moth using entomopathogenic nematodes

Jeanne de Waal, Antoinette Malan, Matthew Addison

University of Stellenbosch, Western Cape, Stellenbosch, South Africa

Introduction: Previous control measures of codling moth, *Cydia pomonella* (L.) Lepidoptera: Tortricidae), an established key pest of apple and pear fruit in South Africa, was grounded predominantly on the use of broad spectrum insecticides. Concerns such as resistance of codling moth to certain insecticides and the negative environmental effect of continuous pesticide use have forced the industry to consider alternative methods which are environmentally friendly and serve as an alternative to pesticides, such as entomopathogenic nematodes (EPNs). Using EPNs as inundatively applied microbial biopesticides for the control of codling moth in South African apple and pear orchards was therefore investigated.

Methods: A survey was conducted to isolate endemic EPN strains from soils. Strains obtained were molecularly identified to species level. Strain efficacy was examined in the laboratory. Overall field-performance of the most promising strain was investigated, whereby the optimum concentration nematodes required per tree was determined and the addition of adjuvants to increase efficacy was investigated in a quantitative spray-deposition assessment.

Results: Several endemic strains were isolated from 202 soil samples collected, with *Heterorhabditis zealandica* being the predominant species. All isolates were effective against codling moth larvae and morphologically suitability. The most promising isolate selected (SF41, *H. zealandica*) performed best at 25℃, 90% RH and at an appropriate concentration in laboratory experiments. Field trials indicate that EPNs are promising candidates to be used for the control of codling moth.

Conclusion: Entomopathogenic nematodes have great potential for the control of codling moth as part of an integrated pest management strategy under local conditions.

The biological control of codling moth using entomopathogenic nematodes

Jeanne de Waal, Antoinette Malan, Matthew Addison

University of Stellenbosch, Western Cape, Stellenbosch, South Africa

Introduction: Previous control measures of codling moth, *Cydia pomonella* (L.) Lepidoptera: Tortricidae), an established key pest of apple and pear fruit in South Africa, was grounded predominantly on the use of broad spectrum insecticides. Concerns such as resistance of codling moth to certain insecticides and the negative environmental effect of continuous pesticide use have forced the industry to consider alternative methods which are environmentally friendly and serve as an alternative to pesticides, such as entomopathogenic nematodes (EPNs). Using EPNs as inundatively applied microbial biopesticides for the control of codling moth in South African apple and pear orchards was therefore investigated.

Methods: A survey was conducted to isolate endemic EPN strains from soils. Strains obtained were molecularly identified to species level. Strain efficacy was examined in the laboratory. Overall field-performance of the most promising strain was investigated, whereby the optimum concentration nematodes required per tree was determined and the addition of adjuvants to increase efficacy was investigated in a quantitative spray-deposition assessment.

Results: Several endemic strains were isolated from 202 soil samples collected, with *Heterorhabditis zealandica* being the predominant species. All isolates were effective against codling moth larvae and morphologically suitability. The most promising isolate selected (SF41, *H. zealandica*) performed best at 25℃, 90% RH and at an appropriate concentration in laboratory experiments. Field trials indicate that EPNs are promising candidates to be used for the control of codling moth.

Conclusion: Entomopathogenic nematodes have great potential for the control of coding moth as part of an integrated pest management strategy under local conditions.

IRM policies and compliance: A stakeholder's perspective from India

Dattatray Shirale, Shivraj Devkar, Prasanna Padmasali, Chandrashekhar Chaporkar, Srinivas Parimi

Maharashtra Hybrid Seeds Co. Ltd., Jalna, Maharashtra, India

Bollgard® (Bt) cotton in India is commercialized and cultivated on approximately 60% of the cotton growing area. Bt cotton in India is grown since 2002 and recently Bollgard II® was commercialized in 2006. Since Bollgard® was commercialized there are around 25 companies marketing more than 150 Bollgard® and Bollgard II® hybrids in different parts of the country. The production of cotton in India doubled in the past six year period of Bt cotton commercialization. One of the regulatory requirements for the sustainability of the Bt crops in India is to plant a refuge besides resistance monitoring in populations as a part of Insect resistance management (IRM) plan. Current IRM plan for the Bt cotton necessitates the growers to plant 5 rows or 20% crop as refuge planted around the Bt crop. Increase in yield and monetary benefits from growing Bt cotton encouraged growers to plant more acreage each year. However, planting the crop following the regulatory requirements has been a challenge for the stakeholders. We conducted a survey among 400 cotton growers from different part of the country with an objective to better understand these challenges and refuge compliance among them. In this presentation we discuss various issues related to IRM plan(s), awareness among growers through various stakeholders specifically the technology providers, refuge compliance, and/or any reasons for non-compliance of IRM plans.

Insects, plants, diversity and spatial scale in the Cape

Serban Proches[1], Richard Cowling[2]

[1]University of KwaZulu-Natal, Durban, South Africa, [2]Nelson Mandela Metropolitan University, Port Elizabeth, South Africa

It has been argued that the remarkable plant diversity of the Cape Floristic Region is not paralleled by an equally diverse insect fauna. Here we present the results of extensive plant surveys and insect collections in various vegetation types in the Cape. We show that fynbos vegetation (a mediterranean-type shrubland characteristic to the Cape) is not particularly insect-poor, and that its insect fauna is largely vegetation-specific, although sharing species with both arid vegetation ("karoo") and summer-rainfall grasslands. Subtropical thickets in the Eastern Cape have a distinctive insect fauna of rainforest affinities. This latter vegetation type is composed of distantly related plants (high phylogenetic diversity), thus accommodating a high diversity of insect herbivores at the local scale; however, insect species turnover between thicket patches is limited. On the other hand, fynbos, similar to karoo and grassland vegetation, has lower plant phylogenetic diversity, a consequence of most component lineages having radiated recently. Nevertheless, numerous insect species from fynbos, grassland and karoo, in particular those belonging to flightless lineages, have localized distributions, given the highly dissected geography of the region.

Insect versus wind pollination in the South African cycad *Stangeria*

Serban Proches[1], Steven Johnson[2]

[1]University of KwaZulu-Natal, Durban, South Africa, [2]University of KwaZulu-Natal, Pietermaritzburg, South Africa

Stangeria eriopus represents an isolated South African cycad lineage previously thought to be wind pollinated. We found the scent of *Stangeria* to mimic that of rotten fruit, the main volatiles being esters (ethyl and propyl acetate, 1-butanol, 2-methyl-acetate), ketones and aldehydes. Unlike in most cycads, there was no evidence of thermogenesis. The main insect visitors were sap and rove beetles (Coleoptera: Nitidulidae, Staphilinidae), and fruit flies (Diptera: Drosophilidae), but only sap beetles were able to effect pollination under experimental conditions. Since sap beetles are also pollinators of *Cycas* and of several ancient angiosperm families, their role in the pollination of *Stangeria* adds interesting details to the role this group has played in the history of plant-pollinator interactions.

Evolution of fungal enzymes in the attine ant symbiosis

Henrik H. De Fine Licht, Morten Schiøtt, Jacobus J. Boomsma

Centre for Social Evolution, University of Copenhagen, DK-2100 Copenhagen, Denmark

The attine ant symbiosis is characterized by ancient but varying degrees of diffuse co-evolution between the ants and their fungal cultivars. Domesticated fungi became dependent on vertical transmission by queens and the ant colonies came to rely on their symbiotic fungus for food and thus, indirectly, on fungal enzymes to break down the plant material brought in by the ants as fungal substrate. The more than 210 extant fungus-growing ant species differ considerably in colony size, social complexity and substrate-use. Only the derived leaf-cutting ants are specialized on using fresh leaves as garden substrate, whereas the more basal genera use leaf litter, insect feces and insect carcasses. We hypothesized that enzyme activity of fungal symbionts has co-evolved with substrate use and we measured enzyme activities of fungus gardens in the field to test this, focusing particularly on plant decomposing enzymes. We further obtained gene sequences coding for specific enzymes and used them to reconstruct the fungal symbiont phylogeny and to compare the trees obtained with those known from sequence information of genes that have no specific link to enzyme function. Differences in fungus garden enzyme activity across ant genera could indeed be partially explained by substrate differences. This implies that fungal enzyme activity has likely coevolved with the genus- or species-specific substrates that the ants use to manure their fungus garden. Plant decomposing enzymes are thus not only essential for the symbiosis in general, but have contributed specifically to the evolution of the symbiosis.

The value of changing phenotypes: Herbivore population consequences of induced plant responses

Andre Kessler[1], Katja Poveda[2]

[1]Cornell University, Ithaca, NY, United States, [2]Georg August University, Göttingen, Germany

Introduction: Plants respond to insect herbivore damage with an array of changes in primary and secondary metabolism. Some of these metabolic changes can cause increased resistance of the plant to current and subsequent herbivore attack and may function as direct and indirect defenses. Such induced resistance effects have been extensively studied but very little is known about their role in structuring arthropod communities, influencing insect herbivore population dynamics, and conversely the distribution of herbivory within plant populations.

Methods: We used field and laboratory choice and preference bioassays and analyzed the herbivore-induced secondary metabolite production of the plants to study the effect of herbivore-induced responses of *Solidago altissima* plants on the population dynamics of the larvae of the specialist Chrysomelid beetle *Trirhabda virgata*.

Results: *T. virgata* damage results in an increased production of secondary metabolites that is correlated with a higher resistance of the plants to beetle attack. Moreover, *Trirhabda* larvae move actively away from the damage site and choose undamaged over damaged plants on their way through the plant population. This plant response-mediated alteration in larval behavior causes a change of beetle and damage distribution within the plant population over the season, from a clumped distribution early in the season to an equal distribution later in the season.

Conclusion: The data demonstrate that herbivore-induced plant responses can have dramatic effects on herbivore population dynamics, which likely has significant effects on community composition and productivity.

The ecology and acoustic biology of the duetting bushcricket *Leptophyes punctatissima*.

Patricia Ash, Marion Hall, David Robinson

The Open University, Milton Keynes, United Kingdom

Introduction: The flightless bushcricket *Leptophyes punctatissima* communicates using ultrasound. We report the habitat and food plants exploited, the distribution of instars in the habitat and the sites from which males call, part of a long-term study of acoustic biology and mate choice.

Methods: Three sites were studied. They were surveyed using belt transects and the percentage cover of all the species of plant in each square meter, were recorded. The position of each immature *Leptophyes* instar and the plant that it was on when first spotted was noted. Observations on adult mating behaviour were made at night adults being located using directional ultrasound detectors. Food choice experiments were conducted with immature instars.

Results: Although *Leptophyes* is present at all sites, the vegetation is different. Wood sage is only present at one site and early instars were found almost exclusively on that plant, usually clumped and close to the ground. Food choice experiments in the laboratory showed that the immature instars preferred wood sage, even if they had been collected from a habitat where it was absent. Mating is rapid and difficult to observe and some adult males have been located singing 14m above the ground implying a long journey down for the female to lay her eggs.

Conclusions: The results suggest that there are food preferences and, given the small size of the hatchlings, the site at which eggs are laid the previous year would be expected to be close to an acceptable food plant.

Towards agro-ecological management of sugarcane stalk borers in South Africa and Reunion: a synthesis of results and perspectives

François-Régis Goebel, Mike Way

CIRAD, Montpellier, France

Introduction: In the last 10 years surveying and formal experiments have concentrated on elucidating the main factors that impact on the major sugarcane borers *Eldana saccharina* Walker and *Chilo sacchariphagus* Bojer on commercial and small-scale farms in South Africa and Réunion.

Results: Synergies appear in the research findings for these species. The following factors had a significant impact on damage levels : cultivar type, age of cane, soil nitrogen and soil silicon level, and biodiversity richness. As such, an Integrated Pest Management (IPM) approach is proposed for control of these particular pest species. The IPM strategy would ideally encompass a combination of recognised control tactics, principles and complementary management practices. In this instance these would likely include implementation of biological control programmes, use of breeding resistant varieties, adoption and monitoring of correct applications of fertilizer in terms of quantities and promoting farming practices among grower communities that conserve habitat diversity on sugarcane farms. Levels of complexity of the landscape structure, coupled with the existence of a fragmented habitat, also impact on the population dynamics of pest species. Accordingly cognisance of these factors is also important in our endeavour to develop a holistic management strategy within sugarcane fields.

Conclusions: Following on from past findings this paper discusses future research work that take into account all the ecological processes influencing the abundance, richness, and diversity of insects in these specific sugarcane agrosystems.

Sensory Map Formation in the Drosophila Olfactory System

Marc Lattemann, Oezkan Adymir, Britta Kuhlmann, Thomas Hummel

WWU Muenster, Muenster, Germany

Introduction: A striking feature of olfactory system organization is the evolutionarily conserved arrangement of olfactory receptor neuron (ORN) terminals into an odortopic map. In mouse and Drosophila, ORNs expressing the same odorant receptor, distributed over the surface of the sense organ, form connections to a common set of CNS dendrites spatially segregated into distinct synaptic glomeruli. In the mouse, odorant receptors play an instructive role in ORN targeting but, despite the anatomical and physiological similarities, targeting of fly ORNs seems to be independent of odorant receptor function.

Methods: To uncover the molecular basis of wiring specificity in the Drosophila olfactory system, we have performed a large-scale genetic mosaic screen and identified mutations that lead to ORN class specific changes in axon targeting or odorant gene expression.

Results: Here we present the functional characterization of two signaling molecules, Dscam and Semaphorin-1a. We demonstrate that *Dscam* mutant antennal ORNs frequently converge onto ectopic glomeruli throughout the AL but that these ectopic glomeruli still contain single ORN class innervation, indicating that ORN axons of the same sensory class recognize each other and induce glomerular convergence independent of their target area. In contrast, removal of Sema1a in ORN-specific somatic mosaics does not interfere with the axonal projection towards the AL target area but disrupt local axon sorting between neighboring glomeruli.

Conclusions: From these data we propose a model in which connection specificity in the olfactory system is achieved through a series of inter-axonal signaling events leading to a progressive refinement into distinct synaptic units.

Phylogeny of Cleroidea (Coleoptera) inferred from 18S ribosomal DNA

Milada Bocakova, Ladislav Bocak

[1]*Department of Biology, Faculty of Education, Palacky University, Olomouc, Czech Republic,*
[2]*Department of Zoology, Faculty of Science, Palacky University, Olomouc, Czech Republic*

The Cleroidea is one of important beetle superfamilies housing almost 10,000 species of worldwide distribution, and belong to a very diverse Cucujiformia series. The modern concept of Cleroidea proposed inclusion of melyrids, while other groups as dermestids, passandrids, bothriderids, and ciids were excluded. Currently the Cleroidea consists of 7 families. Distinctive coloration of some checkered beetles and other groups as well as extensible glands of Malachiinae appear to be aposematic signal. While basal cleroid groups are fungivorous (Trogossitidae: Peltinae), many cleroids are predaceous or polyphagous, and a lot of Melyridae feed preferentially on pollen. The monophyly of this group was challenged by latest molecular analyses. In this study we performed molecular phylogenetic analyses of small ribosomal subunit sequences (18S) of 38 outgroup and 115 cleroid taxa representing 5 families. In contrast to previous published molecular analyses, the results show cleroids including Phloiophilidae as monophyletic group although the low support values are very low. The internal relationships show several features never revealed before. The Trogossitidae were shown to be a paraphyletic assemblage. Results of our analyses further placed the subfamily Trogossitinae as a sister group of checkered beetles, which is in agreement with predatory feeding habits of these groups. Further, the Melyridae were shown to include Prionoceridae, while lately proposed family Mauroniscidae was supported as one of early cleroid splits.

Reasons for successes and failures of microbial control products and businesses in Europe

Juerg Huber

Julius Kühn-Institute, Institute for Biological Control, Darmstadt, Germany

In Europe (EU) about 8 microbial strains are approved as active ingredients of pesticides and more than 20 are in the pipeline, waiting for registration (most of them “old” a.i.).

Success or failure of a product depends on two key elements: the product itself and the market situation (the real market, not the potential one). The market has to be shared with competitors and is further reduced by the fact that in most cases only a small proportion of the potential buyers are inclined to actually buy the product. Therefore, apart from an optimal selection of the target pest, the other factor a company can try to manipulate in order to increase the sales of its products, is the behaviour of the buyer.

What reasons a farmer could have to choose a specific microbial control agent ? (1)The most convincing argument is always low costs. This can be achieved either by a low price of the product, or by financial support (through subsidies from the government - as they are foreseen in the framework of the EU modulation procedures – or directly from consumers, willing to pay better prices for agricultural produce grown without chemical pesticides). (2)The product has to be effective and reliable. (3)A farmer might be forced to use a biocontrol agent if no conventional alternatives are available (either because the pest is resistant against most other means of control or because legislation bans the use of chemical pesticides for reason of environmental or consumer protection). (4) Finally, the decision of a farmer can also be influenced by pressure from the public (to use environmentally more friendly or safer methods) and by good marketing and farmer’s support from the side of the company.

Some of the point listed above can hardly be influenced by the producer; they are the realms of legislators (pesticide ban; registration costs) or even the individual consumer. But several traits which can decide about success or failure of a product are under the control of the producer: A successful biopesticide has to be (1) effective and reliable (right choice of microbial; formulation), (2) cheap to produce (production method), and (3) in demand (market analysis; promotion; support). Producers are well advised to concentrate on these features rather than complain about issues beyond their control as, e.g. high registration cost or hurdles built up by regulators against their products.

The biotic and abiotic controls on ant community structure

Sarah Wittman[1], Nathan Sanders[2], Aaron Ellison[3], Erik Jules[4], Nicholas Gotelli[1]

[1]University of Vermont, Burlington, VT, United States, [2]University of Tennessee, Knoxville, TN, United States, [3]Harvard Forest, Harvard University, Petersham, MA, United States, [4]Humboldt State University, Arcata, CA, United States

Introduction: In ant communities the interaction of competition and temperature has been used to describe diversity patterns on local and continental scales, how communities are affected by disturbance, and how non-native species are able to invade and dominate assemblages. We pair null model analyses with field and laboratory experiments to disentangle the role of interspecific competition and temperature in controlling the structure of ground-foraging ant communities in forests of the Siskiyou Mountains of southern Oregon.

Methods: To assess the potential role of competition as a structuring agent, we used null model analyses to ask whether species partition either space or time. To understand the role of thermal tolerance as a structuring agent, we conducted thermal tolerance experiments in the laboratory. Finally, we conducted a field experiment in which we manipulated temperature and competition by a dominant species (*Formica moki*) to investigate which factor had the greater impact on the ant community.

Results: Although the foraging activity of species broadly overlapped across a range of times and temperatures, the peaks of activity for each species were spaced at regular intervals of soil surface temperature. Species decreased abundance in shaded plots was a direct effect of shading and was not an indirect effect of competitive interactions. Most strikingly, the response of species to shade additions was successfully predicted by the results of the thermal tolerance experiment.

Conclusions: Collectively, our results suggest that ant thermal tolerance may mediate competitive effects in habitats that experience strong diurnal and seasonal fluctuations in temperature.

Evidence for the evolutionary nascence of a novel sex determination pathway in honey bees

Martin Beye, Martin Hasselmann, Tanja Gempe, Morten Schiøtt, Carlos Gustavo Nunes-Silva, Marianne Otte

Genetics, Duesseldorf, Germany

Sex determination in honey bees (*Apis mellifera*) is governed by heterozygosity at a single locus harbouring the *complementary sex determiner* (*csd*) gene, in contrast to the well-studied sex chromosome system of *Drosophila melanogaster.* Bees heterozygous at *csd* are females, whereas homozygotes and hemizygotes (haploid individuals) are males. Although at least fifteen different *csd* alleles are known among natural bee populations, the mechanisms linking allelic interactions to the development program are still obscure. Here we report a new component of the sex-determining pathway in honey bees, encoded 12 kb upstream of *csd*. The gene, *feminizer* (*fem*), is the ancestrally conserved progenitor gene from which *csd* arose. FEM shares the same arrangement of SR-/proline-rich-domain with the *Drosophila* key sex-determining gene *transformer* (*tra*). Like *tra*, the *fem* transcript is alternatively spliced and encodes a functional product only in females. We show that RNAi-induced knockdown of *fem* results in male bees, indicating that the *fem* product is required for entire female development. Furthermore, RNAi-induced knockdown of *csd* results in the male-specific *fem* splice variant suggesting that the *fem* gene implements the switch of developmental pathways controlled by heterozygosity at *csd*. Comparative analysis of *fem* and *csd* coding sequences from five bee species indicates a recent origin of *csd* in the honey bee lineage from the *fem* progenitor and provides evidence for positive selection at *csd* accompanied by purifying selection at *fem*. The *fem* locus in bees uncovers gene duplication and positive selection as evolutionary mechanisms underlying the origin of a novel sex determination pathway.

Love thy neighbour: Argentine ants do not attack non-nestmates

Natasha Palesa Mothapo, Theresa Wossler

University of Stellenbosch, Stellenbosch, South Africa

Introduction: The Argentine ant, *Linepithema humile*, is a widespread invasive species. In the introduced range it is characterized by a social structure known as Unicoloniality, where intraspecific aggression between nests is reduced or absent. This results in the formation of large and spatially expansive 'supercolonies' which lack defined colony boundaries and territoriality. Ants within these 'supercolonies' show very low levels of aggression towards more distant colony members, probably due to the erosion of some important nestmate recognition cues. In line with this observation, we set out to determine the colony boundaries of this ant within the Western Cape Region, South Africa, using behavioural aggression bioassays.

Methods: We collected ants from Elim in the south (30°3'0S, 22°4'60E) to Porterville in the north (33°0'19''S, 18°59'3''E). Pairwise aggression bioassays, with ants, were conducted within and between sites. We extracted and identified cuticular hydrocarbons from individuals for each nest, to relate these signals to worker aggression.

Results: There were very low levels of aggression between individuals within sites, as well as between sites. Except ants from Elim nests where individuals showed very high levels of aggression towards all other ants in this study. The role of cuticular hydrocarbons in nestmate recognition of this ant will be discussed.

Conclusion: Our results suggest a unicolony boundary exists between Elim in the south and all other nests to the north. This suggests that at least two 'supercolonies' exist within this study area, indicating at least two introductions into South Africa.

Desert ants Cataglyphis use olfactory topographical cues to pinpoint their nest entrance

Markus Knaden, Kathrin Steck, Bill Hansson

Max-Planck Institut for Chemical Ecology, Jena, Germany

Cataglyphis fortis forages for dead arthropods that are killed by heat stress in the inhospitable saltpans of Tunisia. Both high surface temperatures and a non-patched food source distribution result in the absence of any trail-laying behaviour in these individually foraging ants. Instead of odour trails, path integration is the fundamental system of long-distance navigation in *Cataglyphis*. This system constantly informs an ant about its position relative to the nest. In order to compensate for errors accumulated during path integration the ants also rely on visual landmarks as geocentric navigational aids. Here we show that, in addition to its visual orientation system, *Cataglyphis* can learn environmental odours and use them to pinpoint the nest entrance. Ants that were trained to a nest entrance being situated within a squared array of four different odours, concentrated their nest search within this array in a test situation. The search accuracy degraded when the odour array was rotated or when the positions of the odours within the array were swapped. Hence, the ants are able to learn not only the association of the nest entrance and the odours but also the spatial distribution of different odours surrounding the nest entrance. A topochemical representation has already been predicted by Forel and v. Frisch. However this is the first time that the use of topochemical cues in the context of landmark orientation could be proven.

Insects, nematodes and fungi: A hodgepodge of multispecies interactions in natural and agricultural systems

S. Patricia Stock

Dept. Entomology, University of Arizona, Tucson, Arizona, United States

In biological control, direct interactions between pairs of species are fairly well known, whereas indirect interactions (involving more than two species) are only beginning to be comprehended. Most studies of indirect interactions have mostly focused on the life history and ecology of these associations, from a bilateral perspective: plant- insect or insect-pathogen interactions. Entomopathogens have a diverse and widespread role in plant–herbivore interactions and both direct effects and indirect effects have been reported. In this respect, insect-parasitic nematodes are significant component of below ground systems and play a major role controlling insect pests and other noxious arthropod populations. Nontheless, very little is known on the impact that other organisms may have in the success of entomopathogens to control herbivore populations in the soil. In this presentation, I will discuss interactions among entomopathogenic nematodes and and other organisms in food webs in natural and agricultural settings. A recent study on multispecies interactions between insect-pathogenic nematodes, plant-pathogenic fungi, herbivores and plants in a Sonoran desert agricultural ecosystem will be considered. The influence of plant-pathogenic fungi on the dynamics of entomopathogenic nematodes, insect herbivores, and plants will be discusse

Optophysiological approaches to dissect neuronal circuits underlying learning and memory in *Drosophila*

Andre Fiala

University of Wuerzburg, Wuerzburg, Germany

Introduction: For many years *Drosophila* has been the geneticist's dream but the physiologist's nightmare, mainly due to the small size of central neurons that makes them almost inaccessible for extensive electrophysiological studies. However, novel genetic tool might help to combine the advantages of *Drosophila* - most notably the possibility to target defined neurons - with physiological techniques. We are using on the one hand DNA-encoded fluorescence sensors to monitor neuronal activity, on the other hand light-sensitive ion channels to depolarize neurons by illumination.

Methods: Using these optical imaging and optical activation techniques we investigate how behaviour is influenced by modulatory neurons. In particular we follow up the hypothesis that two bidirectional modulatory systems might mediate the evaluation of external stimuli as indicative for positive or for negative outcomes, respectively.

Results: Using optical calcium imaging of dopaminergic neurons innervating the mushroom body we show that these neurons are responsive to electric shocks, which are commonly used as punishing stimuli during olfactory associative training procedures. Light-activation of dopaminergic neurons in the larval *Drosophila* brain using channelrhodopsin-2 can substitute for the reinforcing effect of a punitive salt stimulus in an olfactory associative learning paradigm. Activating octopaminergic and/or tyraminergic neurons substitutes for a rewarding stimulus in appetitive learning.

Conclusions: Our experiments indicate that the biogenic amines octopamine or tyramine might act as positive reinforcer in associative learning tasks in insects. Conversely, dopamine is hypothesized to mediate the reinforcing effects of aversive stimuli in associative learning. Arguments for and against this model will be discussed.

Exciting body structures of apterous flat bugs (Heteroptera: Aradidae) of Madagascar - what for?

Ernst Heiss

Tiroler Landesmuseum, Innsbruck, Austria

Introduction: For 180 years after the description of the first Aradid by Linnaeus 1758 (*Aradus corticalis*), apterous forms were regarded as mere larval stages. Only in 1938 N.C.E. Miller recognized wingless Malaysian samples as adults and described on them the first apterous genus Chelonocoris.

After discovering and describing apterous Aradidae from Madagascar by Drake and independantly by Hoberlandt, both in 1957 followed by Usinger & Matsuda and Kiritshenko in 1959 respectively, several new genera and species were recognized since by the author.

Results: While in macropterous species the thorax is dorsally divided into three distinct separated sclerites (pro-, meso- and metanotum), these structures are indistinct in apterous taxa and variously fused to each other and even to the first two abdominal tergites.

Discussion: What for is the question? As all known apterous Aradidae are associated with rainforest habitats where they are found in leaf litter or on wooden parts infested by fungi, no obvious function can be correlated to these curious structures. But even a possible reason for the complete loss of wings is not yet clear. Is it an adaptation and evolutionary process due to rather stable conditions in rainforests or the contrary – that lack of sufficient nutrition in such environments induces the observed development of thoracal structures instead of wings for a better energy balance?

Samples of such dorsal body structures are given and an update of the presently known Aradid fauna of Madagascar and adjacent islands is presented and discussed.

Fossil Neanastatinae (Chalcidoidea: Eupelmidae) — implications for inferences of evolution and relationships of the subfamily

Dr. Gary Gibson

Canadian National Collection of Insects and Arachnids, Agriculture and Agri-Food Canada

Introduction: Neanastatinae is one of three subfamilies comprising Eupelmidae. Putative apomorphies support monophyly of all three subfamilies, but morphological evidence for the monophyly of Eupelmidae is lacking and it has been hypothesized as possibly a paraphyletic grade-level taxon linking Cleonyminae (Pteromalidae) with Encyrtidae and/or Tanaostigmatidae. Hypotheses of relationships derived from molecular data are currently unstable but also do not support a monophyletic Eupelmidae. Phylogenetic analyses combining morphological and molecular evidence of extant taxa are needed to help resolve questions of monophyly and relationships, but the discovery and description of fossil taxa is equally important as a third source of information and test of hypotheses.

Methods: The morphological attributes of five females representing four distinct species of Eupelmidae in Eocene Baltic amber were compared with those of the four extant genera classified in Neanastatinae to test hypotheses of groundplan states, character evolution and relationships.

Results: Two of the species resemble species classified in extant genera of Neanastatinae, though they lack some of the differentiating features hypothesized as groundplan states of the respective genera. The other two species are much less similar to extant Neanastatinae. One exhibits none of the putative apomorphies postulated to support monophyly of the subfamily and has features that suggest some Pteromalidae-like ancestor as well as a possible relationship with the common ancestor of Encyrtidae + Tanaostigmatidae. The fourth species shares a combination of features linking the previous species with the other, more typical, members of the subfamily. As a result, three new genera are recognized in Neanastatinae and hypotheses of groundplan states and character evolution are modified to reflect the new discoveries.

Conclusions: The morphological diversity of extinct and extant Neanastatinae suggests many other fossil taxa remain to be discovered. Baltic amber is comparatively rich in Chalcidoidea and the study of fossils belonging to other families, particularly Pteromalidae, is essential prior to rigorous, stable hypotheses of higher-level relationships among Chalcidoidea.

CATE – Creating a Taxonomic E-Science

Malcolm Scoble

Natural History Museum, London, United Kingdom

Fixed-publication (whether paper, CD-ROM or PDF files) as the medium for descriptive taxonomy is being challenged almost by default and is unlikely to survive in the long-term - at least as the sole means of publication. The future is already apparent in a number of online approaches to revisionary (descriptive, monographic) taxonomy that involve continuous addition and correction of data. Such information comes from single source web pages to databases linked in distributed networks. The ubiquity of the Internet for promoting particular views is likely to be too strong to resist, however persuasive the arguments for control by the codes of nomenclature. This prediction is strengthened by the diminishing workforce of professional taxonomists (who are largely responsible for shaping the Codes) involved in describing life on the planet. While taxonomists may be unable to control taxonomic content in the new and more anarchic medium (other than within their own diminishing community), they do have the opportunity to shape the field to the benefit of their own close community and the much wider (yet undefined) user base.

An Internet-based approach to revisionary taxonomy is being taken in the CATE project (www.cate-project.org). The system allows new taxonomic proposals to be made in an open peer-review process forming part of the workflow. It also provides the opportunity for high quality products to be maintained through the incorporation of well-tested taxonomic standards. There seems much merit in treating taxonomy overtly as an information science, while still regarding it as an intellectual endeavour in its own right. This shift in emphasis is explored by examining the growing influence of e-projects in the changing taxonomy landscape.

Gall midges (Diptera: Cecidomyiidae) in the forest-tree fauna of Turkey

Sabri Ünal, Cihan Cilbircioglu

Kastamonu University, Kastamonu, Turkey

The family Cecidomyiidae is one of the largest of the Diptera. Gall midges are small, inconspicuous flies, but they may be very important both in forest ecosystems and in agroecosystems. The present fauna of gall midges of Turkey includes 71 species belonging to 38 genera. In this study, forest gall midges (Diptera: Cecidomyiidae) fauna of Turkey was examined and deduced this fauna that consists 33 species in 24 genera on 34 host trees species in 15 genera. Of them, 30 species are phytophagous, 1 species is zoophagous, 1 species is phytophagous-inquilines and one species phytosaprophagous.

Plant genotype and herbivory alter ecosystem processes: Extended, evolutionary implications for species genetic interactions.

Jen Schweitzer[1], Joe Bailey[1], Steve Hart[2], Tom Whitham[2]

[1]University of Tennessee, Knoxville, TN, United States, [2]Northern Arizona University, Flagstaff, AZ, United States

Insect herbivory may influence terrestrial ecosystem-level processes in many ways. The indirect impacts of insect-induced alterations of leaf litter, however, may have a consistent impact on ecosystem-level processes as chronic herbivory is more common than outbreaks and leaf litter represents a regular and important source for internal nutrient cycling in forest ecosystems. Furthermore, the effects of genetic variation in plants on ecosystem-level processes are now beginning to be recognized and the effects of individual plant genotypes have been shown to repeatably modify associated arthropod and microbial communities, as well as nutrient cycles of carbon and nitrogen. Utilizing several model plant systems (including *Populus* spp. and *Hammemalis* spp.), here we address how interactions between plant genotype and herbivory by specialist arthropods can modify the impacts of plant genetic variation on ecosystem-level processes. Overall, the data to date suggest that "afterlife" effects of herbivory (by insect species from multiple feeding styles – i.e., gallers and leaf chewers) on leaf litter quality can have extended effects on rates of decomposition and nutrient release and in many cases mediate the effects of plant genetic variation by reducing the overall variation in litter quality and subsequent decay by 22-33% within a population. These results suggest that the interactions between herbivores and genotypes may have predictable effects on variation in ecosystem responses such that herbivores may homogenize the effects of plant genetic variation to stabilize plant-soil feedback interactions.

Revision of *Dilyta* Förster (Hymenoptera: Figitidae: Charipinae) with the description of eight new species

Jordi Paretas-Martínez[1], George Melika[2], Juli Pujade-Villar[1]

[1]Universitat de Barcelona, Barcelona, Spain, [2]Pest Diagnostic Laboratory, Tanakajd, Hungary

Introduction: The genus *Dilyta* includes very small wasps that are hyperparasitoids of Psyllidae (Homoptera) via Encyrtidae (Hymenoptera: Chalcidoidea). *Dilyta* is now represented by three species: *D. subclavata* Förster from Europe, *D. rathmanae* Menke & Evenhuis from Washington state (USA), and *D. africana* (Benoit) from Zaire.

Methods: The type material of all the described species of *Dilyta* has been examined, along with long series of undetermined material loaned from several institutions. The specimens have been studied under stereomicroscopy and with the help of low-vacuum SEM images taken on a Quanta 200 Environmental Scanning Electron Microscope.

Results: Eight new species of *Dilyta* are here described: four from Africa, two from Europe and two from Asia. Morphologically, the four new African species clearly differ from the rest by having the scutellum with only two small apical carinae, instead of the typical inverted U-shaped apical carina of *Dilyta*. Besides this, the differences betwen species can only be found in the proportion of the antennal segments. Moreover, *Apocharips talitzkii* (Belizin) from Moldova is transferred to *Dilyta talitzkii* (Belizin) n. comb. Lastly, the diagnosthic characters of the genus *Dilyta* are discussed and defined.

Conclusions: The genus *Dilyta* is a widespread genus that includes twelve species. The first records of this genus in Asia are presented here, and its distribution in Africa, Europe and North America is widened considerably. There are no records of *Dilyta* in South America and Australia.

Basal phylogenetic relationships in Dictyoptera and Mantodea

Klaus-Dieter Klass

Museum of Zoology, Dresden, Saxony, Germany

Monophyly and placement of Dictyoptera: The Dictyoptera include the Mantodea, Blattaria, and Isoptera, altogether comprising some 9.300 species. Dictyopteran monophyly is unambiguously supported by molecular data and morphological characters (e.g. anterior transverse bridge in tentorium, formation of ootheca with functional differentiations in accessory glands, female subgenital plate coxosternum VII). Dictyoptera are one of 11 principal lineages of Neoptera, whose relationships are altogether not clearly resolved.

Principal dictyopteran lineages and their relationships: Monophyly has been convincingly demonstrated for several lineages inside Dictyoptera: 1) Mantodea. 2) Isoptera + Cryptocercidae (resulting from molecular analyses, association with specific flagellates, and a few morphological characters). 3) Blattellidae + Blaberidae (resulting from the structure of male genitalia and molecular data). 4) Blattidae (male genitalia and molecular data). 5) Polyphagidae (molecular data). 6) Nocticolidae (molecular data). Two further lineages are 7) Lamproblattidae (1 genus) and 8) Tryonicidae (2 genera). The relationships among these 8 lineages vary strongly among the various recent molecular- and morphology-based phylogenetic analyses. Most analyses yield Mantodea and Blattaria (incl. Isoptera) as sister taxa, but one finds a clade Mantodea + Nocticolidae subordinate in Blattaria. (Molecular data for Tryonicidae and Lamproblattidae have not yet been used in large analyses.)

Basal relationships in Mantodea: The structure of the male genitalia strongly supports *Mantoida* + (*Chaeteessa* + (*Metallyticus* and remaing Mantodea). For *Mantoida* and *Metallyticus* this placement has been confirmed by molecular data, which are not yet available for *Chaeteessa*. Characters of wings and forelegs are incongruent with this hypothesis, but are also incongruent with each other.

Plant-insect interactions are controlled by the underworld

Wim Van der Putten

Netherlands Institute of Ecology, Heteren, Netherlands

Interactions between plants and aboveground insects are usually studied without considering interactions between plants and soil biota. However, soil organisms influence plant community composition, plant quality, plant defense and the survival of insects. I will present results of a long-term addition experiment where we exposed species-rich grassland communities to grasshoppers, wireworms and nematodes in a full factorial outdoor experiment. The effects of the grasshoppers on plant community composition depended on the community composition in the soil. Interaction effects were non-linear. I will discuss how interactions in the 'underworld' influence plant community composition and plant-insect interactions.

Above-belowground interactions, global warming, and biological invasions

Wim Van der Putten

Netherlands Institute of Ecology, Heteren, Netherlands

Above- and belowground multitrophic communities play an important role in the control of plant abundance. Global warming may disrupt these interactions, when the individual components respond differently to warming. I will discuss effects of plant range shifts on above and belowground interactions in new habitats. These effects were determined in the field, as well as in controlled greenhouse experiments

Environmental influence on tri-trophic interactions: Plant phenotypic diversity and multiple herbivory

Cesar Rodriguez-Saona[1], Jennifer Thaler[2]

[1]Rutgers University, New Brunswick, NJ, United States, [2]Cornell University, Ithaca, NY, United States

Introduction: Herbivore-induced plant responses can affect the preference and performance of herbivores and their natural enemies. We hypothesize that when herbivores from different guilds feed on plants these interactions are disrupted, and that the abundance of arthropods on plants is influenced by heterogeneity in plant neighbourhood.

Methods: We damaged tomato plants either by caterpillars, aphids, both, or none. Then, we investigated plant-herbivore-natural enemy interactions from the molecular to the organismal levels, including the effects of induced responses on the abundance of herbivores and predators on individual plants and their neighbors in patches of plants.

Results: *At the molecular level*, aphids attenuated several plant defense genes induced by caterpillars. *At the chemical level*, caterpillars increased proteinase inhibitor activity regardless of the presence of aphids. Aphids reduced the C:N ratio but not when caterpillars also fed on the plants. *At the organismal level*, caterpillars reduced oviposition by moths but not when aphids also fed on plants. Caterpillars reduced growth, consumption, and survival of parasitized and unparasitized caterpillars regardless of the presence of aphids. *At the patch level*, plants in homogeneously induced patches contained fewer flea beetles and more lady beetles compared to homogeneously non-induced patches. *At the neighborhood level*, induced plants in heterogeneous patches contained more flea beetles compared to induced plants in homogeneous patches.

Conclusions: Damage by multiple herbivores influenced the plants' inducible responses differently when using molecular, chemical, and organismal measures, and variation in plant neighborhood generated by induced plant responses affected the abundance of herbivores and predators on plants.

Tri-trophic interactions in native and introduced habitats: furanocoumarins, webworms, and *Copidosoma sosares*

Paul Ode[1], Evan Lampert[1], Arthur Zangerl[2], May Berenbaum[2]

[1]North Dakota State University, Fargo, ND, United States, [2]University of Illinois, Urbana, IL, United States

Comparisons of tritrophic interactions in native and introduced habitats are very rare. Yet, they can provide information regarding the selective forces maintaining multitrophic interactions. Likewise, such studies provide insight into how trophic relationships change as a consequence of being introduced into novel environments. *Copidosoma sosares* is a specialist parasitoid of the parsnip webworm (*Depressaria pastinacella*), itself a specialist on furanocoumarin-containing apiaceous host plants. This system is native to Europe, where the predominant host plants are *Pastinaca sativa* and *Heracleum sphondylium*. The webworm is introduced throughout much of the US where it attacks the introduced *P. sativa* and the native *Heracleum lanatum*. *C. sosares* attacks up to 90% of webworms in European and western US populations, but it is absent in eastern US. *C. sosares* clutch size and survivorship is negatively affected by the furanocoumarin, xanthotoxin. We predicted that in populations where *C. sosares* is present (Europe and western US) plants should produce lower levels of xanthotoxin than populations where *C. sosares* is absent (eastern US). While European plants invest less in xanthotoxin than eastern US populations, western US plants produced xanthotoxin in levels as high or higher than eastern US plants. Consequently, *C. sosares* fitness is lower in introduced (western US) populations than in its native European populations. One possible explanation is the recent reestablishment of *C. sosares* to webworms in the western US. Study of this system across three geographic regions with different trophic compositions and histories can give insight into the underlying dynamics involved in biological invasions.

Utilization of attractants/repellents for pest management of *Culicoides* biting midges

Daniel Kline

USDA, ARS, CMAVE, Gainesville/Florida, United States

Introduction: *Culicoides* biting midges are pests of man and livestock worldwide. They cause annoyance due their attacks in high numbers. They can also transmit diseases to man and livestock. An example is the recent outbreak of bluetongue in Europe. Despite their medical and veterinary importance very little information exists concerning their basic biology, ecology or any strategy to control them. This presentation will review current knowledge and recent efforts to develop a pest management strategy based largely on recent knowledge obtained on the chemical ecology of adult biting midges. Emphasis will be placed on their host seeking behavior, but results from recent studies on the association of adult midges and flowering plants will also be presented.

Methods: Various types of traps were operated to determine their efficacy in capturing adult biting midges. Different experimental and commercial attractant lures were also tested.

Results: Propane powered traps were very efficient in capturing large numbers of most species of *Culicoides*. Different species preferred different attractant combinations. The combination of octenol and carbon dioxide was found to be very efficient at collecting large numbers of most species. The addition of lactic acid often reduced collection size.

Conclusions and Future Work: Properly baited and placed propane powered traps seem to be a promising population management technique for some species of biting midges.

Area-wide management of the Asian tiger mosquito

Daniel Kline[1], Gary Clark[1], Dina Fonseca[2], Randy Gaugler[2], Daniel Strickman[3]

[1]USDA-ARS, Gainesville,Florida, United States, [2]NJ Agricultural Experiment Station, Rutgers University, New Brunswick, New Jersey, United States, [3]USDA-ARS, Beltsville, Maryland, United States

Introduction: The Asian tiger mosquito, *Aedes albopictus*, is often responsible for most complaints to urban mosquito control programs, yet there is no clearly defined protocol for controlling this species. We are developing an area wide, multidisciplinary approach, grounded by an economic analysis, which incorporates extensive public education and involvement, with focused application of established biological and chemical control interventions. Our methodology will be developed in two New Jersey counties. In Phase I, we will perform an initial assessment of *Ae. albopictus* abundance, dispersal, population structure, and insecticide resistance status, as well as of its social and economic impact. In Phase II, we will compare *Ae. albopictus* abundance and associated human behavior in two pairs of experimental and control plots of 1,000 homes (up to 640 acres) each. In Phase III, we will expand our control efforts county-wide (>140,000 acres) initially targeting source populations. Throughout the project, the costs of all control procedures will be documented and an economic analysis will be conducted. If we succeed in controlling the Asian tiger mosquito and our strategy is economically sound, we will proceed to Phase IV and expand the initiative nationally by recruiting 12 geographically diverse mosquito control agencies to implement our methodology.

Methods: A 5 year Area Wide collaborative research project was established among federal government, universities and mosquito abatement districts in 2008.

Results: Project has just been initiated. This talk will present overview of objectives and preliminary results.

Conclusions and future work: No conclusions yet.

The threat of insect resistance to phosphine in bulk grain storages in Australia

Manoj Nayak[2], Joanne Holloway[3], Matthew Head[4], Robin Reid[5], Hervoika Pavic[2], Patrick Collins[2]

[1]Cooperative Research Centre for National Plant Biosecurity, Deakin, ACT, Canberra, Australia, [2]Department of Primary Industries and Fisheries, Indooroopilly, Brisbane, Queensland 4068, Australia, [3]NSW Department of Primary Industries, Wagga Wagga Agricultural Institute, Wagga Wagga, New South Wales 2650, Australia, [4]GrainCorp Operations Ltd, North Geelong, Victoria 3215, Australia, [5]GrainCorp Operations Ltd, Toowoomba, Queensland 4350, Australia

Introduction: Australia's $7billion grain industry relies heavily on phosphine fumigant to disinfest stored grain of insect pests. Recently however, development of high resistance to phosphine in four major pest species has become a serious biosecurity threat in the central bulk handling storage system; which adheres to a 'nil tolerance' principle for live insects for marketing grain. As there are no practical alternatives to phosphine, management of resistance is a priority. The development of phosphine fumigation protocols effective against resistant insects is essential to the successful management of resistance.

Methods: Laboratory strains of purified resistant genotypes were exposed as mixed-age cultures (including all life-stages) to a range of phosphine concentrations and exposure periods. The 'time to population extinction' data obtained were used to develop new fumigation protocols and these were verified under commercial conditions at bulk handling storage sites. Cages of mixed-age cultures of resistant strains were placed at different parts of the bulk grain prior to fumigation. Phosphine concentration, temperature and moisture of the grain mass were monitored during fumigation and insect survival was assessed after the fumigation.

Results: Results from this research show that manipulation of concentration and exposure periods is the key to the successful control of strongly phosphine resistant populations of storage pests.

Conclusions: A protocol incorporating a range of phosphine concentration options and exposure periods for use in large central storages was successfully developed. Correct use of this protocol should ensure that the practical life of phosphine is extended in Australia.

Optimizing cotton pollination period by using high stocking rate of honeybee colonies

Marwan Keshlaf[1], Robert Spooner-Hart[1], Robert Mensah[2], Oleg Nicetic[1]

[1]University of Western Sydney, Sydney NSW, Australia, [2]NSW Department of Primary Industries, Narrabri NSW, Australia

Introduction: Cotton is an important world crop and one of the most insecticide-intense cropping systems. Pesticide use in cotton is regarded as a major cause of honeybee losses but with the release of transgenic (Bt) cotton, it was anticipated that pesticide use would be substantially reduced. Reduction of pesticides offers opportunities for increased use of honeybees in cotton, providing benefits to both cotton producers and beekeepers.

Methodology: A study to evaluate the potential of optimizing honeybee, *Apis mellifera*, pollination in the shortest period possible during cotton flowering was carried out in a 2 ha transgenic cotton (Bollgard II) Sicot 71BR crop at Narrabri, Australia in 2007. Thirty honeybee colonies were placed adjacent to the cotton field. The number of honeybee flower visits were recorded over a four week period from two rows of cotton located 60 and 80 m away from the apiary. In addition, the effect of the time of exposure to honeybee pollination on cotton yield and quality was determined by (1) caging five plots for the ten days in peak flowering, (2) caging five plots for four weeks and (3) leaving five un-caged.

Results: Bee visitation to cotton flowers averaged 3.24 bees/ 100 flowers. Cotton yield and lint micronaire were both significantly higher in un-caged plots and plots caged for ten days, compared with control plots.

Conclusions: Honeybees are efficient cotton pollinators, increasing cotton yield and improving lint quality. A period of ten days during peak cotton flowering may be sufficient for honeybee pollination, and could be practicable in IPM programs.

Role of pollen beetles in cotton pollination, and their effect on the foraging behaviour of honeybees

Marwan Keshlaf[1], Robert Spooner-Hart[1], Robert Mensah[2], Oleg Nicetic[1]

[1]UNiversity of Western Sydney, NSW, Australia, [2]New South Wales Department of Primary Industries, NSW, Australia

Introduction: Pollen and nectar of *Gossypium* spp. attract beneficial as well as harmful insects. Pollen beetles, *Carpophilus aterrimus*, were observed in cotton flowers in the field, but there was no published information about whether they pollinated flowers, damaged them or deterred pollinators.

Methodology: A study to investigate the direct and indirect effects of pollen beetles on cotton pollination was carried out in a 2 ha flowering crop of transgenic (Bt) cotton (Bollgard II) at Narrabri, Australia in 2007. Cotton plants were (1) caged to prevent pollinator entry, (2) caged with beetles, and (3) uncaged and exposed to beetles and managed honeybees, *Apis mellifera*, for a period of one week. A further study was conducted whereby (1) single flowers were bagged to prevent insects (2) flowers were bagged with varying numbers of pollen beetles, and (3) flowers were unbagged. The effects of beetles on boll set, yield and lint quality were determined. In addition, their effect on honeybee foraging behaviour was assessed by recording the number of bees visiting cotton flowers containing or not containing beetles.

Results: Plants exposed to honeybees had significantly higher yield and improved lint quality than those not exposed to pollinators or exposed to pollen beetles only. No bolls were produced from flowers infested with ≥10 pollen beetles. Honeybees rarely visited beetle-infested flowers when there was a choice but did visit them when there was no choice.

Conclusion: Pollen beetles do not contribute to cotton yield. Heavy beetle infestations can reduce cotton yield, by direct damage, or indirectly by deterring honeybees from visiting and pollinating cotton flowers.

Improved monitoring of early-season emergence of males, virgin and mated females of oriental fruit moth and codling moth in Australian orchards

Alexandre Il'ichev, David Williams

Department of Primary Industries Victoria, Biosciences Research Division, Tatura, Victoria, Australia

Pheromone mediated mating disruption (MD) is widely used in Australia to protect stone and pome fruit orchards without chemical sprays and produce “clean and green” fruit for domestic and overseas markets. Unfortunately, conventional sex pheromone traps are not reliable for monitoring of pest males under MD. Attracting females of orchard pests to synthetic host-plant volatiles could allow growers to control females and their unlaid eggs and to monitor pest life cycles precisely in orchards treated with MD.

Sex pheromones, food traps and new female attractants were used for detailed daily monitoring of codling moth (CM) in apples and pears, and oriental fruit moth (OFM) in peaches, pears and apples conducted at the beginning of three growing seasons to identify the first catches of males, virgin and mated females. The results demonstrated that OFM males and females emerged in pear blocks earlier than in their preferred host peach. First catches of OFM males and females in food traps in apples were recorded approximately 1 month later than in pears. Also, OFM males were caught in sex pheromone and food traps 2-3 weeks earlier than females in food traps. First mated OFM females were caught in food traps 4-10 days later than the first virgin OFM females. Virgin and mated CM females were caught in traps with new female attractants in pears at similar dates, but about a week later than first males in sex pheromone traps. The results of the daily monitoring of OFM and CM males and females helped to estimate Biofix dates for different fruit varieties more correctly and were used in Day-Degree Models.

The possibility of invasion by the coconut hispine beetle Brontispa longissima into mainland Japan

Ai Yamashita[1], Yukinari Taninoki[2], Keiji Takasu[2]

[1]Graduate school of Bioresource and Bioenvironmental Sciences, Kyushu university, Fukuoka, Japan, [2]Faculty of agriculture, Kyushu university, Fukuoka, Japan

No abstract submitted, or incorrect abstract submitted, or submitted in an inaccessible format.

Ranking of the potential host plants for the invasive Siberian moth in Europe

Natalia Kirichenko[1], Yuri Baranchikov[2], Jean-Claude Gregoire[3], Julie Flament[3], Marc Kenis[3]

[1]VN Sukachev Institute of Forest, Krasnoyarsk, Russian Federation, [2]University Libre de Bruxelles, Brussels, Belgium, [3]CABI Bioscience Switzerland Center, Delemont, Switzerland

Introduction: The Siberian moth *Dendrolimus superans sibiricus* Tschtv. (Lep.: Lasiocampidae) has recently been suggested for regulation as a quarantine pest for EPPO member countries. However, no specific report on European hosts for the pest has been published so far.

Methods: Relative growth rate and mortality of the pest larvae were evaluated on coniferous species widely planted in Europe and having high economical significance. The work was done in the quarantine facilities of the Laboratory of Biological Control and Spatial Ecology, Université Libre de Bruxelles (Belgium) in 2007.

Results: Suitability of the possible host plants for the defoliator decreased from European larch *Larix decidua* P. Mill., Eastern white 5-needle pine *Pinus strobus* L., European silver fir *Abies alba* Miller*.,* Norway spruce *Picea abies* (L.), Scots pine *Pinus silvestris* L. to European black pine *P. nigra austriaca* Arnold (all from Pinaceae). Larvae could also develop on the species from exotic genera *Pseudotsuga, Tsuga* and *Cedrus* (also Pinaceae) what appeared to be highly valuable for larval performance. Conifers from other families: Taxaceae and Cupressaceae were inedible for the pest.

Conclusions: Given the laboratory results, the pest is able to survive and develop on the main European coniferous species, including non-native conifers. Taking into account that more than two thirds of the European forest area consists of pine, spruce, fir and larch the introduction and establishment of the moth in Europe may result in devastations of large areas of forest stands.

Laboratory and field evaluation of formulated *Bacillus thuringiensis* var. *israelensis* as a feed additive for controlling house fly (*Musca domestica* L.) larvae in caged-poultry manure

Lizzy Mwamburi[1], Mark Laing[1], Mike Morris[2], Ray Miller[3]

[1]Department of Plant Pathology, School of Biochemistry, Genetics, Microbiology and Plant Pathology,University of KwaZulu-Natal, Scottsville 3201, Pietermaritzburg, South Africa, [2]Plant Health Products (Pty) Ltd, Nottingham Rd, South Africa, [3]Department of Entomology, School of Biological and Conservation Sciences, University of KwaZulu-Natal,Scottsville 3201, Pietermaritzburg, South Africa

Introduction: Infestations of house flies, *Musca domestica* L., are a continual problem around poultry establishments. The high levels of resistance developed by flies toward organochlorine and organophosphorous compounds have made the efforts to control flies using biological control agents (BCAs) increasingly important.

Methods: Prior to conducting field evaluations, laboratory baseline bioassay data were established on a dose-time response relationship closely simulating poultry house conditions in the laboratory. Acute toxicity of two *Bacillus thuringiensis var. israelensis* (*Bti)* formulations was evaluated against larvae in the laboratory, and against natural populations of *M. domestica* larvae in the field applied in oral feed to chickens and as topical application in the poultry houses.

Results: Baseline bioassay data demonstrated that susceptibility of *M. domestica* larvae increased to a given concentration of *Bti* as the duration of exposure increased. In the laboratory studies, the LC_{50} and LC_{90}values of *Bti* for the larvae ranged between 65 - 77.4 and 185.1 - 225.9µg ml^{-1} respectively. LT_{50} and LT_{90} values were 5.5 and 10.3d respectively. In the field, a concentration of 10g *Bti* kg^{-1} of feed resulted in 90% reduction of larvae for 4wk post-treatment. Furthermore, as the exposure duration increased, the level of *Bti* required to cause a significant mortality decreased. A higher concentration (2g L^{-1}) of *Bti* in spray applications was not significantly more effective than the lower concentration of 1g L^{-1}.

Conclusion: Adding *Bti* to chicken feed is a good potential measure for the management and control of house flies in caged-poultry facilities.

Placement of Isoptera inside the Blattaria seen from the morphological perspective: the key role of the cockroach *Cryptocercus* and the termite *Mastotermes*

Klaus-Dieter Klass, Ariane Barton, Gerda Buder, Ute Eulitz

Museum of Zoology Dresden, Dresden, Saxony, Germany

Phylogenetic evidence: All recent molecular- and morphology-based phylogenetic analyses have confirmed Isoptera to be placed inside Blattaria as the sister group of *Cryptocercus*. Most analyses have obtained *Mastotermes* as sister group to all other termites. This emphasizes the key role of both *Cryptocercus* and *Mastotermes* for evolutionary studies on Isoptera.

Key role of *Cryptocercus*: *Cryptocercus*, like all basal Isoptera, harbours a species-rich community of oxymonadid and hypermastigid flagellates in its hindgut and transfers these to the next generation by anal trophallaxis (unique among insects). *Cryptocercus* shows biparental brood care like incipient termite colonies (and a few blaberid cockroaches). However, there are only few, mostly vague morphological apomorphies common to *Cryptocercus* and termites: somewhat moniliform antennae with low number of flagellomeres; strong similarity between primary and secondary sclerites and large size of primary pulvilli in the proventricle. Recent studies of the head capsule, tentorium, hypopharynx, and leg spination in Dictyoptera have not yielded any further discrete similarities.

Key role of *Mastotermes*: *Mastotermes* is in many morphological aspects more plesiomorphic than all other termites, and more similar to cockroaches than those. The female genitalia include a complete ovipositor, with all elements differentiated to the same extent as in typical cockroaches. Malpighian tubules are numerous, spermatozoa are flagellate (though with many flagella instead of only one). There are bacteriocytes in the fat body, harbouring *Blattabacterium*. There is a distinct anal fan in the hindwing. An ootheca is formed using accessory glands with a peculiar, asymmetrical functional differentiation.

Morphological diversity and species distinction in Mantophasmatodea

Klaus-Dieter Klass, Kai Drilling, Anna Hell

Museum of Zoology Dresden, Dresden, Saxony, Germany

Introduction: Since the initial description of Mantophasmatodea in 2002, 16 extant species have been described, further ones are known but yet undescribed, and four fossil species have become assigned to the taxon. The presentation surveys the distinctive characters in the group.

Methods: Male and female postabdomina were studied under the stereomicroscope; the antennal sculpture and tarsal processes were observed by SEM.

Results: Most differences are found in the male postabdomen. This concerns the shape of the (clasping) cerci (especially their tips); the shape of the vomeroid projection and details of the ridge crossing it; extensions of the left arm of the vomeroid sclerite; the shape of the projection of the subgenital plate; and the presence and shape of several genitalic sclerites. In the females the spermathecal bulb and structural details of the subgenital plate (median division, posterior lobes, shape of anterior apodemes) provide important characters. The antennal basiflagellomeres have a sculpture of ridges forming polygons; their details and distinctness vary among species. The dorsal process in the membrane distal to tarsomere 3 (an autapomorphy of Mantophasmatodea) shows differences in its size and shape, and in the pattern of sawteeth along its margins. The colouration of the compound eyes either includes scattered dark spots (mottled type) or a stripe along the lower margin (striped type). No clearcut interspecific differences were found in the left and right mandibles, the cuticular sculpture of the hindgut (where differentiations are entirely absent), and the glands of distiflagellomeres 1 and 6.

Soil macrofauna effect on plant succession in post mining sites

Jan Frouz[1], Ondrej Mudrak[1], Alena Roubickova[2], Karel Prach[3]

[1]Institute of Soil biology, Ceske budejovice, Czech Republic, [2]Charles University, Prague, Czech Republic, [3]South Bohemian University, Ceske Budejovice, Czech Republic

Introduction: Vegetation, survey in chronosequence of unreclaimed post mining sites distinguished (TWINSPAN) two distinct clusters. The first, young sites cluster was dominated by euritopic and ruderal plants. The second cluster covered sites 24-41 years old; with forest and meadow plants in the primary forest. The earthworm colonisation and consequent humus layer development, was selected by a discriminant analysis as the strongest predictor for the second cluster. Earthworm activity, namely the mixing of organic and mineral layers, is expected to cause vegetation changes.

Methods: To test this set of manipulation experiment was started looking on effect of earthworm on plant growth and establishment in presence or absence of earthworms.

Results: In laboratory, earthworms increased biomass of plants including grass, forbs and leguminous. In plants planted on soil in succession age 10-40year plant performance increased with succession age, however if earthworms were added to youngest soil plant performance was the same as on 40 year soil. In field the worm effect was more pronounced on forbs and grasses then leguminous.

Conclusion: The result indicated that changes in the topsoil mediated by soil fauna played an important role for vegetation succession.

The effect of wood ants on nutrient flow and tree growth in spruce forest

Jan Frouz

Institute of Soil Biology, Ceske Budejovice, Czech Republic

Introduction: Wood ants play important role in forest, we studied their effect on nutrient flow and tree growth in spruce forest.

Methods: Amount of nutrient brought into the nest from various sources was studied by analyzing nest material and food flow and nutrient content. Nutrient distribution and tree growth was studied in four distance from the closest ant hill (0-1m, 5-10 m 50m and more than 200 m) by soil sampling and tree ring analysis.

Results. In one ha of forest amount of P brought to the nests was about the same as amount of P coming to forest soil outside nests. Soil in close vicinity of the nest showed significantly higher content of nutrients than samples in the larger distances from the ant nests. Analysis of the tree rings indicated the fastest growth for trees, that were not attended by ants, located >200m from the ant nest. The second highest growth was observed in the trees that were in close vicinity of the nest.

Conclusion: We expect that depletion for nutrients by honeydew collection from the trees may slow the tree growth. The tree, that grow in close vicinity of the nests may compensate for this nutrient depletion by surplus of available nutrients in immediate surrounding of the nest.

From biological control to invasion: the ladybird *Harmonia axyridis*

Helen Roy[1], Eric Wajnberg[2]

[1]NERC Centre for Ecology and Hydrology, Cambridgeshire, United Kingdom, [2]INRA, Sophia Antipolis Cedex, France

Biotic homogenisation is considered among the greatest threats to global biodiversity. The rapid increase in introduced exotic species worldwide and the potential of these species to become invasive are widely recognised to have ecological and evolutionary consequences. The impact of some invaders is unquestionably negative and they are designated as invasive alien species (IAS). *Harmonia axyridis* Pallas (Coleoptera: Coccinellidae), "the most invasive ladybird on Earth", is undoubtedly one such species. Ladybirds have a long history of use as biological control agents against pest insects and are one of the most loved insects worldwide but *H. axyridis* is extremely unpopular outside of its native range for a number of reasons. First and foremost, *H. axyridis* threatens the diversity of native aphidophagous species through direct competition and as a voracious, polyphagous predator. Second, *H. axyridis* is now considered a pest species because it consumes soft fruit and is adversely affecting the wine and fruit growing industries. Third, *H. axyridis* occurs at high densities in buildings during overwintering and is thus regarded as a human nuisance. In this paper we introduce *H. axyridis* and particularly refer to the collaborative work of scientists across Europe (and USA) that resulted in a special issue of the journal BioControl ("From biological control to invasion: the ladybird *Harmonia axyridis* as a model species"). We conclude that *H. axyridis* should be used as a model to prevent, or mitigate against, subsequent releases of high risk organisms, by contributing to our understanding of the mechanisms involved in biological invasions.

Ecology of learning in insect parasitoids: From gene to behavior

Hans Smid[1], Michaël van den Berg[1], Saartje Hontelez[1], Patrick Verbaarschot[1], Louise Vet[2]

[1]Wageningen University, Wageningen, Netherlands, [2]Netherlands Institute of Ecology, Heteren, Netherlands

Differences in the expression of learning between closely related species create excellent opportunities to study species-typical learning. We find such an opportunity in our model system of two co-existing *Cotesia* parasitoid species that occupy slightly different niches. In the Netherlands, *Cotesia glomerata* mainly attacks the gregariously feeding caterpillars of the Large Cabbage White *Pieris brassicae*, whereas *Cotesia rubecula* is specialized on the solitarily feeding Small Cabbage White *Pieris rapae*. Both species can learn to associate plant odours with the presence of suitable hosts after an oviposition experience, but there are some profound interspecific differences in the functional requirements for the formation of long-term memory (LTM). *C. glomerata* learns fast and already forms LTM after a single learning event, whereas *C. rubecula* is a slow learner that needs three spaced learning events to change its plant preference. We argue that this inter-specific variation in LTM acquisition reflects a difference in the searching behaviour in nature, related to the distribution of their caterpillar hosts. Our current research focuses on the genetic backgrounds of the observed difference in LTM acquisition and consolidation of LTM. We focus on genes known to be involved in LTM formation, especially the transcription factor cyclic AMP-responsive element binding protein (CREB). Our results show that there are several putative memory activating and inhibiting CREB isoforms present in the brains of both *Cotesia* species. The CREB gene may serve as an important substrate involved in the evolution of learning and memory.

Morphological and biochemical characteristics of a cecidomyiid leaf gall of *Machilus bombycina* – a silkworm host plant

Mantu Bhuyan, Jiban J Mahanta, Jeeten Mech, Pranab R Bhattacharyya

North-East Institute of Science & Technology, Jorhat, Assam, India

Introduction: Leaves of *Machilus bombycina,* the primary host plant of silkworm species, *Antheraea assama* are heavily infested by gall midges of the genus *Daphnephila* (Diptera: Cecidomyiidae). Attempts have been initiated to understand the bioecology of the insect and nutritional quality of its leaf galls.

Methods: A survey has been carried out in order to understand the morphology and distribution of the galls which are pest on the leaves of *M. bombycina*. Biochemical analyses of the galls were conducted using standard protocol.

Results: More galls were found on the basal half rather than on the distal half of individual leaves while peripheral sections of plants had greater no of galls than other parts. On average, 10.77 galls were observed per leaf, which were 0.6 mm apart. Mature galls had 11.08 x 3.69 mm diameters, while their larval chamber were 8.22 x 1.31 mm in size. Galls were found to markedly deplete the nutrient contents of adjacent areas of infested leaves and store these nutrients in the galls in addition to the nutritional layer. Higher gall infestations resulted in greater nutritional content of leaves (including the gall tissues), except for carbohydrates, for which a reverse trend was observed.

Conclusion: Galls infesting silkworm host plant, *M. bombycina* were found to bear distinct morphological characters and play marked role on nutritional physiology of the host plant.

Population dynamics of the southern pine beetle in relation to applied silviculture

Robert Coulson[1], Andrew Birt[1], Maria Tchakerian[1], Frederick Stephen[2], James Guldin[3]

[1]Knowledge Engineering Laboratory, Department of Entomology, Texas, United States, [2]Department of Entomology, University of Arkansas, Arkansas, United States, [3]USDA Forest Service, Southern Research Station, Hot Springs, United States

In 2003 the Healthy Forest Restoration Act (HFRA) became US law and thereby provided the statutory means to address the degraded state of public forests in the US. The HFRA is a set guidelines for directed actions that are intended to adjust (and perhaps regulate) the conditions of the forest environment and thereby alter the frequency and amplitude of natural disturbances (fire and insect and disease outbreaks in particular). One of the first efforts to address the HFRA mandate by the USDA Forest Service was to examine the relation of silviculture (the theory and practice of controlling forest establishment, composition, and growth) and outbreaks of the southern pine beetle, Dendroctonus frontalis (Coleoptera: Curculionidae) (SPB). Considerable previous research on this relation has been reported. In essence, susceptible habitat patches for the SPB include stands containing mature loblolly, shortleaf pine, and slash pine with high basal area and stagnated radial growth. Such stands are considered to be high hazard. Simulation models for the SPB have been developed which mimic population growth in susceptible stands. We are using established knowledge of the SPB/forest silviculture relation to develop a computer based system (SPBsilvix) to evaluate (1) the impact of SPB infestation occurring in specific forest stands and the (2) to assess the risk of infestation in stands occurring in proximity to outbreaks. SBPsilvix is an interactive integrative computer-based system that links spatial data, tabular information, and simulation models from a variety of sources. Interpreted results are provided through the INTERNET.

Insect traces in Antarctic fossil forests: a modern day comparison

Claire M. McDonald[1], Jane E. Francis[1], Steve G.A. Compton[1], Alan Haywood[1], Allan Ashworth[2], Luis Felipe Hinojosa[3], John Smellie[4]

[1]University of Leeds, Leeds, United Kingdom, [2]North Dakota State University, North Dakota, United States, [3]Universidad de Chile, Santiago, Chile, [4]British Antarctic Survey, Cambridge, United Kingdom

Insect body fossils from Antarctica are very rare, yet many collections of Eocene Fossil leaves from Antarctica provide insect trace fossils, indicating that insects were an important component of the unique forests that once grew in south polar regions. These insect traces provide an excellent opportunity to examine the palaeoecology of Antarctica. The fossils studied include Eocene leaves from both Seymour Island and King George Island on the Antarctic Peninsula. A database of all insect traces on the Antarctic fossil leaves was compiled and analysed in terms of the diversity of palaeoherbivory. The fossil leaves are diverse with several different plant families present such as Nothofagaceae and Cunoniaceae. The range of traces that were found includes leaf mines, leaf galls and general leaf chewing, of which both marginal and non-marginal examples were present.

To provide a greater understanding of ancient herbivore intensity and diversity in Antarctica, modern insect traces on Nothofagus leaves, and their associated insects, were examined from the temperate forests in Chile, the modern day analogue of the Antarctic forests during the Eocene. Modern traces show a similar diversity of damage types to that seen in the Eocene, but the intensity of damage appears to be greater now.

The conservation and use of entomopathogenic nematodes and fungi in Chile

Steve Edgington[1], Dave Moore[1], Andrés France[2], Loreto Merino[2]

[1]CABI, Ascot, Berkshire, United Kingdom, [2]INIA, Chillán, XIII Region, Chile

Introduction: This is a Darwin Initiative study on the diversity of entomopathogenic nematodes (EPN) and fungi (EPF) in Chile and an assessment of their use as biological controls. The study is a collaboration between CABI and the Instituto de Investigaciones Agropecuarias (INIA).

Methods: EPN and EPF surveys were carried out in six zones in Chile, covering some of the principle habitats, including desert, sub-Antarctic, temperate rainforest and 'Mediterranean' areas within the central valley. Soil samples were live-baited for EPN and EPF and selected isolates were subsequently profiled for a number of ecological, physiological and behavioural traits, including environmental tolerance, growth characteristics and virulence.

Results: Surveys revealed 90+ and 300+ isolates of EPN and EPF respectively (~ 9 % and 30 % 'positive' hit), including isolates of both EPN and EPF from the Atacama Desert and Tierra del Fuego. Virulence assays showed selectivity amongst the isolates towards a number of key agricultural insect pests. Recent profiling of a thrashing, rather long EPN revealed that the isolate will travel at least 17 cm in 120 h to reach a host and is also capable of significant infection at 6 °C in humid soils. Interestingly no stages of this EPN were able to survive 0 °C for 24 h, even if contained within a host.

Conclusions: EPN and EPF isolates have been recovered from all survey sites in Chile, from a range of habitats, including some environmental extremes. Profiling has revealed interesting traits that may assist in using isolates for biological control.

The *Varroa destructor* invasion in South Africa: doing nothing can be the best response.

Mike Allsopp

ARC-Plant Protection Research Institute, Stellenbosch, South Africa

The varroa mite (*Varroa destructor*) has become an near-global pest of Western honeybee (*Apis mellifera*) colonies, both natural and managed, and in many parts of the world a continuous flow of novel pesticides and other control strategies has been required to prevent collapse of the honeybee population. The strategy chosen in South Africa, however, following the detection of the mite in 1997 was to do nothing and to allow susceptible honeybee colonies to die. This live-and-let die approach has resulted in the South African honeybee population becoming essentially tolerant to the varroa mite within ten years, and without a collapse in the honeybee population. It is suggested that the sub-optimal vitality of unmanaged African honeybee colonies, in which the varroa mite is now just one of a battery of pests and diseases in natural equilibrium with their host, is preferable to lengthy and likely futile efforts on the pesticide or biocontrol treadmill. Doing nothing was clearly the correct response to the arrival of varroa mites in South Africa, and the same is true for *Vespula germanica* and other insect invaders. It is suggested that efforts at control might frequently frustrate the development of natural tolerance and are often of questionable long-term value.

Male and female *Culex* mosquitoes match their flight tones at frequencies beyond their auditory range.

Ben Warren[1], Gabriella Gibson[2], Ian Russell[1]

[1]School of LIfe Sciences, University of Sussex, Sussex, United Kingdom, [2]Natural Resources Institute, University of Greenwich at Medway, Kent, United Kingdom

Introduction: Mosquitoes produce sexually dimorphic wing-beat frequencies (*wbfs*), with multiple harmonics. The flight tones produced alter in response to sound stimuli. This study explored the auditory interactions between pairs of *Culex quinquefasciatus* and *Cx pipiens*.

Methods: The *wbf*s of pairs of *Culex* in tethered-flight were recorded with a particle velocity microphone. Mechanical tuning curves were measured with a laser diode interferometer directed at the base of the antennae. The electrical responses of the antennae to sound were measured with an extracellular electrode from the pedicels.

Results: The resonant frequency of the JOs of the females of both species ~300Hz and are broadly tuned, whereas males are tuned to higher frequencies (*Cx quinquefasciatus* ~ 330 Hz and *Cx pipiens* ~ 380 Hz) and are more narrowly tuned. In tethered flight, male-female pairs responded to the sound of the other by altering their respective *wbfs*, converging on their nearest shared harmonic. The fundamental *wbf* of the male is at least 1.5 times higher than that of the female and the closest shared harmonic can be > 1000 Hz, which exceeds the sensitive frequency ranges of the mechanical tuning of their antennae and the neural tuning of their JO. However, the electrical tuning curves shows they also respond to low frequencies (10–80 Hz); during auditory interactions they may detect the *difference* between their respective frequencies, usually < 20 Hz when they are close to synchrony.

Conclusion: *Culex* mosquitoes interact through alterations in flight tone by mechanisms not fully understood.

In vivo visualization of odor propagation along the olfactory pathway of the *Drosophila* brain

Andre Fiala, Thomas Völler

Department of Genetics and Neurobiology, Wuerzburg, Germany

Introduction: Animals are able to differentiate a large variety of odors with respect to their chemical identity and concentration. We ask how different odor identities and intensities are represented in the brain of the fruit fly *Drosophila melanogaster* at various levels of processing, from sensory neurons to mushroom body neurons.

Methods: We presented several odors at different concentrations to the antennae of the fruit fly while monitoring calcium activity in different parts of the olfactory pathway. We have used the genetically encoded, FRET-based calcium sensor Cameleon 2.1 because of the minimization of movement artefacts due to its ratiometric properties, a good signal-to-noise ratio and high fluorescence intensity in the non-activated state. The expression of this calcium sensor in three different neuropils by specific Gal4-driver lines enabled us to trace the processing of the presented odor concentrations along a part of the olfactory pathway: in olfactory sensory neurons terminating in the antennal lobe, in olfactory projection neurons in the antennal lobe, in terminal arborisations of projection neurons in higher brain regions, and in Kenyon cells, the intrinsic neurons of the mushroom body.

Results and Conclusions: The results indicate that odor-evoked calcium responses in all these investigated neuropils show an odor concentration dependent activation. We have found no indication for any concentration-invariant activity at any stage of olfactory processing.

The epicuticular waxes as a plant defence barrier towards grain aphid

Agnieszka Wojcicka[1], Bogumil Leszczynski[1], Roman Warzecha[2]

[1]University of Podlasie, Siedlce, Poland, [2]Institute of Plant Breeding and Acclimatisation, Radzikow, Poland

Introduction: Physical and chemical characters of plants, especially their chemical constitutes are in the first line of their defense towards herbivorous insects. The present paper reports on role of the epicuticular waxes of triticale in its defense towards the grain aphid, *Sitobion avenae* (Fabricius).

Methods: The experiments were carried out on waxy covered (RAH 122) and wax-less (RAH 366) triticale hybrids. Feeding deterrents/stimulants from surface of the waxy triticale RAH 122 were extracted with dichloromethane, chloroform and ethanol. Seedlings of the wax-less hybrid RAH 366 were sprayed with the previously obtained surface extracts from the waxy RAH 122. The grain aphid feeding behavior on wax-removed and on sprayed with wax extract seedlings was studied using the EPG method (electrical penetration graphs) in 10 independent replicates.

Results: Removal of the surface wax compounds shortened non-probing period of the grain aphid on the waxy hybrid. Extracts from RAH 122 hybrid applied on seedlings of wax-less hybrid RAH 366, showed a strong reduction in penetration of peripheral plant tissues and prolonged the non-probing period. Generally, chemicals extracted from heavy-waxy hybrid reduced the aphid feeding on wax-less triticale.

Conclusions: Results presented here suggest that chemicals occur within epicuticular waxes layer of the triticale play an important role in its acceptance by the grain aphid.

Beyond the wasp-waist: Mesosomal anatomy and phylogeny of apocritan Hymenoptera

Lars Vilhelmsen[1], Istvan Miko[2], Lars Krogmann[3]

[1]Natural History Museum of Denmark, Copenhagen, Denmark, [2]Vas County Plant Protection and Soil Conservation Service, Tanakajd, Hungary, [3]Staatliches Museum für Naturkunde, Stuttgart, Germany

Introduction: We present the results of the first comprehensive investigation of the skeleto-musculature of the mesosoma across Hymenoptera, and analyse the resulting data set to elucidate the higher level phylogeny of the order.

Methods: Specimens were dissected and investigated with SEM and light microscopy. More than 270 morphological characters were scored and analyzed in TNT under different weighting conditions.

Results and Discussion: Relationships of basal, non-apocritan Hymenoptera were very similar to results of previously published analyses. At the base of Apocrita, the relationship Xiphydriidae + (Orussidae + (Stephanidae + other Apocrita)) was consistently reproduced. Within Apocrita, most superfamilies were retrieved as monophyletic, with the exception of Proctotrupoidea, Chrysidoidea, and Vespoidea. Aculeata were usually not monophyletic and Ichneumonoidea usually came out as sister to the majority of Aculeata. Cynipoidea were usually placed as the sistergroup of Proctotrupoidea + Platygastroidea, the latter being nested deeply within the former. Chalcidoidea was sometimes placed as sister to the remainder of the Proctotrupomorpha. Mymarommatidae and Maamingidae usually came out as sister groups, but the placement of this clade varied. Evaniomorpha excluding Stephanidae was always retrieved, with Evanoidea being monophyletic and Ceraphronoidea sister to Megalyridae. In general, within Apocrita relationships above the superfamily level were weakly corroborated and subject to substantial change under different analytical conditions. The mesosomal dataset provides substantial useful phylogenetic information and clade support at various taxonomic levels within Hymenoptera. However, the mesosomal dataset is highly homoplasious and additional sources of characters are needed to produce a more robust phylogeny for Apocrita.

Movement towards favourable microhabitats on the apple tree by *Cydia pomonella* caterpillars

Silvia Dorn, Ute Kuehrt, Joerg Samietz, Sibylle Stoeckli, Karsten Mody

ETH Zurich, Applied Entomology, CH 8092 Zurich, Switzerland

Introduction: While many studies focus on external feeders on plant leaves, little is known on cues guiding caterpillars within fruits. Neonate Cydia pomonella caterpillars bore quickly into apple fruit, then feed several weeks within the fruit before leaving it to search a cocooning site.

Methods: To determine temperature selection of feeding larvae, apple trees with newly infested fruits were radiated with infrared lamps under controlled conditions. After 3.5 weeks, thermal response of feeding larvae within apples was quantified by distribution of the feeding tunnels over each the radiated and the shaded hemisphere. Temperature selection of final-instar larvae was assessed in a cylindrical temperature gradient area.

Results: Caterpillars feeding inside fruits select the radiated, warmer hemisphere for building feeding tunnels. The proportion of larval cavities in the warmer hemisphere is positively related to increasing apple temperatures on that side, as well as to the temperature difference between the warm and the cold side. In contrast, final-instar larvae in search of cocooning sites show no temperature preference.

Conclusions: Beyond biotic factors known to influence larval movement, temperature appears to shape spatial microhabitat use even in internal feeders. Codling moth larvae change their behaviour during development from cryptic basking to no thermal preference, according to changing benefits, needs and constraints. Temperature as a driving force for movement in this species is further confirmed by a recent analysis of spatial distribution of fruits with larval damage on trees in two different environments.

Combining top-down with bottom-up forces to control bruchids: larval parasitoid and protein-based host plant resistance

Silvia Dorn[1], Guido Velten[1], Anja S. Rott[1], Ine Schmale[1], Cesar Cardona[2]

[1]ETH Zurich, Applied Entomology, CH 8092 Zurich, Switzerland, [2]Centro Internacional de Agricultura Tropical (CIAT), AA 6713 Cali, Colombia

Introduction: For the control of a coleopteran pest feeding within stored bean grains, we investigated the potential of a larval parasitoid in combination with protein-based plant resistance. This pest, the bruchid Acanthoscelides obtectus, infested the beans in 80% of the observed cases already in the field (Colombia). This infestation, invisible at harvest for the farmer, can lead to a complete yield loss within a few months storage period, rendering on-farm storage difficult.

Material: To evaluate the natural storage protein arcelin as a bottom-up force and the natural antagonist Dinarmus basalis as a top-down force, bioassays were carried out on beans with different relative arcelin content.

Results: All arcelin-containing bean lines consistently prolonged bruchid development and affected fitness of bruchid females, as indicated by their reduced body mass. The parasitoid accepted hosts on all bean lines, and parasitoid fitness was not impeded by arcelin. Even under conditions mimicking temporal complexity of bruchid infestations in the field, bruchid suppression is significantly higher on arcelin-containing bean lines than on arcelin-free cultivars.

Conclusions: Arcelin as a bottom-up force not only suppresses the bruchid Zabrotes subfasciatus as has been previously demonstrated, but also supports the proposed two-component integrated pest management system against the discussed bruchid A. obtectus. It extends the time frame during which parasitoids can attack the host successfully, and directly reduces its population growth rate. The storage protein arcelin appears to be harmless to the ectoparasitoid D. basalis, which therefore holds great promise as a top-down force in this system.

IPM practices on insect populations on stored rice in Portugal

Ines Pires[1], Diogo Lemos[1], Claudia Santos[2], Blaine Timlick[3], Maria Otilia Carvalho[4]

[1]Saludaes, SA, Oliveira de Azemeis, Portugal, [2]SOS Cuétara, Pombal, Portugal, [3]Canadian Grain Commission, Winnipeg, Manitoba, Canada, [4]Tropical Research Institute of Portugal - IICT, I.P., Lisbon, Portugal

Portugal is the biggest consumer of rice in Europe and consequently a large number of farmers and industries are associated with rice production and processing. In Portugal, rice is usually planted in April and harvested after August. Prior to processing, rice is stored as paddy on farm or in co-operatives until the end of winter when the remainder of the rice is transported to the processing facility.

As a tool to assist in rice storage decision making, monitoring programmes for environmental conditions and insect activity were conducted on farms and at rice milling facilities, in several warehouses, bins and granaries, containing paddy and brown rice and distributed through the three main rice production regions: Mondego, Tejo and Sado Valleys.

Monitoring on-farm storages, more insect species were identified than in rice mill. The main insect species were fungus-feeders. At rice mills, the main insect species caught were commodity feeders with the most abundant species being *Sitophilus* spp. (*S. zeamais* and *S. oryzae*) and *Tribolium castaneum*.

The studies conducted on five varieties of rice, Gladio, Fani, Eurosis, Ariete (paddy) and Suriname (brown rice), stored in granary and bin structures belonging to one rice mill, showed that grain temperature of stored rice was different among varieties and among paddy and brown rice and Gladio variety was the most susceptible to *Sitophilus* spp attack.

Chemically-Induced anosmia in mosquitoes: A novel way to prevent host finding

Ulrich Bernier[1], Kamlesh Chauhan[2], Daniel Kline[1], Donald R Barnard[1]

[1]USDA-ARS-CMAVE, Gainesville, FL, United States, [2]USDA-ARS-IICBL, Beltsville, MD, United States

Introduction: Hundreds of volatile to semivolatile chemical compounds on the skin of humans and other animals act as kairomones and allomones to produce host-seeking or host-avoidance by mosquitoes and other haematophagous insects. We have spent a decade examining the effect of these human-produced emanations on the host-seeking behavior of the anthropophilic mosquito species, *Aedes aegypti* L. and *Anopheles albimanus* Weidemann. Single compounds act as weak attractants alone, e.g. L-lactic acid but attract synergistically when combined in blends of two to three compounds. Within blends, the release rate and relative abundance of each compound can have a significant impact on attraction. Furthermore, there are some compounds that when added in trace amounts can inhibit the host-seeking ability of these mosquitoes in laboratory behavioral assays.

Methods: Analysis of human skin emanations was accomplished using gas chromatography-mass spectrometry. Bioassays were performed with a dual-port triple cage olfactometer using approximately 75 females, aged 6-10 days, per assay.

Results: Several compounds identified tentatively in human skin emanations suppress or inhibit host-seeking of mosquitoes when trace amounts of these were single compounds are combined with either synthetic attractant blends or attractant odors from human volunteers. We examined 42 compounds similar in chemical structure to the compounds in human emanations that inhibit host-seeking in mosquitoes. Of these, 24 produce significant inhibition of attraction from host-seeking *Ae. aegypti*. A subset of 12 of these compounds has been tested against *An. albimanus* and also inhibits host-seeking in this species.

Conclusions and Future Work: We believe that these compounds produce anosmia in mosquitoes and hope to characterize the physiological basis for this effect in the near future.

Spinosad 45 SC – the novel pesticide for the management of chilli pests

Monilal Chatterjee

Bidhan Chandra Agril University, Kalyani, West Bengal, India

Introduction: Chilli is an important vegetable as well as spices crop in Indian Agriculture. Though India ranks first in the world with reference to area and production of chilli, however the average productivity is very low in comparison to other countries. A major constraint in chilli production is direct damage to fruit by *Helicoverpa armigera* (H) and *Spodoptera litura* (F) and damage by thrips (*Scirtothrips dorsalis*) at vegetative growth of plants. As chilli is one of the most popular and profitable crop, farmers everywhere feel the need to protect such high value crops from any type of damage caused by insect pests. They often use synthetic insecticides indiscriminately, and insect resistance to insecticides and resurgence are very common in the tropics.

Methods: To control chilli thrips and fruit borers efficiently, a new organic pesticides Spinosad 45 SC with novel mode of action has been developed recently. To determine the effectiveness of this new pesticides at different doses compared with traditional chemicals effect on natural enemies and compatibility to other insecticides, fungicides and urea, two field experiments were done over two seasons. They compared five pesticides (Spinosad 45 Sc @ 45, 56 & 73 g a.i./ha, Imidacloprid 20SL @ 40 g a.i., Chlorpyrifos 20 EC @ 500 g a.i., Endosulfan 35 EC @ 525 g a.i. and Fipronil 5 Sc @ 40 g a.i./ha) with untreated control. All other agronomic practices were standard, and a blanket sprays to control mites was applied when necessary. First spraying was done with the appearance of thrips and thereafter three sprays at fortnightly interval were followed.

Results: The results showed that Spinosad 45 % SC at 56 and 73 gm a.i./ha gave best control of thrips up to 14 days in both seasons. It has also reflected in yield parameter. Similarly the fruit borer infestation was sharply reduced in Spinosad treated plot that was closely followed by Fipronil. In another observations Spinosad showed less hazard to natural enemies viz. *Menochillus* sp., *Syrphus* sp. And *Chrysoperla* sp. at different doses compared to untreated control. The compatibility of Spinosad with Quinalphos, Carbendazim and Urea was well and no phytotoxicity was noted at any stages of the crop growth .

Conclusions: Spinosad is a naturally derived insecticide produced by fermentation of bacterium, *Saccharopolyspora spinosa* and consists of a mixture of related Spinosyn toxins, principally Spinosyn-A and D. It acts as contact and stomach poison (Dow, 1997, Salgado, 1997; Thompson *et al.* 2000). It has novel mode of action, disrupts the functions of GABA receptors of small neurons in the central nervous system. Spinosad is considered to be 'fast-acting' insecticide provides 7 to 14 days of control have practically no odor, moderately strong soil absorption and degrades rapidly in the environment. It offers excellent selectivity to beneficial organisms with low environmental risk to human beings and has potential use in Integrated Pest Management (IPM) systems.

HIPV, HIPPO and IPM: Telling plants to pull in their defenders

David James[1], Vincent Hebert[2], Deborah Brooks[1], Lawrence Wright[1], Tessa Grasswitz[1], Castle del Conte Sandra[1]

[1]Washington State University, Prosser, Washington, United States, [2]Washington State University, Richland, Washington, United States

Deployment of synthetic methyl salicylate (MeSA), a herbivore-induced plant volatile (HIPV), in controlled release dispensers (CRD) in hops and grapes in the Pacific Northwest (PNW) of the United States has been demonstrated to increase populations of beneficial insects, improve conservation biological control (CBC) and suppress pests. Other synthetic HIPV (e.g. hexenyl acetate, methyl jasmonate) have also been shown to attract beneficial insects in the field. Identifying and understanding the chemical-ecological and eco-physiological mechanisms mediating beneficial insect attraction to HIPV, is a current focus of this project. Determining whether beneficial insects are recruited by direct attraction or whether plants are stimulated by synthetic HIPV to produce their own beneficial insect-attracting volatiles, is a key question. Preliminary results from laboratory experiments indicate that hop plants exposed to CRD of MeSA emit a different profile of volatiles compared to unexposed plants. Some of these volatiles from MeSA-exposed plants are known attractants of beneficial insects and/or repellents for pests. Turning on or telling plants to produce their own natural enemy attractants is an appealing idea and strategy, and may be responsible for much of the success seen hitherto in improving natural enemy populations and CBC in PNW grapes and hops. Field experiments using agricultural spray oil formulations with 2% MeSA applied to hop and grape plants, have demonstrated recruitment of some natural enemy species. This might be a more cost-effective and practical way of delivering HIPV to plants. This project is a good example of a crop protection application of chemical ecology: turning HIPV into HIPPO (Herbivore-Induced Plant Protection Odors)

Termite-fungus interactions: Are semiochemicals involved in the defense behaviour of the termite, *Macrotermes michaelseni*?

David . M. Mburu, Lynett Ochola, Nguya .K. Maniania, Peter. G. N. Njagi, Linus. M. Gitonga, Mary.W. Ndung'u, Ahmed Hassanali

[1]Icipe-African Insect Science for food and Health, Nairobi, Kenya, [2]Icipe-African Insect Science for food and Health, Nairobi, Kenya, [3]Icipe-African Insect Science for food and Health, Nairobi, Kenya, [4]Icipe-African Insect Science for food and Health, Nairobi, Kenya, [5]Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya, [6]Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya, [7]Icipe-African Insect Science for food and Health, Nairobi, Kenya

Introduction: Termites encounter diverse array of infective and symbiotic fungi in their hemiedaphic habitats. How these hemiedaphic insects cope in habitats with infective fungi is not well understood.

Objectives: To explore the relationship, if any, between virulence and repellency of fungus, *Metarhizium anisopliae* against termite, *Macrotermes michaelseni* and identify the mediating signals.

Materials and Methods: 15 isolates of *M. anisopliae* were screened for their virulence against *M. michaelseni* at standard conditions. Of these, virulence of 9 selected isolates was determined at different doses and LC_{50} values obtained. In a preliminary study, the repellency of a highly pathogenic isolate of *M. anisopliae* (ICIPE30) against *M. michaelseni* was tested in a Y-olfactometer. To establish if the repellency of the different isolates correlate with their virulence, the RC_{50} and LC_{50} values, respectively, were determined. Fungal volatiles were collected from the most and the least repellent isolates. GC-MS and GC-EAD profiles were obtained.

Results: The virulence and repellency of the different isolates showed a positive correlation. The GC-MS profiles obtained showed qualitative and quantitative difference in volatiles collected.

Conclusion: Our results suggest that termites have defensive behavioural repertoire to detect infective fungi through olfaction and avoid direct physical contact. The results suggest that the avoidance behaviour is mediated by differential semiochemical signals.

Tribolium spp. as model insects for pesticide efficacy studies

Frank Arthur, Jeff Lord

USDA-ARS-GMPRC, Manhattan, Kansas, United States

Stored-product insects can infest stored raw agricultural commodities, processed and packaged warehouses, and urban distribution and retail centers. There are a variety of important pest species, with varying degrees of susceptibilities to insecticides, and researchers often must make choices as to which species are appropriate for laboratory and field studies.

Tribolium castaneum, the red flour beetle, and *Tribolium confusum*, the confused flour beetle, are often used for pesticide studies, particularly those involving treated surfaces or exposure studies with aerosol insecticides. Adults of these species are often more tolerant to insecticides compared to other stored-product beetles, and therefore are good indicators species. Also, they are important economic pests, particularly in mills and warehouses. They are cosmopolitan and found in a variety of stored-product environments, including bulk grains. Finally the adults of *T. castaneum* rarely fly unless temperatures are above 27°C, and *T. confusum* does not fly at all. Consequently, they can be placed in open Petri dishes and directly exposed to aerosol insecticides in actual field trials. They can also be used in laboratory studies in which adults are exposed on different treated surfaces. Finally, the two species often differ in their susceptibility to insecticides, depending on a variety of factors, including the specific strains being tested, the actual insecticide, and methods of exposure.

Although *Tribolium* species can be found in stored raw commodities, they may not be as useful for pesticide studies on treated grains compared to internal feeders such as *Rhyzopertha dominica* and weevils of the genus *Sitophilus*. In these types of studies, progeny production is often measured in addition to direct mortality of adults. However, depending on the commodity and region of the world, Tribolium spp. can be an important component of the pest complex.

Sexual cannibalism and male risk-taking behavior in the Chinese praying mantid

William Brown

State University of New York at Fredonia, Fredonia, NY, United States

Introduction: Praying mantids are famous for the act of sexual cannibalism. Previous work in my laboratory showed that males actively assess the risk imposed by individual females and alter their mating behavior to avoid cannibalism. Here I examine the level of risk taking by males with varying prior experience with mates. Specifically, I hypothesized that males will alter rate of approach, extent of courtship, and degree of cautiousness with which they approach hungry, rapacious females depending on their perception mate availability.

Methods: We collected adult praying mantids (*Tenodera aridifolia*) from wild populations in Autumn 2006 and 2007 and placed individual males into either (a) high or (b) low female encounter treatments to alter male perception of mate availability. Subsequent to the treatments we tested the behavior of males under 2 conditions of differing risk of sexual cannibalism, either (a) approaching a hungry female head-on (high risk), or (b) approaching a well-fed female from behind (low risk).

Results: Males responded to the differing risk of cannibalism by altering approach to females. As predicted, males with prior exposure to females displayed the greatest difference in behavior, slowing down their approach and mounting from a greater (and probably safer) distance in response to level of risk. In contrast, males without prior exposure to females approached both high- and low-risk females relatively rapidly and closely, indicating greater overall risk taking.

Trees as mediators of pathogen-insect interactions: The role of systemic induced resistance

Pierluigi Bonello[1], Daniel Herms[2], Thomas Gordon[3], David Wood[4], Nadir Erbilgin[5], Donald Cipollini[6]

[1]Dept. of Plant Pathology, The Ohio State University, Columbus, Ohio, United States, [2]Dept. of Entomology, The Ohio State University, Wooster, Ohio, United States, [3]Dept. of Plant Pathology, University of California, Davis, California, United States, [4]Div. of Insect Biology, University of California, Berkeley, California, United States, [5]Dept. of Renewable Resources, University of Alberta, Edmonton, Alberta, Canada, [6]Dept. of Biological Sciences, Wright State University, Dayton, Ohio, United States

Plant defense theory revolves around plant responses to herbivory by animals, especially arthropods, with significantly less reference to what could be called “microbial herbivory”, *i.e.* parasitism of plants by symbiotic microbes, *e.g.* pathogens. The virtual absence of this microbial component has constrained a comprehensive understanding of plant defense, given the increasing evidence that plant-associated microbes can be potentially strong modulators of plant-herbivore interactions.

Coniferous trees are often dominant species in both boreal and temperate forests, wherein they play critical roles in ecosystem function. In natural environments, ecosystem stability appears to be the norm, notwithstanding the co-occurrence of insect and microbial species inherently capable of killing their host trees. Adaptive plasticity of host trees involving inducible mechanisms of resistance against invading organisms is likely to play a crucial role in these interactions. We hypothesize that systemic induced resistance (SIR) elicited by pathogens and mutualists represents a common and important phenomenon in coniferous trees, allowing for a balanced allocation of resources between growth and defence. We also propose that the growth/differentiation balance hypothesis (GDBH) should be integrated with the SIR hypothesis to provide a fuller and more mature extension of existing plant defence theory. Several lines of evidence will be provided in support of these hypotheses along with proposed future lines of investigation.

Products and services of the Armed Forces Pest Management Board, USA

Stanton Cope, Sharon Spradling, Richard Johnson

Armed Forces Pest Management Board, Forest Glen, MD, United States

The Armed Forces Pest Management Board, located in Forest Glen, Maryland, USA, provides a wide variety of products and services that are useful to medical entomologists, public health personnel and preventive medicine professionals. This presentation will review all available products and services and demonstrate a step-by-step methodology of how to access them from our website at afpmp.org.

Temperature-controlled colour change in the chameleon grasshopper (*Kosciuscola tristis*) (Orthoptera: Acrididae).

Kate Umbers, Gregory Ian Holwell, Adam James Stow

Macquarie University, Sydney, NSW, Australia

The chameleon grasshopper can change colour from black to pale turquoise in just 30 minutes. This condition is likely to have a thermoregulatory function and is unique amongst arthropods. This study investigated the environmental factors that influence colour change in the chameleon grasshopper. The only previous work on colour change in the chameleon grasshopper was carried out by Key and Day in 1954. Our aim was to identify any relationship between ambient temperature, light level and time of day and the colour of chameleon grasshoppers. In caged field experiments, we employed spectrophotometry, digital photographs and a laser thermometer to measure the colour and temperature of grasshoppers and their environment. We found that grasshoppers kept at higher temperatures were significantly paler than those kept at lower temperatures. We show that this response is independent of circadian patterns and light intensity.

Evidence for transitions to sociality in the small carpenter bees (Apidae: Ceratinini)

Sandra Rehan[1], Miriam Richards[1], Michael Schwarz[2]

[1]Brock University, St. Catharines, Ontario, Canada, [2]Flinders University, Adelaide, South Australia, Australia

Introduction: Presocial taxa are vital to understanding the origins of sociality and the evolutionary steps from solitary to social life. Many authors have inferred incipient sociality in *Ceratina* and suggested their potential for understanding the origins of sociality. Ceratinini is a primarily subsocial lineage, with mothers known for their longevity, nest loyalty throughout the breeding season, and extended maternal care. Both solitary and social behaviour is reported within the tribe, but these observations lack a phylogenetic context. A phylogenetic framework is imperative in order to reveal evolutionary transitions between solitary and social behaviour.

Methods: Ceratinini comprises a lone genus, *Ceratina*, that represents 23+ subgenera of cosmopolitan distribution. To date, representatives from 13 subgenera have been sampled for phylogenetic analysis based on sequences of one nuclear (EF1α-F2) and two mitochondrial (COI and cyt b) genes. Maximum parsimony and Bayesian analyses were used to infer phylogenetic relationships.

Results: Maximum parsimony and Bayesian analyses produce similar topologies and high support of subgeneric nodes. The continental endemism of most morphologically described subgenera is well supported genetically and geographically. However, a few subgenera appear to be biogeographically disjunct, as well as paraphyletic, suggesting a need for revision of their taxonomic status. Mapping social behaviour onto a consensus tree reveals basal subsociality for the tribe, and at least two evolutionary transitions to sociality.

Conclusions: *Ceratina* offer key insights into the transition from subsocial to social states. With subsocial preadaptations set, a few taxa have achieved sociality under the right combination of ecological and behavioural circumstances.

The utility of molecular diagnostics in biological control: evaluating non-target effects associated with introduced parasitoids

Tara Gariepy, Russell Messing

University of Hawaii at Manoa, Department of Plant and Environmental Protection Sciences, Kapaa, Hawaii, United States

Direct and indirect non-target effects associated with exotic parasitoids can be difficult to predict and measure using conventional rearing and dissection techniques. Host and parasitoid mortality that occur during rearing can limit the accuracy of information obtained from field-collected samples, and dissection does not always provide accurate identification of parasitoids to the species level. However, polymerase chain reaction (PCR)-based techniques provide rapid and accurate identification of parasitoid species, and are not affected by mortality issues associated with host rearing. Furthermore, information regarding multiparasitism and hyperparasitism of individual hosts can be obtained using PCR-based techniques, and may provide additional insight on multitrophic interactions and interspecific competition among parasitoids that share the same host. Here, we provide case studies to demonstrate the utility of PCR-based assays in both pre- and post-release studies on classical biological control agents. Molecular diagnostic tools for detection and identification of parasitoids within host insects provide a unique approach to study host-parasitoid, parasitoid-parasitoid, and parasitoid-hyperparasitoid interactions in field-collected insects. A better understanding of these interactions in the field may improve the success of natural enemy establishment and suppression of pest populations and may be used to predict and measure potential non-target effects.

Long-term sustainable area-wide mating disruption program with improved monitoring tools for oriental fruit moth and codling moth in Australian orchards

Alexandre Il'ichev

Department of Primary Industries Victoria, Biosciences Division, Tatura, Victoria, Australia

Area-wide pheromone mediated mating disruption (MD) has been successfully used for long-term and sustainable Integrated Pest Management (IPM) programs in Australian orchards. Initially, hand-applied MD dispensers were used to treat individual orchard blocks and only known hosts of oriental fruit moth (OFM) and codling moth (CM). An increased incidence of pest damage on the borders of MD treated blocks adjacent to blocks without MD treatment stimulated an area-wide application of MD for better crop protection. An initial area-wide MD program, with more than 1,100 ha of 40 contiguous orchards covered with MD dispensers, applied to all fruit trees in the Cobram region of northern Victoria, Australia, substantially improved protection against OFM damage during 3 years. When the initial program was finished, a number of small growers stopped area-wide MD applications and returned to the conventional insecticide spay program on pome fruit with MD treatment of only stone fruit. This resulted in an increase of OFM damage to the neighbouring properties where area-wide MD treatment continued. Affected local growers took the initiative to continue this area-wide MD program as a self-sufficient community approach and re-established MD across the whole Cobram region.

Later area-wide MD program to control OFM and CM has been successfully established in Greater Shepparton and Invergordon regions of northern Victoria. Both OFM and CM have the ability to infest new hosts and could quickly build up population level in orchards without proper MD treatment. Reliable monitoring of these pest in orchards treated with MD is crucial for sustainable pheromone-based IPM. New host-plant attractants were tested to improve monitoring of these pests, particularly mated females in the orchards treated with MD. Semiochemical-based IPM and selective area-wide MD programs are the key elements in development of cost effective strategies for pest control while protecting the environment by reducing pesticide pressure in orchards.

The butterfly bell curve: linking behavior, brains, and life history in the study of host learning

Emilie Snell-Rood, Wulfila Gronenberg, Goggy Davidowitz, Daniel Papaj

University of Arizona, Tucson, AZ, United States

Introduction: Learning allows animals, including insects, to exploit rare or novel environments. In nature, hostplants of butterflies generally bear green foliage, and many butterflies show innate preferences for green during host search. However, butterflies may encounter hosts of other colors, such as red. This work sought to determine if butterflies can learn uncommon colors in relation to oviposition and if such learning is associated with costs, such as increased neural tissue, that might maintain innate color biases.

Methods/Results: In field cage assays, host search in both the pipevine swallowtail butterfly, *Battus philenor* and the cabbage white butterfly, *Pieris rapae*, is innately biased towards green, yet females readily learn red in association with oviposition on red hosts. In the cabbage white, full-sib families varied in initial green bias and ability to learn red hosts. The capacity to learn red was associated with larger brains and less mature ovaries at emergence, suggesting a 'production cost' of learning. However, regardless of genetic background, the size of certain brain regions increased and fecundity decreased with experience learning red hosts, suggesting an 'operating cost.' Finally, cabbage whites originating from agriculturally-intensive areas had a stronger green bias, suggesting that costs may select against learning in constant or predictable crop settings.

Conclusions: Host learning in butterflies is maintained by benefits of using novel hosts but in less variable environments the costs of learning, in terms of neural tissue and delayed reproduction, may favor innate biases in host cue preference.

Juvenile Hormone as a regulator of plasticity in adulthood: from butterflies to beetles

Emilie Snell-Rood[1], Daniel Papaj[1], Goggy Davidowitz[1], Wulfila Gronenberg[1], Armin Moczek[2]

[1]University of Arizona, Tucson, AZ, United States, [2]Indiana University, Bloomington, IN, United States

Introduction. Many organisms cope with environmental variation through the development of suites of traits appropriate to local conditions. Such phenotypic plasticity is often mediated by endocrine regulators with many downstream effects. While we know much about how hormones, such as juvenile hormone, mediate plasticity during larval and pupal development, we know much less about how it mediates plasticity in adults confronted with changing internal or external environments.

Methods. This study investigated the effects of JH on mediating host learning in adult butterflies. It is known that early in adulthood, JH regulates reproductive development in Lepidoptera; given that learning is costly, we predicted that JH may antagonistically link investment in learning and neural tissue to investment in reproduction.

Results. Adult butterflies (*Pieris rapae*) treated with methoprene (a JH analog) were, relative to controls (treated only with the solvent), less likely to increase their ability to locate novel (red) hosts over two days of learning. Instead, they were more likely to search for innately-preferred green colors. Furthermore, prior to host-learning, hormone-treated butterflies developed relatively smaller mushroom bodies, regions of the insect brain involved in learning.

Conclusions. This research supports the idea that JH has a suite of effects in adult insects. Further insights will depend at least in part on our understanding of the downstream targets of JH action. We end by highlighting several experimental avenues designed to identify and characterize interactions between JH and its targets using recently developed gene function and genomic approaches in polyphenic horned beetles, *Onthophagus*.

Development and application of a genetically engineering strain WG-001 of *Bacillus thuringiensis*

Ziniu Yu, Ming Sun, Ziduo Liu, Jianhong Li

National Engineering Research Center for Microbial Pesticides, Wuhan, China

Eight strains highly toxic to lepidopteran, dipteran, and coleopteran insects isolated from 1800 *Bacillus thuringiensis* strains stored in our lab had been screened, and their insecticidal crystal protein genes *cry1Ab*□*cry1Ac*□*cry1Ea*□*cry1C*□*cry2Ab* and *cry1A* , and assistant protein gene *P19* and *P20* had been cloned. Three plasmids with different functions were constructed with replication vectors of pBMB9741□pBMB 2062 and pBMB 607□ resolution vectors of pBMB 801 and pBMB1808, and integration vectors of pBMB R14, pBMB f7, pBMBr13 and pBMBF13, respectively.

Through gradually increasing culture temperature, nine non-crystallous mutant strains were screened. plasmid-free derivative strain BMB171 had highest transformation efficiency among four vectors transformed. The function of upstream promoters of target gene *cry1A* and *cry1D* of their effects on cry-lacZ fusion gene's transfection and regulation was analyzed, and difference of expression and regulation of target genes *cry1A* and *cry1D* was analyzed in different strains. It indicated that gene expression was related to early-stage carbon resource and cell metabolization.

The engineering strains with various functions were constructed. Fermentation medium and culture condition of highly effect engineering strain WG-001 were optimized, and fermentation dynamics and productive technique of the strain WG-001 was investigated. The safety certificate of the strain WG-001 was acquired in 2005 after Mid-test in laboratory done by China Agriculture Genetic Engineering Safety Assessment, Environment release and commercialized test. Large-scale production of the strain WG-001 was done with potency 60000IU/mg of technical powder and 8000IU/mg of oil emulsion. WG-001 had been applied to control agricultural and forestry pest, such as *Helicoverpa armigera*, *Plutella xylostella*, *Tryporyza incertulas* and *Dendrolimus punctatus*. Some product of WG-001 had been exported in abroad.

Next generation repellents of public health value

Scott P Carroll

University of California, Davis, CA, United States

Insect repellents provide flexible means of personal protection to fill inevitable gaps in other control measures– gaps currently most profound in tropical regions of the developing world. Safe and effective repellents based on deet, picaridin, IR3535 and PMD are available; properly deployed, such products could in theory limit disease outbreaks. However, currently available repellents have not been developed specifically to address public health needs, and thus suffer from several (surmountable) logistic limitations. These include affordability, distribution, duration of efficacy, and user acceptance (particularly important when daily use is critical to disease prevention). Positive developments include formulation improvements that increase the cosmetic appeal of deet and the duration of efficacy of IR3535. In addition, a new, affordable PMD-based repellent is being developed to enter local markets in impoverished regions. Vital to such initiatives is US Environmental Protection Agency approval, which is globally influential, but difficult to attain due to increasingly stringent and costly human research subject oversight.

Evolution in response to climate change and species invasions

Scott P Carroll

University of California, Davis, CA, United States

The biological consequences of climate change and species invasions should be studied from an evolutionary perspective. Affected populations, whether *in situ* or displaced, invading or invaded, may exhibit substantial adaptation within a few generations. Swift adaptation may avert extinction, permit establishment after colonization, or, in invaded communities, act to limit the spread or impact of an invader. I will summarize recent findings on evolution in response to climate change and species invasions, and discuss the potential for *adaptive biological management* of disrupted communities.

The impact of floral resource subsidies and landscape context on biological control in forage brassicas

Mattias Jonsson[1], Steve Wratten[1], Cory Straub[2], Hannah Buckley[1], Brad Case[1], Raphael Didham[3], Roddy Hale[1]

[1]Lincoln University, Lincoln, New Zealand, [2]University of Wisconsin, Madison, United States, [3]University of Canterbury, Christchurch, New Zealand

Introduction: The intensification of agricultural production systems has resulted in a severe decline in biodiversity and this is likely to lead to deteriorating ecosystem services such as biological control. Several studies have shown that complex landscapes with a high proportion of non-crop vegetation have higher densities of natural enemies and tend to have lower pest numbers than do simpler landscapes dominated by agriculture. However, it is not known how best to design landscapes to maximise biological control. Conservation biological control aims at improving the conditions for natural enemies of pests, for example by adding flowering plants that can provide non-prey food as well as shelter. To date, conservation biological control research has usually focused on plots or single fields while ignoring processes at larger spatial scales. However, it is likely that the effect of local measures depend on the composition of the surrounding landscape. In the research project presented here we firstly investigate how vegetation composition at different spatial scales surrounding fields of forage brassicas in New Zealand determines biological control of the key pests diamond back moth, *Plutella xylostella* and cabbage grey aphid, *Brevicoryne brassicae.* Secondly we study if the effect of local conservation biological control measures, in the form of floral resource subsidies is influenced by landscape features. Analysis and field experimentation are still under way. Key results from both these studies will be presented.

The impact of flowers and omnivory on a four trophic level food web – implications for biological control

Mattias Jonsson, Katherine Robinson, Steve Wratten, Shona Sam

Lincoln University, Lincoln, New Zealand

Introduction: Many insect predators feed on nectar and/or pollen and increasing the availability of such resources can improve biological control. If such resources also increased the fitness of predators' enemies, this may affect the likelihood of success of biological control programmes. The lacewing *Micromus tasmaniae* is a true omnivore that as an adult feeds on both flowers and aphids, whereas the parasitoid wasp, *Anacharis zealandica* is a life-history omnivore, feeding on lacewings at the larval stage and flowers as an adult.

Methods: In a series of laboratory bioassays and a field cage experiment we explored how flowering buckwheat affected longevity, oviposition and population dynamics of lacewings and parasitoids at different levels of aphid availability.

Results: The effect of flowering buckwheat on lacewing longevity and oviposition depended on aphid availability, having a positive effect only at low aphid densities. Buckwheat significantly increased parasitoid longevity. In field cages, buckwheat decreased the density of lacewings when the aphid density was high, probably because of increased parasitism rates. Towards the end of the experiment when the aphid populations had declined, the effect of buckwheat on lacewing density became positive, probably because lacewings were starving in the absence of flowers and with low prey availability.

Conclusion: Flowers may benefit species at the fourth trophic level and this may reduce the populations of predators of pests. More effective biological control may be achieved by providing food plants that selectively benefit predators of pests but have a lesser or no effect on their antagonists.

Historical biogeography of selected species of cicada within the tribe Platypleurini (Hemiptera: Cicadidae).

Benjamin Price, Martin Villet, Nigel Barker

Rhodes University, Grahamstown, South Africa

Molecule-based phylogenetics, and in particular comparative phylogeography of phytophagous insects, can prove useful in identifying places and processes central to the origin and maintenance of biological diversity. Cicadas in particular have proven useful as tools for examining the effects of distribution, host plant association and geographic barriers on gene flow in species. The family (Cicadidae) is subdivided into about 20 tribes, of which the tribe Platypleurini is predominantly African. Molecular studies have shown that the platypleurine cicadas are a fairly ancient tribe within the cicadas and have indicated that the group dispersed in a southward and westward radiation from East Africa. The process of biodiversification has apparently involved host plant switching (though altered host-finding cues), modified acoustic signalling, altered habitat preferences, and population genetic effects brought about by climate change and sea-level fluctuations. The high rates of endemism shown by these insects can assist in generating insight into the radiation and diversification of the platypleurines, which is crucial to a mechanistic understanding of biodiversity.

Modelling the responses of tsetse to climate change: from mechanisms to macroecology

John Terblanche[1], Steven Chown[2], John Hargrove[3]

[1]Dept Conservation Ecology & Entomology, Stellenbosch, South Africa, [2]Centre for Invasion Biology, Stellenbosch, South Africa, [3]SACEMA, Stellenbosch, South Africa

As the vectors of trypanosomiasis, what some have called a neglected tropical disease, tsetse are of considerable medical and veterinary significance in sub-Saharan Africa. In consequence, understanding the factors determining their population dynamics, spatial variation in abundance and geographic distributions has long been of interest. For several species, large-scale, largely bioclimatic modelling work has identified temperature and saturation deficit as significant factors influencing spatial variation in abundance. Small scale work on population dynamics has identified temperature as a major direct and indirect contributor to mortality in the adults, and saturation deficit a source of mortality in the pupae. However, the mechanisms by which physiological tolerances translate to population dynamic effects and to large scale distributions have yet to be fully explored. Here we do so for *G. pallidipes* and *G. morsitans* from southern Africa, using laboratory and field-based physiological data, field collected population data, and a model combining the two. Using the model we also make predictions for changes to populations of these species using a gradual temperature increase model typically applied to climate change effects and models incorporating extreme thermal events that are also predicted to increase. In so doing we also provide information on a much-debated topic in evolutionary biology: the contribution of rare, extreme events, and more common sub-lethal events to population dynamics and evolutionary change.

Development and demonstration of Earth Observation technology for identifying potential mosquito larval habitats in Kilifi, Kenya.

Charles Mbogo[1], Jiangui Liu[2], Janet Midega[1], Joseph Nzovu[1], John Bennett[1], Mark Kampfer[1], Tom Hirose[1]

[1]Kenya Medical Research Institute, Kilifi, Kenya, [2]Noetix Research Inc, Ottawa, Ontario, Canada

Introduction: Malaria is a serious health problem in the Sub-Saharan region of Africa, Latin America and tropical areas in Asia, affecting approximately 300 million people and causing over 1 million deaths each year. Solutions are needed by governments and health organizations to combat with this disease. Remote sensing and GIS techniques are useful for generating thematic map layers that identify the spatial and temporal variability of malaria risk. This information can be invaluable for allocating limited resources in an effective way. Under the TIGER initiative and the support from Canadian Space Agency, Noetix Research in collaboration with the Kenya Medical Research Institute are working on a project to develop technologies based on earth observation data for malaria risk mapping. This paper reports our results using remote sensing data and digital elevation model (DEM) to map potential mosquito larva habitats in Kilifi district, Kenya.

Methods: Shuttle Radar Topographic Mission (SRTM) DEM was used to map topographic features, such as slope, depressions, streams and topographic wetness index. SPOT image was used for vegetation and soil wetness mapping. Multi-temporal synthetic aperture radar (SAR) images were obtained for 2006 and were used for mapping wetland features, such as permanent and ephemeral water bodies, areas that are potential to cumulate water during precipitation. Field surveys were carried out to deploy sample sites, record larval status, and characterize the physical environmental conditions of the sites. The ability for mapping mosquito larvae habitat using remote sensing data generated thematic layers was evaluated using statistical analysis. Our data shows that the thematic layers can correctly identify over 60% of the sites, representing a fair agreement with the observations.

Conclusions: Multi-temporal Radarsat SAR images are useful in developing thematic layers which are useful in mapping potential mosquito larval habitats or environmental factors that regulate vector-borne disease transmission.

RNA interference (RNAi) with allatoregulating neuropeptide genes from *Gryllus bimaculatus* (Ensifera: Gryllidae) and *Spodoptera frugiperda* (Lepidoptera: Noctuidae) and its effects on reproduction

Klaus H. Hoffmann, Manuela Klim, Sandra Merz, Mehriye Sertkol, Stephanie A. Westerlund, Martina Meyering-Vos

Animal Ecology I, University of Bayreuth, Bayreuth, Germany

Double-stranded (ds) RNA gene interference is an efficient method to silencing gene expression in a sequence-specific manner. Here, we show that dsRNA targeting genes for allatoregulating neuro-peptides in the Mediterranean field cricket, *Gryllus bimaculatus* (type-A allatostatins; FGLamide allatostatins), and the fall armyworm, *Spodoptera frugiperda* (type-C allatostatin or Manse-AST, Spofr allatotropin-2), injected into freshly moulted last instar larvae or adults produced a rapid and long lasting reduction in the mRNA levels in various tissues. The effects lasted for up to 7 days. Following dsRNA injections, the juvenile hormone titers in the haemolymph (as measured by HPLC-mass spectrometry) were clearly affected in a peptide- and stage-dependent manner resulting in significant changes in adult development and reproduction:

(1) Type-A allatostatin dsRNA injection induced a reduced body weight gain in larval and adult crickets and the imaginal moult was incomplete.
(2) Silencing the allatostatin type-A expression also reduced the egg and testes development in crickets, and the oviposition rate was drastically reduced in both species.
(3) Following injection of either type-C allatostatin or allatotropin-2 dsRNA into last instar larvae of *S. frugiperda*, the last larval stage was prolonged. In prepupae, the juvenile hormone titer was decreased, but the animals pupated and moulted normally.
(4) In adult moths, gene silencing for both peptides clearly reduced the oviposition rate.

The present study confirms the effectiveness and specificity of gene silencing of allatoregulating neuropeptides by RNAi. Thus, RNAi can be used in order to prove putative functions of the various types of allatoregulating neuropeptides in different insect orders.

Supported by the Deutsche Forschungsgemeinschaft (ME-2034/1-3 and GRK 678/2)

Cloning and characterization of the genes responsible for larval body color mutants in the silkworm, *Bombyx mori*

Yan Meng[1], Susumu Katsuma[1], Takaaki Daimon[1], Kazuei Mita[2], Yutaka Banno[3], Toru Shimada[1]

[1]Department of Agricultural and Environmental Biology, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Yayoi 1-1-1, Bunkyo-ku, Tokyo 113-8657, Japan, [2]Insect Genome Research Unit, National Institute of Agrobiological Sciences, Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan, [3]Institute of Genetic Resources, Graduate School of Bioresource and Bioenvironmental Sciences, Kyushu University, Hakozaki 6-10-1, Higashi-ku, Fukuoka 812-8581, Japan

Hundreds of mutant strains of the silkworm *Bombyx mori* are valuable genetic bioresources, quite a few of which are related to body color pigment formation. *red blood* (*rb*, 21-0.0) is a recessive mutant with larval skin reddish, whose hemolymph turns red in the air although hemolymph from normal strains turns black in melanization. *lemon* (*lem*, 3-0.0) is another recessive mutant, which grows normally but body color is deep yellow. *lem^{l}*, a *lem* allele, is homozygous lethal immediately after the first ecdysis with bright yellow skin. Previous studies showed that the red body color was caused by abnormal accumulation of 3-hydroxykynurenine in *rb* strain, and that a large amount of 7,8-dihydropteridin was accumulated in the integument of *lem* larvae. Recently, we successfully identified the candidate genes, i.e. *kynureninase* (*BmKyn*) for *rb* and *sepiapterin reductase* (*BmSpr*) for *lem* and *lem^{l}* using *B. mori* EST databases. Kynureninase is an important enzyme in the kynurenine pathway of tryptophan metabolism. *BmKyn* encodes a 406-aa protein. A single nucleotide mutation, which substitutes isoleucine for threonine at residue 102, was found in the *BmKyn* ORF of *rb* strains. This mutation resulted in a marked reduction of BmKYN activity as compared to that of normal type. Sepiapterin reductase catalyzes the biosynthesis of tetrahydrobiopterin in the metabolic processes of guanosine triphosphate. An abnormal forward stop codon in the *BmSpr* ORF caused 5-aa deletion in the *lem* strains. We also found that 27 nts were tandemly inserted into *BmSpr* ORF of *lem^{l}* mutant resulting in an addition of 9-aa residues. Our data suggest that BmSPR activity deficiency leads to *lem* larvae body color deep yellow, and that BmSPR activity loss is responsible for *lem^{l}* larvae lethality.

The impacts of alien plants on native pollinators

Caroline Nienhuis, Jane Stout

Trinity College Dublin, Dublin, Ireland

Introduction: Invasive alien plants can impact native plant communities directly and indirectly but little is known about their effects on native pollinators. The invasive alien *Impatiens glandulifera* (Balsaminaceae) was used to investigate the effects of alien plant removal and density on native pollinator assemblages and native co-flowering plants.

Methods: Pollinator assemblages in sites where *I. glandulifera* was absent, present and had been experimentally removed were assessed by measuring insect visitation to *I. glandulifera* and artificial potted native plant communities. Mark-recapture experiments were conducted to estimate bumblebee utilisation of all sites.

In addition, bumblebee foraging behaviour on *I. glandulifera* and native co-flowering plants was examined. The effect of *I. glandulifera* plant density on bumblebee visitation to native plants, deposition of alien pollen on native plant stigmas and subsequent seed set was assessed.

Results: Although the presence and/or removal of *I. glandulifera* did not affect insect abundance, bees, especially bumblebees showed high visitation levels to the alien. Invaded sites did not attract a greater abundance or diversity of bumblebees.

Bumblebee species differed in foraging behaviour with low levels of flower constancy potentially causing improper pollen transfer. Although high *I. glandulifera* densities seemed to facilitate visitation to native plants, high alien density significantly decreased seed set of some native plants.

Conclusions: Its high nectar secretion rate and sugar concentration make *I. glandulifera* an extremely attractive nectar source for bumblebees. Self-incompatible perennial plants, in particular those relying on cross-pollination and growing at low densities may be greatly affected by *I. glandulifera*.

Monitoring fruit flies (Diptera: Tephritidae) in Africa

Mervyn Mansell, Jeffrey Austin, Kenneth Nagata

Animal and Plant Health Inspection Services (APHIS), United States of America Department of Agriculture (USDA), Pretoria, South Africa

Fruit flies are among the world's worst pests of cultivated fruits and vegetables. They endanger food security globally, especially in Africa and are a serious impediment to trade. Africa is home to a number of economically important flies, including Mediterranean fruit fly, generally regarded as the world's most dangerous fruit pest. Besides the indigenous taxa, four additional species have recently invaded Africa, further compromising Africa's trade potential and food security. Millions of dollars are spent annually on phytosanitary measures to control Tephritidae and to prevent the establishment of invasive populations in pest free countries.

At least 12 species of indigenous Tephritidae are of economic significance in Africa: *Ceratitis capitata* - Mediterranean fruit fly, *C. rosa* – Natal fruit fly, *C. fasciventris*, *C. anonae*, *C. cosyra* – Marula fruit fly, *C. silvestrii*, *Dacus bivittatus*– Pumpkin fly, *D. ciliatus* – Lesser pumpkin fly, *D. vertebratus* – Jointed pumpkin fly, *D. frontalis*, *Trirhithrum coffeae* – Coffee fly, *T. nigerrimum*, *Bactrocera oleae* – Olive fly, as well as several in Madagascar (*Ceratitis malgassa* – Madagascan fruit fly, *C. catoirii* – Mascarene fruit fly, *Dacus demezzeri*). In addition, four species of *Bactrocera* have recently invaded Africa: *B. zonata* – Peach fly, *B. invadens* – Invader fly, *B. cucurbitae* - Cucurbit fly, *B. latifrons* – Solanum fly.

A number of countries in Africa have established surveillance programmes and one has a sterile male facility to enhance phytosanitary capacity. An overview is provided of the pest species and phytosanitary measures to counter them.

Novel application of pollen to augment predatory mite populations

Phyllis Weintraub[1], Carmit Tal[1], Eric Palevsky[2], Yonattan Maoz[2], Moshe Coll[3], Samuel Gan-Mor[4]

[1]Agricultural Research Institute (ARO), Gilat Research Center, Israel, [2]ARO, Newe-Ya'ar Research Center, Ramat Yishay, Israel, [3]Faculty of Agricultural, Food and Environmental Quality Sciences, Hebrew University, Rehovot, Israel, [4]ARO, Volcani Center, Bet Dagan, Israel

Introduction: Pollen supplements have been demonstrated to improve the efficacy of biological control agents. However, supplements have not been used beyond small trials because of the arduous application. We have developed an efficient application unit for orchards, greenhouse and field crops and report preliminary results.

Methods: A patented pollen application unit, which places an electrostatic charge on pollen, was used to deliver corn pollen to seedling peppers (affected by *Polyphagotarsonemus latus*) and avocado trees (affected by *Oligonychus perseae*). Plants were treated with pollen then predatory mites (*Amblyseius swirskii* and *Euseius scutalis*, respectively) were released. Pest and predator populations were monitored by rinsing leaves in 80% EtOH or by direct observation.

Results: On greenhouse peppers we obtained significantly more *A. swirskii* for a period of 26 days after 1 pollen application as compared to non-pollen treated plants, in field trials there were fewer *P. latus* on plants in which the predators were supplemented with pollen. At the end of a 6-week potted avocado trial, there were significantly more predators and fewer pests as compared to non-pollen-treated plants. Pollen supplements of natural occurring *E. scutalis* in avocado orchards showed similar trends.

Conclusions: The goal of this work is to improve the biological control provided by generalist predators by allowing their early establishment. These initial trials demonstrate the beneficial effects of pollen supplements on *A. swirskii* and *E. scutalis* in greenhouse and field trials. Optimum pollen density and application rates, effect of pollen on pests and IGP have yet to be determined.

Relating ichneumonoid phylogeny to global diversity patterns

Donald Quicke, Owen Jones, Andy Purvis

Imperial College London, Silwood Park Campus, Ascot, United Kingdom

Species-richness varies in complex ways across the globe and among phylogenetic lineages. Clade diversification is shaped by both organism traits and features of their environments, but most data sets are too small to allow these two kinds of influence to be separated. High-diversity cosmopolitan clades showing many independent geographic and biological transitions are needed in order to distinguish the two effects.

The results of new phylogenetic analyses of a cosmopolitan insect group, the Ichneumonoidea, are used to investigate this further. A 1001 taxon molecular (28S rDNA) and a combined molecular-morphological data set is used to generate Ichneumonidae phylogeny estimates using a range of alignment algorithms. The data set comprises representatives of all subfamilies, all except three tribes and all but one of the genera highlighted as placed uncertainly. These trees were used to construct lineage through time plots to which models of diversification rate such as Yule process, or birth-death models, etc. were fitted. The slopes of these models provide estimates of 'birth' and/or 'birth-death' rates for the included lineages.

Diversification rates are estimated for the whole tree and for subsets of lineages from different regions (tropical or temperate) and with different functional traits (idiobiont or koinobiont). The effect of geography and life-history on our diversification rate estimates was then examined. By repeating analyses under a range of diversification models we the statistical support for each. These results will help to explain current ichneumonoid diversity patterns and go some way to addressing hypotheses of distribution patterns in other taxonomic groups.

Potential of entomopathogenic nematodes for the control of false codling moth, *Thaumatotibia leucotreta*, (Lepidoptera: Tortricidae) in laboratory bioassays

Antoinette Malan[1], Sean Moore[2]

[1]*Department of Conservation Ecology and Entomology, University of Stellenbosch, Stellenbosch, Western Cape Province, South Africa,* [2]*Citrus Research International, Humewood, South Africa*

Introduction: False codling moth (FCM), *Thaumatotibia leucotreta* (Meyrick), is an endemic key pest of citrus in South Africa. None of the current control measures target the soil stages of FCM. The inundative use of entomopathogenic nematodes (EPNs) against the soil stages of FCM offers a window period for the control of FCM.

Methods: A survey for EPN in citrus orchards from three provinces of South Africa was conducted. The nematodes were identified to species level using molecular techniques. Specific strains effective against FCM larvae and pupae were selected by means of laboratory bioassays, which included 24-well plates, sand and soil assays.

Results: A total of 164 samples were collected and trapped with wax moth or mealworm for the presence of EPNs. Nematodes were isolated from 33 samples with a 20% recovery rate. The species identified during the survey were *S. khoisanae*, *Steinernema* sp., *Heterorhabditis bacteriophora* and *H. zealandica*. Mortality was found to be high for late instar FCM larvae, while mortality for pupae were much lower. All three of the selected EPN species performed well in different soil types and infectivity was high. *Heterorhabditis bacteriophora* gave 100% control in all soil types tested, followed by *H. zealandica* (99%) and *S. khoisanae* (81%). Time of persistence for the three species and minimum concentration of infective juveniles for field trails were obtained using soil bioassays.

Conclusions: Results in the laboratory indicate EPNs to be of great potential as biological control agents against the soil stages of FCM as part of an IPM system.

Early experience with alternative prey affects adult performance in predatory mites

Peter Schausberger, Daniela Hoffmann, Andreas Walzer, Hasan Rahmani

University of Natural Resources and Applied Life Sciences, Department of Applied Plant Sciences and Plant Biotechnology, Institute of Plant Protection, Vienna, Austria

Learning in the context of foraging is a widespread phenomenon in both vertebrate and invertebrate animals. Among arthropods, learning has been mainly studied in insects and within insects in eusocial and parasitoid hymenopterans. In contrast, learning is far less well documented for predatory arthropods, in particular mites. Studies on mites dealt with herbivorous spider mites and long-distance olfactory learning by predatory mites. There exist no reports about the effects of learning in early life on adult performance. However, experience with a given prey in the early stages of life may have profound impacts on feeding performance of adults. Moreover, although learning is generally assumed to be adaptive, the adaptive significance of learning has been rarely documented. I here give two examples of how learning in the juvenile phase may affect predation performance and fitness of adult predatory mites. The first example deals with adaptive learning in the specialist predatory mite *P. persimilis*. Adults emerging from juveniles experienced with alternative prey attacked this prey sooner than those emerging from inexperienced juveniles. Learning was adaptive because it increased the survival prospects of adults. The second example shows that adult generalist predatory mite females, *Neoseiulus californicus*, have an improved predation performance on the alternative prey western flower thrips, *Frankliniella occidentalis*, after having had contact with this prey in the early stages of development. I argue that the putative learning mechanisms are priming/sensitization and/or food imprinting.

The role of advertisement, rewards, and defense against insect herbivores in the pollination biology of African cycads (*Encephalartos*)

John Donaldson[1], Terence Suinyuy[2], Steven Johnson[3]

[1]South African National Biodiversity Institute, Cape Town, South Africa, [2]University of Cape Town, Cape Town, South Africa, [3]University of KwaZulu Natal, Pietermaritzburg, South Africa

Early models of insect pollination in cycads were based on angiosperm examples in which pollinators are attracted to reproductive structures by floral rewards and advertising. Subsequent studies have shown that cycad pollination may involve more complex push-pull systems in which insects are both attracted to and dispersed from cones by attractant and repellant compounds, and cyclical patterns of cone thermogenesis. We present data from studies on the African cycad genus, *Encephalartos,* to test hypotheses based on the push-pull model. We also examine how pollination involving insect herbivores may be especially complex in *Encephalartos* because it has a higher diversity of insect herbivores than any other cycad genus, including the only known cycad seed predators. As a result, there is a tradeoff between attracting pollinators and defense against herbivory. Preliminary data from olfactometer experiments, analysis of cone volatiles, and insect responses to plant defensive compounds indicate significant differences in pollination systems between *Encephalartos* and other relatively well studied systems such as Australian *Macrozamia* species. Data from *E. villosus* indicates that volatile compounds vary at different times of day, over the lifespan of the cone, and between male and female cones, and these differences are coupled to changes in insect behaviour. Our studies of responses to apparent defensive compounds (macrozamin, BMAA) show that they can act as both deterrents and feeding stimulants for different herbivores, although their role in determining pollinator specificity is still not clear.

Who goes first? Arrival order influences reproductive success in two species of group-living beetles *Ips grandicollis* and *Dendroctonus ponderosae* (Coleoptera: Curculionidae)

Tanya Latty[1], Mary Reid[3], Matthew Symonds[2]

[1]University of Sydney, Sydney, New South Wales, Australia, [2]University of Melbourne, Parksville, Victoria, Australia, [3]University of Calgary, Calgary, Alberta, Canada

In group-living animals, individuals can choose to either join established groups or to start new groups. Individuals who found new colonies are called pioneers. By arriving first, pioneers may benefit from lower competition. However, if a resource is dangerous, pioneers may suffer high injury/mortality rates. Here we examine pioneering in two group-living bark beetles: the mountain pine beetle (*Dendroctonus ponderosae,* herein MPB**)** which colonises living trees, and the eastern fivespined bark beetle (*Ips grandicollis),* herein *Ips*) which colonises dead trees. By attacking living trees, MPB pioneers may face an increased risk of mortality due to tree defences. We predicted that successful pioneers would produce more offspring than joiners because of lower competition (the primary cause of larval mortality). As expected, MPB pioneers were found to have high mortality rates (12%). Surprisingly, successful pioneers produced fewer offspring than joiners, suggesting there is no reproductive benefit associated with pioneering. Given the costs, why do individuals pioneer? We tested the hypothesis that pioneering in MPB is condition-dependent such that individuals become pioneers only when they have run out of energy. We found that individuals in poor condition were indeed more likely to pioneer than individuals in good condition.

In contrast to MPB, *Ips* colonises dead trees which lack active defence mechanisms. Pioneer mortality is therefore negligible. We predicted that *Ips* pioneers would benefit from lower competition. Contrary to our expectations, *Ips* pioneers had lower reproductive success than joiners, suggesting that tree defences do not fully explain why pioneers suffer poor reproductive success.

The potential for biocontrol in stored products in general, with specific attention to application of parasitoids against *Sitophilus granarius* in grain stores at low temperatures

Lise Stengaard Hansen

Aarhus University, Department of IPM, Danish Pest Infest. Laboratory, Kgs. Lyngby, Denmark

Introduction: This presentation will give an overview of the current state of biocontrol in stored products. An EU-funded COST Action Working Group, active during 2000-2006. evaluated the possibilities in different sectors: grain stores, mills and bakeries, pasta factories, stored nuts and dried fruit, etc. Three situations were identified with the greatest potential for widespread application: (1) empty room treatment against mites, beetles and moths, (2) treatment of bulk commodities against *Sitophilus* spp. and mites, and (3) application of egg-parasitoids against moths in packaged products. As an example, results of research concerning the larval ectoparasitoid *Lariophagus distinguendus* (Hym.: Pteromalidae) for biological control of the granary weevil *Sitophilus granarius* (Col.: Curculionidae) will be presented. This weevil is an important pest in grain stores in cool temperate climates, e.g. Northern Europe. Here, aeration of stores is carried out in order to bring grain temperatures down to about 5°C in the first months after harvest. Investigations were conducted on the effect of low temperatures on *L. distinguendus*: a) life table parameters and parasitoid induced mortality (PIM) and b) survival during exposure to a simulated winter.

Results: *L. distinguendus* can develop and reproduce at temperatures as low as 16°C. In addition, the parasitoid population did not seem to be affected by the low temperatures, as opposed to its host. Some mortality was observed in *S. granarius* after exposure to 6°C for >4 weeks. This indicates that *L. distinguendus* will be able to survive winter conditions and resume its activity when grain temperature increases in spring.

Effects of spruce budworm (*Choristoneura fumiferana*) outbreaks on fire hazard in central Canada's boreal forest landscapes

Richard Fleming[1], Jean-Noel Candau[2]

[1]Canadian Forest Service, Natural Resources Canada, Sault Ste. Marie, Canada, [2]Unite de Recherches Forestieres Mediterraneennes Institut National de la Recherche Agronomique (INRA), Domaine St Paul, Canada

Introduction: During its periodic outbreaks, the spruce budworm (SBW) defoliates extensive forest areas and has occasionally been blamed for subsequent wildfire.

Methods: To better understand the SBW-wildfire interaction at landscape scales, we studied the spatiotemporal relationships between these two major disturbance types as reflected in historical survey records.

Results: Within the vast region defoliated at least once by SBW since 1941: fires tended to occur 3-9 years after an outbreak; the strength of this interaction and the start and duration of this 'window of opportunity' for wildfire varied geographically; fires occurring within the 'window of opportunity' accounted for over half of the 2,710, 000 ha burnt.

Conclusions: SBW outbreaks have a discernible effect on wildfire at landscape scales. These results can be partly explained by the interaction of two opposing processes operating on different time scales. Fuel production and restructuring during SBW outbreaks increases fire hazard and opens the 'window of opportunity' for wildfire. Fuel decomposition later closes this 'window'.

Clinical evaluation of plant-based insect repellents against malaria in the Bolivian Amazon and coils in China

Nigel Hill

London School of Hygiene & Tropical Medicine, London, United Kingdom

Background: Insecticide treated nets (ITN's) are highly effective in Africa where the main malaria vectors bite indoors late at night. However, outside Africa mosquitoes often feed before local inhabitants retire to bed or prefer to feed outdoors where ITN's are less likely to be as effective. We have been investigating methods of personal protection which may prove beneficial as an alternative or in combination with ITN's. Anti-mosquito products such as repellents and mosquito coils are widely used yet there is very little robust evidence of clinical reduction of insect-borne disease from their use.

Repellents: A randomised, placebo-controlled clinical study of over 4,000 individuals conducted in the Bolivian Amazon found a significant 80% reduction in clinical malaria cases in the group using plant-based insect repellent plus ITN's compared to a placebo plus ITN. The study proves that in areas where the local vector bites in the early evening the effectiveness of ITN's can be dramatically enhanced by using repellents.

Mosquito coils: A new clinical study has just been completed in the border area of China / Myanmar where over 7,000 individuals were randomised into 4 arms; mosquito coils, LLIN, coils+LLIN or a no-treatment control. Each individual was screened for *P. falciparum* / *P. vivax* each month by rapid diagnostic test over an entire high risk season. Findings from the study will be presented.

Future Studies: A range of traditional mosquito control measures used by inhabitants of remote / isolated regions will be summarised and candidates for further investigation will be suggested.

Communities of ants and carabid beatles after clear cut of spruce forest: the effect of site age and landscape position.

Adam Vele[1], Jaroslav Holusa[1], Jan Frouz[2]

[1]Forestry and game management research institute, Prague, Czech Republic, [2]Institute of soil Biology, Ceske Budejovice, Czech Republic

Introduction: What affects insect community site conditions or clearcutting history in surrounding areas?

Methods: The communities of ants and carabid beetles were studied in spruce forest clear-cuts using pitfall traps on five chronoseuences 500-2000m apart, each containing five neighboring plots different age.

Results: In total 13 and 64 species of ant and carabids were found. Shading was principal factor that directly or indirectly affect ant and carabid community along succession. However for both, the difference between chronosequences was more important than differences between succession stages. The influence of succession stages near the pitfall trap, in 50m and 300m diameter from the trap was compared using CCA and variation partitioning. Proportion of individual succession stages in 300m around the sampling point was more important for community composition condition in sampling site itself.

Conclusion: Shading was the most important succession driver. Beside conditions in the site itself the community was strongly affected by availability of a optimal habitat in surrounding landscape, more suitable habitat is in surrounding more likely higher density will be in both optimal and suboptimal habitat.

Metabolic resistance to insecticides in the dengue vector *Aedes aegypti*

Shavanthi Rajatileka[1], William C. Black IV[2], Chamnarn Apiwathnasorn[3], Yuwadee Trongtokit[3], Pradhya Somboon[4], Mark J.I. Paine[1], Philip McCall[1], Hilary Ranson[1]

[1]Liverpool School of Tropical Medicine, Liverpool, United Kingdom, [2]Colorado State University, Fort Collins, Colorado, United States, [3]University of Mahidol, Bangkok, Thailand, [4]Chiang Mai University, Chiang Mai, Thailand

Dengue fever and dengue haemorrhagic fever are major causes of mortality and morbidity and present a substantial public health and socioeconomic problem throughout the Tropics. Currently, control of the vector mosquito *Aedes aegypti* is the only method of controlling disease transmission. However resistance to the limited number of insecticides available for vector control in *Ae. aegypti* populations is impeding control programmes. Determining the molecular basis of insecticide resistance will facilitate vector control programmes by enabling the development of 'early warning systems' for emerging resistance. Metabolic resistance, whereby the rate of insecticide detoxification is enhanced, is a very common but poorly understood resistance mechanism. The over-expression of GSTe2 an Epsilon class GST has already been shown to cause resistance to DDT in the malaria vector *Anopheles gambiae* and in *Ae aegypti* from Thailand. In this study we have determined the level of insecticide resistance in six field populations of *Ae. aegypti* from Thailand. High levels of DDT resistance and low to moderate levels of pyrethroid resistance are present throughout Thailand. Using Quantitative PCR analysis we have investigated the expression levels of selected candidate detoxification genes in adult females and identified genes whose expression correlates with the resistance profile. In addition to the preliminary analysis of the qPCR data, western blot analysis and immunolocalisation experiments implicate several Epsilon class glutathione-S-transferases as being involved in insecticide resistance. We report progress on the development of diagnostic assays to detect these metabolic resistance mechanisms in field populations of *Ae. aegypti*.

Viability of *Beauveria bassiana* formulations for the control of stored product pests

Bryony Taylor, Belinda Luke

CABI-Europe UK, Egham, United Kingdom

Introduction: This study investigated the viability of several formulations of two isolates of *Beauveria bassiana* currently being trialled as biopesticides in the stored product pest environment.

Methods: 0.1g of *B. bassiana* conidia from isolates IMI 386243 and IMI 389521 were formulated in: mineral oils, powder (conidia +/- electrostatic powders, +/- lumogen tracers, +/- bulking agents), emulsifier, 0.05% Tween 80 or as conidia only. Formulations were sonicated for 3min to break up aggregations of conidia, stored at 5℃ and 25℃ and assessed regularly for viability.

Results: After 365 days all IMI 389521 formulations stored at 5℃ displayed excellent germination (>90%), apart from Tween 80 where viability dropped below 50% after 150 days storage. Formulations stored at 25℃ showed good viability (except Tween 80 formulation with <5% germination after 28 days) with germination generally above 80% up to 243 days and dropping below after 300 days. All IMI 386243 formulations showed good germination (>80%) after 183 days at 5℃, except the emulsifier and Tween 80 formulations in which viability dropped below 10% within 15 days. Good germination was observed at 25℃ for the 28 days, before a drop in viability after 77 days, and after 183 days viability dropped below 60% in general. Emulsifier and Tween formulations displayed a rapid loss in viability.

Conclusions: IMI 389521 retained viability better than IMI 386243 under storage when formulated. Tween is a poor formulating agent for both isolates and the emulsifier is not suitable for isolate IMI 386243.

Genomic signature of reproductive success among competing fire ant queens

Yannick Wurm[1], John Wang[1], Kenneth G Ross[2], Laurent Keller[1]

[1]Université de Lausanne, Lausanne, Switzerland, [2]University of Georgia, Athens, United States

Division of labor between reproductive and non-reproductive individuals is a key characteristic of social insects societies. During an ant colony's life cycle, both the number and reproductive status of queens can vary greatly. Little is known about the factors controlling which queens are reproductive, nor about their genetic basis. Examining gene expression, this study aims to identify what determines reproductive success among candidate replacement queens in an orphaned fire ant colony.

A mature monogyne fire ant colony comprises a single mother queen, territory, thousands of workers and up to several hundred virgin queens. Upon the mother queen's death, many virgin queens shed their wings and begin reproductive development. They thus forgo a mating flight in hope of becoming the replacement queen. Over the following weeks, workers execute almost all reproductive queens. The surviving queen is thus "elected" to replace her mother.

The workers base their collective decision on cues provided by the virgin queens as reproductive development begins. In our artificial orphaning setup, we examined whether virgin queens that shed their wings faster are more likely to become replacement queens than queens that shed their wings slower. This was not the case. Instead, our data indicate the importance of another, genetic component. Using microarrays, we identified major molecular-physiological changes in orphaned queens: more than 2,000 genes are differentially expressed after orphaning, including several involved in Juvenile Hormone degradation. Interestingly, one of these degradation genes was among 100 genes differently expressed between likely replacement queens and queens likely to be executed.

Thermal imaging establishes behavioural fever in the desert locust, *Schistocerca gregaria* during mycosis

Victoria Hunt, Gary Lock, Keith Charnley

University of Bath, Bath, United Kingdom

Introduction: The desert locust *Schistocerca gregaria* is a major agricultural pest which periodically is responsible for considerable economic damage. A bio-pesticide based on the fungus *Metarhizium anisoplia* var. *acridum* has been developed as an alternative to chemical pesticides. However, field trials have reported varied success. This is thought to be in part due to the locusts' ability to thermoregulate. During infection with a pathogen, locusts seek out higher environmental temperatures. This 'behavioural fever' has been associated with both an improved immune response and a direct detrimental effect on the pathogen. For the first time we have shown in detail how fever develops during the early stages of mycosis.

Method: An Indigo Systems Omega Infrared camera was used to measure locust body temperature. The development of behavioural fever was recorded in the desert locust, *Schistocerca gregaria* during mycosis. Characteristic green spores were observed to grow from surface sterilized cadavers confirming *M.a.*var *acridum* as the causative infective agent.

Results: The onset of fever in infected locusts occurred before the fungus was present in the haemolymph. Fever was sustained throughout day light hours reaching temperatures *ca.* 8 ° C above that of controls. Consistent with previous work, fever delayed the development of disease.

Conclusion: Behavioural fever is an adaptive response. Locusts are able to detect a fungal infection before it has reached the haemolymph and respond by selecting higher environmental temperatures in anticipation. Infrared imaging provides a non-invasive, more accurate alternative to previously used thermocouple-based measurements of temperature.

The underpinning science and practice of intercropping, mixed cropping and undersowing for control of insect pests of crop plants

John Pickett

Rothamsted Research, Harpenden, United Kingdom

It is essential that there is a sound scientific base for any habitat management strategy to be sustainable. Furthermore, this type of management strategy, as with all others, must represent a robust and effective intervention. Undoubtedly, the most potent and manageable intervention, which at the same time allows acceptable yield and economy of labour or inputs, exploits semiochemicals for manipulating pests and their biological or biochemical antagonists. Intercrops provide a means of disrupting pest and pathogen development in the main harvestable stand, but this can also be achieved by mixed cropping. Trap cropping can provide an opportunity to use strategies more expensive to apply for population control and where special considerations need to be maintained, for example for use of beneficial pathogens. Besides the need to identify appropriate semiochemicals and plants for habitat management strategies, there are also opportunities for plant breeding and heterologous gene expression to create new companion crops. Not only are these approaches required to satisfy new demands on world agricultural production, but this situation requires that all companion crops have their own value, for example as animal feed or industrial crops, for fine chemicals through to bioenergy.

Non-host repellents for arthropod vectors of pathogens: evolutionary aspects and practical exploitation

John Pickett[1], Michael Birkett[1], Ahmed Hassanali[2], James Logan[1], A Jennifer Mordue[3], Lester Wadhams[1]

[1]Rothamsted Research, Harpenden, United Kingdom, [2]ICIPE, Nairobi, Kenya, [3]University of Aberdeen, Aberdeen, United Kingdom

Botanicals: By conveying a strong plant cue, these materials interfere with the normal host location of carnivorous and haematophagous biting flies and other arthropods. Where plant essential oils are involved, these are highly volatile and can be readily lost. These agents also often cause dermatitic problems. The nepetalactones under current development by us may avoid some of these problems. However, as with synthetic repellents derived from structure-activity relationship studies, hosts can easily be detected through the botanical cues.

Non-host species: Although the response to compounds from, related but, non-host species is more deeply embedded in the behavioural ecology of arthropod vectors than for botanically derived repellents, it is still possible for hosts to be detected in the presence of non-host species. For example, human beings are easily located by highly anthropophilic mosquitoes, such as *Anopheles gambiae* s.s., even when surrounded by numerous cattle. However, compounds derived from waterbuck, a non-host for tsetse fly, repel tsetse flies and there are compounds derived from the African hunting dog, a non-host for ticks, potentially useful against ticks.

Host derived repellents: Individuals within an animal population, e.g. bovine or human, can be extremely unattractive to even the most anthropophilic arthropods. We have proved this to be due to the presence of additional compounds which can themselves be used as repellents on normally attractive human beings and will be dealt with in detail by James Logan in this Symposium 9.9.

Genes, networks, and the evolution of phenotypic plasticity: first insights from genomic approaches in horned beetles

Emilie Snell-Rood, Amy Cash, Teiya Kijimoto, Justen Andrews, Armin Moczek

Indiana University, Bloomington, IN, United States

Introduction: Complex, integrated phenotypes emerge during ontogeny through interactions between genotype, environmental conditions, and developmental processes. However, little is known about how such interactions evolve to give rise to novel traits, and which genetic and developmental mechanisms distinguish the ontogenies of canalized and plastic traits.

Methods: We studied gene expression underlying a phenotypic novelty - horns - in the beetle *Onthophagus nigriventris*, using spotted cDNA microarrays. Specifically, we compared genes whose expression is associated with canalized, sex-specific differences in horn expression to those associated with environment- (nutrient) dependent expression of horns in alternative male morphs.

Results: Our results suggest large scale cooption of pre-existing genes and pathways in the origin of beetle horns. A subset of these genes are non-intuitive candidates given their known functions in other organisms. In addition, our microarrays suggest that a number of genes found only in *Onthophagus* may play a role in the integration and diversification of horns. Finally, genes vary in the degree to which their expression is relatively specific to alternative phenotypes.

Conclusions: Genomic approaches provide powerful tools to begin characterizing genetic networks underlying the evolution, integration, and diversification of novel traits. These analyses of co-expressed genes lay the foundation for exploring how the gene network architecture underlying phenotypic plasticity may constrain or foster diversification within and between species. For instance, sets of genes expressed in a highly modular and specific manner may be far less constrained than those expressed as an integrated unit.

Climatic effects on pestilence: parsing the processes and predicting the patterns

Matthew Ayres

Dartmouth College, Hanover, NH, United States

Since the early 1990s, it has been hypothesized that the projected trajectory of climate change would have rapid consequential impacts on biotic disturbance in forests. The argument was mainly based on two points: (1) even in the absence of directional changes in climate, forests throughout the world are strongly influenced by episodic events of pestilence, and (2) insects are very responsive to climatic variation because of their short generation time, high reproductive potential, and physiological sensitivity to temperature and food quality. The most likely potential pathways of ecological change include: direct effects of temperature on insects; effects of temperature, soil moisture, or cloud cover on plant defenses, nutritional suitability, and compensatory growth; and effects of temperature on community interactions between herbivores and their predators, competitors, and mutualists. There are now numerous examples of insect populations whose distribution and abundance have changed in ways that are consistent with the expected effects of climate change. Some globally noteworthy examples of recent pestilence may be attributable to climate change during the last two decades. Presumably there have been some other impacts that are positive from the perspective of traditional forest management. Biological responses have been uneven across insect species and forest systems, and have not usually been predictable in their details. There is a need for well validated models for any forest system that can predict changes in biotic disturbance given specific scenarios of climate change. I offer the following suggestions to facilitate progress: (1) develop, test, and refine general qualitative hypotheses that can predict when and where impacts will be large vs. small, and positive vs. negative; (2) develop programs of focused studies in systems with high importance and a high probability of consequential impacts; and (3) conduct multi-faceted tests (including meteorology, physiology, and population ecology at least) of explicit mechanisms by which climatic variation is theoretically transduced into biotic disturbance.

How to select a limited number of non-target species for host specificity testing?

Peter Mason[1], Ulrich Kuhlmann[2]

[1]Agriculture and Agri-Food Canada, Ottawa, Ontario, Canada, [2]CABI Europe-Switzerland, Delemont, Jura, Switzerland

Selection of appropriate species for host specificity testing of candidate biological control agents is the first critical step in the process to determine potential impacts once the need for pest suppression is justified and one or more potential agents have been identified. The centrifugal phylogenetic method has been suggested as the primary method for use in selecting non-target species for testing candidate entomophagous biological control agents. However, this approach may not always be feasible because of taxonomic uncertainties and the greater number of taxa that could be required in testing compared to weeds. Furthermore, other parameters such as the phenology, feeding niche or the common habitat of target and non-target species may be more meaningful, at least for some biological control agents.

We proposed methods for setting up test species lists for arthropod biological control programmes that are scientifically based and ensures that all aspects of potential direct impacts are considered. Moreover, the methods take into consideration possible practical constraints associated with arthropod host specificity screening to ensure that the number of non-target host species selected for testing is manageable.

New insights in venation pattern morphology of Paleozoic insects

Jakub Prokop[1], André Nel[2], Dong Ren[3]

[1]Charles University in Prague, Faculty of Science, Department of Zoology, Praha, Czech Republic, [2]Muséum National d'Histoire Naturelle, Laboratoire d'Entomologie, Paris, France, [3]College of Life Sciences, Capital Normal University, Beijing, China

Introduction: Paleozoic insect fauna greatly differs from Mesozoic and Cenozoic ones. Insects are entirely known as compression fossils or 3-D from siderite nodules. Wing venation is the most common structure preserved on Paleozoic insect fossils. Besides the venation pattern morphological limitations due to various adaptations and pattern stability within the certain groups it remains crucial structure for systematic of Paleozoic insects. Unfortunately many fossil taxa described by some authors are based on fragmentary material of different body structures those are usually misguided. Such enthusiasm caused noise in systematic and generates further difficulties to make any serious comparison with other taxa. The aim is finding of significant venation characters on newly discovered material and revision of selected Paleozoic fossils.

Results: Current research in several institutional and private collections enabled study and of a new Upper Carboniferous material of palaeopterous and neopterous insects from several localities in Euro-America and China. The first results of comparative studies mainly based on wing venation pattern morphology revealed new significant characters for taxonomy and phylogeny of different insect groups (e.g., Ephemeroptera: Syntonopteridae, Palaeodictyopterida: Homoipteridae, Namuroningxiidae, Odonatoptera: Meganeuridae and others). Contemporary studies extend our knowledge on past insect diversity and display variability of venation pattern in evolution. Moreover, those results provide support for palaeogeography, such as evidence for a Euro-American connection during the Late Carboniferous.

Effects of milkweed modularity on foraging by monarch larvae at different scales

Stephen Malcolm, Tammi Roberts, Barbara Cockrell

Western Michigan University, Kalamazoo, Michigan, United States

Introduction: Mobile, holometabolous insect herbivores are confronted with diet qualities that are influenced at small scales by plant and larval interactions and at large scales by adult responses to a variable hostplant landscape. Monarch butterflies in eastern North America migrate between overwintering resources in Mexico and larval milkweed resources distributed across much of the continent, east of the Rocky Mountains. At a continental scale adult monarchs can choose to oviposit among an array of approximately 115 species of milkweed in the genus *Asclepias.* These plants vary considerably according to defense investment and modularity. Once the adult choice has been made in space and time, their larvae then choose where to forage according to plant modularity and the plant's response to larval feeding.

Methods: Here we examine the implications of these foraging scales with larval feeding experiments, in both the laboratory and field, that manipulate defense expression in different *Asclepias* species and examine feeding behavior, growth and sequestration by larvae.

Results and conclusions: Our results show that both adults and larvae make foraging decisions in response to both small and large-scale variation in plant quality and may help to explain the nature of selection for long-distance migration in this mobile insect herbivore.

Does the southern monarch butterfly, *Danaus erippus,* migrate?

Stephen Malcolm, Allister Malcolm, Barbara Cockrell

Western Michigan University, Kalamazoo, Michigan, United States

Introduction: Anecdotal evidence from Argentina suggests that the southern monarch butterfly, *Danaus erippus,* migrates in southern South America much like its northern congener, *D. plexippus.* Other than these seasonal observations nothing is known about the distribution and abundance of *D. erippus* in South America, south of the equator. In contrast to the northern monarch, which has an array of approximately 115 species of *Asclepias* to exploit as a larval host plant, *D. erippus* has only 10 *Asclepias* species available throughout South America. Here we examine the seasonal movements of *D. erippus* in Bolivia using hostplant sequestered cardenolides as fingerprints of host origin.

Methods: We collected *D. erippus* adults at 3 different times of the year in various locations in Bolivia and analysed their steroidal cardenolides by HPLC. We also measured fat content, wing size, wing wear and reproductive status of adults. The bursa copulatrix was dissected from all females and analysed separately for possible male contributions to cardenolide profiles. In the field we also searched for milkweeds at a range of altitudes and searched for immatures of *D. erippus.*

Results and conclusions: Adult *D. erippus* in Bolivia are some of the best defended butterflies known, with extremely high cardenolide concentrations. The plants most commonly exploited as larval host plants in Bolivia were *Asclepias curassavica* at lower altitudes*, A. boliviensis* at mid altitudes and *A. barjoniifolia* at altitudes up to 4,000m. We conclude that *D. erippus* is both a seasonal latitudinal migrant as well as a seasonal altitudinal migrant, but that there is no evidence for the dense overwintering aggregations that characterize *D, plexippus.*

Dynamics and impact of chemical defence expression in a plant-aphid-coccinellid interaction

Stephen Malcolm[1], John Couture[2], Brett Blaauw[1]

[1]Western Michigan University, Kalamazoo, Michigan, United States, [2]University of Wisconsin, Madison, Wisconsin, United States

Introduction: Specialist insect herbivores that sequester plant chemical defenses pose a problem for plants; should they induce defenses to try and remove herbivores, or should they reduce defenses to make the herbivores more vulnerable to natural enemies in the third trophic level. We examine these bottom-up and top-down hypotheses in a milkweed, aphid, coccinellid system with laboratory experiments that manipulate the dynamics of source-sink interactions among three trophic levels.

Methods: We manipulated the density of the aposematic aphid, *Aphis nerii* on the neotropical milkweed, *Asclepias curassavica,* to determine the cardenolide response of the plants to aphid phloem-feeding and the consequent sequestration of these steroidal defences by the aphids at these densities. We then took aphids at different densities and fed them to newly emerged, 4th instar larvae of the coccinellid *Coccinella sepempunctata* and measured their functional response to aphid density.

Results and conclusions: Milkweeds show a U-shaped reduction-induction cardenolide response to aphid density, with reduction of cardenolides at low aphid density in comparison to aphid-free controls and induction above constitutive levels at high aphid densities. This plant response resulted poorly defended aphids at low density and well-defended aphids at high density. The plant response generated a domed, or type 4 functional response in coccinellid larvae to *A. nerii* density. This response destabilizes tritrophic interactions characterized by sequestered chemical defences when examined with Rosenzweig-MacArthur models of tritrophic dynamics.

Modular Ecological Design: A fruit and vegetable polyculture system

Joseph Kovach

Ohio State University, Wooster, OH, United States

Introduction: The layout of crops (alternating high and low crops) could improve pest management while limiting pesticide use and increasing yields. The goal of this project is to determine the optimal layout (in terms of economics, pest density and efficiency) of an intensive polyculture system that can be used by the small urban farmer.

Methods: This experiment began in 2005 with 4 treatments (18.2 m x 13.3 m) replicated 4 times on 0.54 hectares. The treatments are a solid row planting, a checkerboard, a mixed row and a mixed row on raised bed. Each treatment is a mixture of 8 crops (4 woody fruit commodities and 4 herbaceous commodities) arranged in different patterns and heights. To increase temporal diversity each crop has an early, mid and late harvest. For the perennial crops (apple, peach, blueberry, raspberry, strawberries), different cultivars were selected for different harvest times, for the annual crops (tomatoes, soybeans, snap peas) three planning dates were used. Insect and disease pests were monitored regularly throughout the growing season and harvest evaluations were conducted on each commodity. In 2007, Haygrove high tunnels were placed over 1 replicate of each treatment.

Results: Aphids, mites and powdery mildew densities were much higher on crops grown in the high tunnels. The raised bed treatment had the most insect biodiverstiy. Of the crops grown, peaches and strawberries had the most insect biodiverstiy and tomatoes the least.

Conclusions: This agroecosystem is stabilizing and is on track to meet the project goals.

Age specific fecundity and temperature dependent population growth rate of *Eurygaster integriceps* Put. (Heteroptera: Scutelleridae) at four constant temperatures

Shahzad Iranipour[1], Aziz Kharrazi Pakdel[2], Gholamreza Radjabi[3]

[1]University of Tabriz, Tabriz [2]University of Tehran, Karaj, [3]Plant Pests and Diseases Institute, Tehran, Islamic Republic of Iran

Introduction: Sunn-pest, *Eurygaster integriceps* Put. is the most important insect pest of wheat and barley in Iran. A demographic study was carried out in order to determine effect of temperature on fitness of the pest.

Methods: Fertility life tables of the pest were constructed in four constant temperatures 22, 25, 27, and 30 ± 1℃ on MAHDAVI wheat kernels. Both finite and intrinsic rates of population increase, gross and net reproductive rates, intrinsic rates of birth and death, cohort generation time, doubling time, total fecundity per female and adult life time components were compared among temperatures.

Results: Significant differences were observed in all statistics. Intrinsic rate of natural increase, r_m increased linearly by temperature ($r^2 = 0.89$, $P < 0.01$). It was estimated as 0.0126, 0.0381, 0.0541, and 0.0789 females/ female/day in above mentioned temperatures respectively. An opposite trend was observed in generation time ($r^2 = 0.93$, $P < 0.01$), as the longest and the shortest generation times were measured 121 and 40 days at 22 and 30 ℃ respectively. Net replacement rate was significantly lower at 22 ℃ than other temperatures. It was about one fifth of them (4.57 vs. 22.17 to 25.83 females/ female/ generation). Total fecundity per female was ranged from 123.07 at 22 ℃ to 209.36 at 30 ℃. Adult life time as well as its components was affected by temperature. Oviposition period was the longest course among life time periods. Thermal threshold and effective temperature required for pre-oviposition development were estimated as 20 ℃ and 68 degree-days respectively.

Discussion: The best fitness and the most reproductive output of sunn-pest *Eurygaster integriceps* was occurred at 30℃ among studied temperatures.

An international cooperative effort to protect *Opuntia* cactus resources in the American Southwest and Mexico from the South American cactus moth, *Cactoblastis cactorum*

Joel Floyd[1], Kenneth Bloem[2], Stephanie Bloem[2], James Carpenter[3], Stephen Hight[4], Arturo Bello[5], Walther Enkerlin[6]

[1]USDA, APHIS, PPQ, Riverdale, Maryland, United States, [2]USDA, APHIS, PPQ, Raleigh, North Carolina, United States, [3]USDA, Agriculture Research Service, Tifton, Georgia, United States, [4]USDA, Agriculture Research Service, Tallahassee, Florida, United States, [5]Dirección General de Sanidad Vegetal, Mexico City, D.F., Mexico, [6]North American Plant Protection Organization, Ottawa, Ontario, Canada

The South American Cactus moth, *Cactoblastis cactorum*, was intentionally introduced to an island in the Caribbean in the 1950's and eventually made its way to the Florida peninsula by 1989. In 2004, the United States Department of Agriculture's (USDA) Animal and Plant Health Inspection Service (APHIS) and Agriculture Research Service (ARS) began a joint effort to establish a barrier to its spread along the US Gulf Coast before reaching areas of significant *Opuntia* diversity. Since 2006, the Mexican government's Secretería de Agricultura, Ganadería, Desarrollo-Rural, Pesca y Alimentación (SAGARPA), through the North American Plant Protection Organization (NAPPO), has been cooperating to help fund the monitoring and prevention of the spread of this pest in on the continent. There has been technology transfer with survey methods and sterile insect release in Mexico. Other cooperation has occurred with state departments of agriculture, agencies, and environmental groups that manage lands in trapping and setting up sentinel sites for visual monitoring of plant populations for early stages of infestation. The program has been successful in slowing the spread and raising awareness with other cooperators such as national parks, wildlife refuges, ranchers, nursery operators, and home owners.

Can extra-floral nectaries facilitate predation by cursorial spiders in row crop agroecosystems?

Robert Pfannenstiel, Joseph Patt, Felix Wäckers

[1]USDA-ARS Subtropical Agricultural Research Center, Weslaco, TX, United States, [2]Centre for Sustainable Agriculture, Lancaster Environment Centre, Lancaster University, Lancaster, United Kingdom

Introduction: Extrafloral nectaries are a significant resource for many natural enemies. However, the importance of extrafloral nectar to cursorial spiders (Anyphaenidae, Miturgidae, and Clubionidae), which are common foliage inhabitants, is not understood. Our laboratory and field studies are examining the relationship between nectar availability and these spiders' potential to act as biological control agents in row crops.

Methods: Sentinel eggs of pest moths (*Helicoverpa zea* and *Spodoptera exigua*) were used to measure levels of spider predation in cotton, corn, and soybean fields. Estimates of the level extrafloral nectar consumption by spiders were made in cotton fields. Laboratory studies evaluated the impact of nectar consumption on growth and survivorship; acceptance and assimilation of sugars from nectar and honeydew; and, the influence of contact and olfactory cues on searching behavior for nectar and prey.

Results: Cursorial spiders were the dominant predator of lepidopteran eggs in cotton but were less important in crops that lacked extrafloral nectaries. Spiders in cotton were commonly detected as positive for fructose, indicating that they had fed on nectar within the previous three days. Laboratory diet studies demonstrated that nectar consumption could significantly improve their survival, growth, and development. Behavioral studies showed that they were stimulated by nectar aromas and could learn to recognize and remember novel aroma cues. In combination, these data suggests that cursorial spiders are adapted for finding and utilizing extrafloral nectar and that nectar availability significantly increases their role as biological control agents in cotton vs. other crops.

Predator biodiversity strengthens herbivore suppression

William Snyder, Gretchen Snyder, Deborah Finke, Cory Straub

Washington State University, Pullman, WA, United States

Concern over biodiversity loss, especially at higher trophic levels, has led to a surge in studies investigating how changes in natural enemy diversity affect community and ecosystem functioning. These studies have found that increasing enemy diversity can strengthen, weaken, and not affect prey suppression, suggesting that multi-enemy effects on prey are context-dependent. In a series of field experiments we have examined the relationship between natural enemy species diversity and the suppression of aphids on pea, potato, and collard plants. We have found that, across a range of predator, aphid, and plant species, aphid biological control consistently strengthens with higher predator biodiversity. However, we have found that plant traits, such as surface chemistry, can dramatically alter the strength of predator biodiversity effects. Field and laboratory experiments indicate that members of our aphid predator community differ in where they forage on plants, perhaps contributing to complementary resource partitioning among species. Thus, plant traits that accentuate or diminish interspecific differences in foraging behavior may likewise strengthen or weaken predator-predator complementarity, and thus the relationship between predator biodiversity and herbivore suppression.

Evolutionary riddles and phylogenetic twiddles: the sternum V gland in Trichoptera

Marie Djernaes, Felix Sperling

University of Alberta, Edmonton, Alberta, Canada

Introduction: The sternum V gland is found throughout Trichoptera and the most basal Lepidoptera and generally produces sex pheromones. The present study focused on morphology and microstructure of this gland in an evolutionary context.

Results and Discussion: All Trichoptera and Lepidoptera studied had a gland opening muscle that inserts on the gland duct just inside the gland orifice. In most Trichoptera the gland opening muscle originates mesad on the cuticle of sternum V while in Lepidoptera this muscle originates on the anterior edge of sternum VI. Four trichopteran families (Glossosomatidae, Hydroptilidae, Rhyacophilidae and Philopotamidae) have a gland opening muscle of the lepidopteran type. Glossosomatidae, Hydroptilidae and Rhyacophilidae belong in the problematic suborder Spicipalpia which may be basal within Trichoptera. However, the fourth spicipalpian family, Hydrobiosidae, has a typical Trichopteran gland opening muscle. Philopotamidae is considered basal within the suborder Annulipalpia. However, philopotamid females have fenestra on sternum IV, otherwise found on females in the lepidopteran families Eriocraniidae, Neopseustidae and Nepticulidae.

Gland opening muscles originating on the anterior edge of sternum VI are found both in Lepidoptera and some Trichoptera. Thus it might be assumed that this type is ancestral and that the trichopteran type is a later development. However, this raises the question of one or several origins of the trichopteran type. A single origin would place Glossosomatidae, Hydroptilidae, Rhyacophilidae and Philopotamidae as basal within the Trichoptera, a placement that disagrees with recent phylogenetic studies. Multiple origins posit that morphologically indistinguishable muscles can arise independently as apparent neoformations.

Reduction of respiration by aggregate formation in *Parastrachia japonensis*

Sumio Tojo[1], Lisa Filippi[2]

[1]Department of Applied Biological Sciences, Saga University, Saga-Shi, Saga Prefecture, Japan, [2]New College of Hofstra University, Hempstead, N.Y, United States

Nymphs of the univoltine shield bug, *Parastrachia japonensis* grow by feeding on the drupes of their sole food plant, which are provisioned by their female adult and available for only two weeks a year in late June. New adults which emerge in late July soon enter diapause until reproductive stage in next May, live mostly in aggregated conditions and can survive more than one year on only water. Diapausing adults have a high tendency to form clusters with no sexual bias. When three to 40 insects were enclosed in chambers of equal volume used to measure respiration, oxygen consumption was reduced to nearly half that when a single individual was enclosed. However, this reduction in metabolic rate was lost when the bugs were prevented from having physical contact with other individuals, partly lost by being enclosed with dead individuals, totally lost with the ones being washed with dietylether, and not influenced by humidity. No such effect of aggregation on respiration was found in adults in the reproductive stage, nor in two other diapausing bugs, *Erthesina fullo* and *Plautia crossata*, which hibernate in groups. These results indicate that the reduction in oxygen consumption in *P. japonensis* is due mostly to physical contact with other individuals and partly to chemical cue that functioned to settle them down and resulted in a greatly reduced respiration rate. This trait is an effective strategy that allows diapausing adults to conserve energy and prolong survival until reproductive stage.

Insecticidal formulation with African nutmeg *Monodora myristica* (Gaertn) dunal seed extracts for the control of cowpea seed beetle, *Callosobruchus maculatus* (Fabricius) (Coleoptera: Bruchidae}

Chris.O. Adedire, Olabinmpe.O Okosun

Federal University of Technology, P.M.B. 704, Akure, Nigeria, Akure,Ondo state, Nigeria

Introduction: Plant-derived biopesticide such as plant powder and oils exert various physiological and behavioral activities on stored product insect .These are relatively cheaper and ecologically more tolerable than convectional chemical pesticides.

Method: Insecticidal bioassays involving *Monodora myristica* (Gaertn) Dunal seed extracts using: methanol, ethanol, acetone, Pet-ether, n-hexane and water as solvents were accomplished at ambient tropical conditions of temperature and relative humidity. The extracts at 0.5**%** (v/w) were evaluated for insecticidal activity on *Callosobruchus maculatus* using mortality, oviposition and progeny development as *indices.*

Results: Steam distillate and non-polar extracts of hexane and pet ether significantly ($p<0.05$) reduced oviposition and evoked high mortality of *C. maculatus* compared with other solvent extracts. When the bruchids had the choice of oviposition media, the mean number of eggs laid on cowpea seeds treated with steam distillate was significantly lower than those laid in other treatments. The adult that emerged from the seeds with different African nutmeg treatments was significantly lower (0-22%) than that of the untreated seeds (55%).

Conclusion: Steam distillate of *M.myristica* could serve as a potent protectant of cowpea seeds against *C. maculatus* infestation and damage.

Ecological risk assessments for the invasion of *Bombus terrestris* in Japan

Yoko Kawate Kunitake, Koichi Goka

Josai International Univeristy, Chiba, Japan

The large earth bumblebee, *Bombus terrestris*, has been recognized as an invasive alien species and greatly expanding its distribution over the native range. In Japan, since the first introduction in 1991, a lot of individuals of this species including queens and males have escaped from the commercial colonies into the field. As a result, *B. terrestris* have naturalized in Japan, especially on the northern island, Hokkaido.

In this talk, I will review the progress of studies for ecological risk assessment of *B. terrestris* in Japan, based on the following ecological aspects; 1) competition with native bumblebee species 2) hybridization with native species 3) transmission of alien parasites into the field 4) disturbance against the reproduction of native flora through changing interaction among pollinators.

I will also introduce the invasion status and the process of *B. terrestris* in Japan. This study demonstrates how selected key factors affect the distribution of naturalized population. We have found that the landscape components (forest coverage rate), not the local propagule pressure (the number of commercial colonies), is the critical factor. However, the effect of landscape components on the distribution of *B. terrestris* varied among regions. This is possibly because of large difference in the propagule pressure among regions. Understanding such state dependent process in the invasion ecology is considered to be important for the future study and for the practical control of invasive bumblebees.

Consequences of temperature fluctuations on tritrophic systems plants-aphids-parasitoids: adaptation to climate change and biocontrol

Thierry Hance, Alexis Descampe, Herve Colinet

Université Catholique de Louvain, Louvain-la-Neuve, Belgium

Introduction: Global warming predictions mask regional situations where likely outcomes will be more frequent heat or cold waves, droughts and extreme precipitation events. For tritrophic systems, the increase in temperature fluctuation and the occurrence of more frequent extreme will be a greater challenge than the gradual increase in average temperature. Temperature changes may influence differently the biology of each component species of a system, provoking a destabilisation in their population dynamics that may lead to the extinction of part of the system. The impact of climatic changes is likely to be more important in higher trophic levels that depend on the capacity of the lower trophic levels to adapt to these changes.

Methods: We analyzed the effects of low and fluctuating temperature on the life-history traits of parasitoids and interactions with their aphid hosts and possible consequence on biological control.

Results: Four trends can be identify: 1) Differential modification of the development time or diapause pattern (timing or rate) of one of the partners of the trophic systems may change the temporal synchronisation between host and parasitoid and may result in aphid outbreaks. 2) The temperature-induced size variation produces also changes in parasitoid fecundity and survival. 3) Parasitoid searching behaviour is affected after exposition to low temperature. 4) In the opposite, if during cold exposure temperature raises during several hours, survival, fecundity and some behavioural traits are clearly improved. Such fluctuating temperatures correspond to changes in some proteins expression as shown by the proteomic profiles obtained under different conditions. In consequence, fluctuating temperature may perhaps compensate at least partially more frequent exposure to extreme temperature.

Conclusions: It appears that impact of climate changes on trophic systems should be studied under systemic and multidisciplinary approaches.

Exocrine glands in the legs of ants

Johan Billen

University of Leuven, Leuven, Belgium

Ants no doubt can be considered walking glandular batteries, as their tiny bodies contain a plethora of exocrine glands, the secretions of which play crucial functions in the social organization and the communication system of their colonies. Although the head, thorax and abdomen appear the most obvious sites where such glands can be found, also the appendages like antennae and legs contain a number of glands. This talk reviews the various glands that are known from the ants' legs.

The first leg gland to be reported in literature (by Reinhard Leuthold in 1968) was the tibial gland in the hindlegs of *Crematogaster* ants, with a function in the elaboration of trail pheromones. This pioneer report was later supplemented with several additional descriptions, with especially Bert Hölldobler and our own work extending the knowledge of the variety of exocrine glands in the legs of ants. At present, this variety comprises 20 different glands that can be found among the various ant species that have been studied, with glands occurring in all leg segments (coxa, trochanter, femur, tibia, and tarsal segments). Some glands are found in all species (such as the pretarsal arolium gland), although most are more restricted, and occur in a single genus or species. Several of these glands, especially these in the hindlegs, produce trail pheromones. Other functions reported for leg glands include functions like antenna cleaning, lubricant production, and elaboration of sex pheromones.

Potential for host plant-mediated genetic differentiation in a tritrophic system

Betty Benrey

University of Neuchatel, Neuchatel, Switzerland

Many insect species are distributed over populations that live in different habitats where they experience different environmental conditions. If gene flow among these populations is limited and natural selection operates differently in different habitats, this can lead to genetic divergence and local adaptation.

We study a tritrophic system comprised of several species of beans (wild and cultivated), bruchid beetles that feed on these beans, and the parasitoids that attack the bruchids. Insects that emerged from beans collected throughout Mexico were used for microsatellites and mitochondrial DNA analyses. For bruchids, most of the between-population genetic differentiation was explained by geographic distance and not by variation in their host plant. Interestingly, isolation by distance was only evident for populations that originated from wild beans and not from cultivated beans. This can be explained by long-distance migrations of beetles on domesticated plants resulting from human exchanges of bean seeds.

Three parasitoid species of the genus *Horismenus* showed some degree of isolation by distance. For one of the species it was found that individuals collected from one bean species were genetically distinguishable from individuals from another bean species, even within populations. Behavioural assays confirmed that these genetic groups were closely associated to the plant of origin: female wasps were more attracted to the odour of the bean species from which they were collected than to the odour of an alternative bean species. These results imply that plants can contribute to the genetic structuring of the parasitoid populations, possibly leading to host race formation.

Current pest status, life-cycle and ecology of *Hieroglyphus perpolita* (Uvarov, 1932) (Acrididae: Orthoperta) of Pakistan

Riffat Sultana, M.Saeed Wagan

Department of Zoology, University of Sindh, Jamshoro, Pakistan, Hyderabad, Palestinian Territory, Occupied

Introduction: The species of genus *Hieroglyphus* are very important from economic point of view they are major pest of paddy, sugarcane, wheat, and maize in Pakistan Among the all species of *Hieroglyphus H.perpolita* (Uvarov) goes to totally oppose extreme regarding their habits and habitat .Its habits and habitat are mostly associated with the presence of *Saccharum bengalense* locally called Sarkanda.

Material and Methods: The stock culture consisted of nymphs & adults were collected mostly from the *S. bengalense* having thick and coarse (thorny) leaves, near the cultivated field of *Z*ea *mays* and *Arachis hypogaea* with the help of traditional insect hand-net as well as by hand picking. In the field the collected material was transferred into polythene bags for transfer to the laboratory where collected material was killed and preserved by standard entomological method.

Results: Incidence of *H.perpolita* reported significantly highest during the months of July and August than the other months. They go through six nymphal stages becoming adult. They live an aggregation except few adults found on cultivated field. They seem to prefer thorny bushes rather than other plants, which do not provide protection from enemies. The eggs were also laid in the root of same plants, which remain undisturbed when nearby land is ploughed for cultivation. *S. bengalense* was report as new host plant of *H.perpolita* from Pakistan for the first time.

Conclusions: The results of such type of study will be instrumental in understanding and devising population management strategies, which could help to avoid or prevent any possible future outbreak.

Specific adaptations to plant chemical defences in a generalist herbivore: Detoxification of isothiocyanates by glutathione-S-transferases in midguts of *Spodoptera littoralis*

Katharina Schramm[1], Jonathan Gershenzon[1], Ute Wittstock[2]

[1]MPI for Chemical Ecology, Jena, Germany, [2]IPB, TU Braunschweig, Braunschweig, Germany

Introduction: Generalist insect herbivores feed on numerous plant species, yet how do they cope with the many different chemical defences they encounter? Possible strategies include avoidance, insensitivity to toxins or detoxification and excretion. Brassicaceae (e.g. cabbages, rapeseed or Arabidopsis) use glucosinolates for their defence, which are the precursors of toxic isothiocyanates and other compounds that are released upon tissue damage, for example, after herbivore attack. Some specialist Brassicaceae feeders have developed biochemical mechanisms to avoid the toxicity of isothiocyanates. We employed *Spodoptera littoralis* (Lepidoptera), whose larvae feed, amongst others, on Brassicaceae, to study the metabolism of the glucosinolates in a generalist herbivore.

Methods and Results: Analysis of the faeces of larvae which had fed on different Brassicaceae, including Arabidopsis transgenics, revealed that glutathione conjugates of isothiocyanates occur whenever isothiocyanates are formed in the food plant. *S. littoralis* was able to form glutathione conjugates from a large variety of isothiocyanate structures. The conjugation was shown to be catalysed by glutathione-S-transferases in the larval gut, inducible by feeding on isothiocyanate-containing diets. The identification of the specific enzymes responsible for isothiocyanate detoxification by two-dimensional protein separation is in progress, as is a molecular approach for identifying the corresponding genes. Future investigations will explore the costs of this detoxification ability and determine whether glutathione-*S*-transferase activity can cope with the range of isothiocyanates present in potential hosts.

Conclusion: In *S. littoralis*, one pathway of detoxification of isothiocyanates derived from glucosinolates with variable side chains is the enzymatic conjugation with glutathione.

Resistance management for Bt crops: from theory to reality

Anthony Shelton

Department of Entomology, Cornell University/NYSAES, Geneva, New York, United States

In the decade leading up to the first commercial release of transgenic-insecticidal crops expressing proteins from *Bacillus thuringiensis* (*Bt*), several deployment strategies designed to delay resistance were proposed. These strategies were built on a considerable body of theoretical and empirical work on resistance to conventional insecticides. However, *Bt* crops were considered a special case since target insects were exposed to toxins over the entire season. Thus, *Bt* plants were more akin to conventionally bred, insect-resistant plants than most conventional, short-lived insecticides. For various political, social, ecological and economic reasons, in many countries *Bt* crops have been introduced with requirements for managing the evolution of resistance. However, the scope and adoption of such requirements is variable within and between countries. Despite this variation, since their introduction in 1996, *Bt* cotton and *Bt* maize have been grown on more than 162 million ha worldwide with minimal evidence of resistance evolution. This situation is in stark contrast to most conventional insecticides and has been credited to proactive insect resistance management (IRM) strategies, as well as characteristics of the insects themselves and the ecology into which *Bt* crops have been introduced. Present and future challenges remain for IRM and it is important that the agricultural sectors (scientific, grower, regulatory and producers) that work with *Bt* crops remain vigilant to ensure the long-term successful performance of this first wave of transgenic-insecticidal crops.

Resistance management for Bt crops: from theory to reality

Anthony Shelton

1Department of Entomology, Cornell University/NYSAES, Geneva, New York, United States

In the decade leading up to the first commercial release of transgenic-insecticidal crops expressing proteins from *Bacillus thuringiensis* (*Bt*), several deployment strategies designed to delay resistance were proposed. These strategies were built on a considerable body of theoretical and empirical work on resistance to conventional insecticides. However, *Bt* crops were considered a special case since target insects were exposed to toxins over the entire season. Thus, *Bt* plants were more akin to conventionally bred, insect-resistant plants than most conventional, short-lived insecticides. For various political, social, ecological and economic reasons, in many countries *Bt* crops have been introduced with requirements for managing the evolution of resistance. However, the scope and adoption of such requirements is variable within and between countries. Despite this variation, since their introduction in 1996, *Bt* cotton and *Bt* maize have been grown on more than 162 million ha worldwide with minimal evidence of resistance evolution. This situation is in stark contrast to most conventional insecticides and has been credited to proactive insect resistance management (IRM) strategies, as well as characteristics of the insects themselves and the ecology into which *Bt* crops have been introduced. Present and future challenges remain for IRM and it is important that the agricultural sectors (scientific, grower, regulatory and producers) that work with *Bt* crops remain vigilant to ensure the long-term successful performance of this first wave of transgenic-insecticidal crops.

IPM and insect-protected transgenic plants: Thoughts for the future

Anthony Shelton[1], Jörg Romeis[2], George Kennedy[3]

[1]Department of Entomology, Cornell University/NYSAES, Geneva, New York, United States, [2]Agroscope Reckenholz-Tänikon Research Station ART, Zurich, Switzerland, [3]Department of Entomology, North Carolina State University, Raleigh, North Carolina, United States

Transgenic maize and cotton varieties expressing insecticidal proteins from the bacterium, *Bacillus thuringiensis* (*Bt*), have become important components in integrated pest management (IPM) programs globally. In 2006, *Bt* maize and *Bt* cotton were grown in 13 and 9 countries, respectively. *Bt* plants have provided opportunities and challenges to managing insect pest complexes, but overall their use has resulted in strong economic and environmental benefits. Their adoption rate has been dramatic. Only 11 years after their introduction, they were grown on 32.1 million ha in 2006. In some parts of the world, *Bt*-transgenic varieties dominate the crop area. For example, *Bt* cotton makes up 65% of the total cotton acreage in China, 59% in Australia, 56% in the USA and 42% in India. Adoption of *Bt maize* has reached 75% in the USA. Thus, *Bt* plants have turned what was once a minor foliar insecticide (*Bt*) into a major control strategy. Other *Bt* commodities are expected to be registered in the near future. Additionally, new insecticide molecules are being developed for expression in plants and plant genes are being altered to affect biochemical pathways that elicit insect resistance. Adoption of *Bt* plants should be viewed within the larger context of food systems, cultures, human values, politics and the roles and responsibilities of science in the modern world. Such a context helps explain the variable adoption rates of *Bt* plants on a global basis and helps provide insights for the future deployment of insect-resistant plants.

Trap cropping in pest management strategies

Anthony Shelton, Francisco Badenes-Perez

[1]*Department of Entomology, Cornell/NYSAES, Geneva, New York, United States,* [2]*Department of Entomology, Max Planck Institute for Chemical Ecology, Jena, Germany*

The concept of trap cropping fits into the ecological framework of habitat manipulation of an agroecosystem for the purpose of pest management. Interest in trap cropping, a traditional tool of pest management, has increased considerably in recent years as a result of concerns about potential negative effects of pesticides on human health and the environment, pesticide resistance, and general economic considerations of agricultural production. Recently, we proposed a broader definition of trap cropping that encompasses the inherent characteristics of the trap crop plants themselves as well as the strategies associated with their deployment. Inherent characteristics of a trap crop may include not only natural differential attractiveness for oviposition and feeding, but other attributes that enable the trap crop plants to serve as a sink for insects or the pathogens they vector. Successful deployment of trap crops within a landscape depends on the inherent characteristics of the trap crop and the higher value crop, the spatial and temporal characteristics of each, the behavior and movement patterns of insect pests, and the agronomic and economic requirements of the production system. Thus, trap cropping is more knowledge-intensive than many other forms of pest management. From a commercial standpoint, we consider that currently there are only 10 cases of successful applications of trap cropping in agricultural and forest systems. Ultimately, the combination of insect and trap crop characteristics and practical considerations determines the success of a trap cropping system.

The roles of floral colour and scent in a shift from wind to insect pollination in the sedges (Cyperaceae)

Peter D. Wragg, Steven D. Johnson

University of KwaZulu-Natal, Pietermaritzburg, KwaZulu-Natal, South Africa

The shift from wind to insect pollination was a key transition in the early evolution of flowering plants. Several lineages have subsequently reverted to wind pollination, in association with loss of floral attractants (bright colour, floral scent) and rewards (nectar). Here we present the first experimental evidence for a switch back to insect pollination in one of these wind-pollinated lineages, the family Cyperaceae. We focused on *Cyperus obtusiflorus* var. *obtusiflorus* in the KwaZulu-Natal coastal grasslands. Flowers from which insects, but not wind, were excluded showed a significant 98 % reduction in seed set compared to open pollinated controls, indicating that insect pollination was more important than wind pollination. Bees, beetles and flies visited the white, scented inflorescences of *C. o.* var. *obtusiflorus* more often than the brown, unscented inflorescences of the co-flowering, wind-pollinated *Pycreus oakfortensis* (nested within *Cyperus*). We explored the cues responsible for attractiveness to insect pollinators. Colour was more important than scent in attracting insects to artificial inflorescences: white artificial inflorescences attracted more insects than brown ones, but those mimicking the scent of *C. o.* var. *obtusiflorus* with a blend of ocimene, linalool, benzyl alcohol and phenylethyl alcohol were no more attractive than unscented controls. In a wind tunnel, wind transported pollen of *P. oakfortensis* more effectively than pollen of *C. o.* var. *obtusiflorus*. Thus, there appears to be a tradeoff between effectiveness of insect pollination and effectiveness of wind pollination in these sedges.

An instructional DVD on collecting entomological evidence from crimes scenes

Richard W. Merritt[1], Ryan K. Kimbirauskas[1], Mark E. Benbow[1], John R. Wallace[2], Jeffery K. Tomberlin[3]

[1]Michigan State University, East Lansing, MI 48824, United States, [2]Millersville University, Millersville, PA 17551, United States, [3]Texas A&M University, College Station, TX 77843, United States

This DVD was created by forensic entomologists to fulfill the immediate need to standardize practices for collecting entomological evidence. The material is intended to instruct forensic crime scene investigators, detectives, and associated personnel on how to collect specimen samples and field data in a way that will be scientifically valuable and credible in court. The DVD includes an overview of forensic entomology and the decomposition of an animal model has been time-lapsed to demonstrate the association of insects with various stages of decay. Insects commonly found with human remains are shown and factors that influence insect activity and development are described. Crime scene photographs and video are used to aid in the recognition of what information should be collected during death investigations. A list of equipment needed to process entomological evidence is given, and the collection and preservation of insect specimens has been clearly demonstrated in a step-by-step procedure. The main purpose of this DVD is to standardize the practices which are critical to the development of postmortem intervals and the utilization of insects as evidence during criminal investigations. The entire training video is 22 minutes; however, the multi-media format provides self-paced instruction and allows the viewer to select specific modules for quick referencing.

Shed leaves revitalized by a galling insect

Makoto Tokuda[2], Shigeru Takahashi[3], Masashi Suzuki[4], Naoki Mizusawa[5], Seiichi Nishimura[6], Junichi Yukawa[7], Takema Fukatsu[4]

[1]National Institute of Agrobiological Sciences, Tsukuba, Japan, [2]RIKEN Plant Science Center, Yokohama, Japan, [3]National Agricultural Research Center, Tsukuba, Japan, [4]National Institute of Advanced Industrial Science and Technology (AIST), Tsukuba, Japan, [5]The University of Tokyo, Tokyo, Japan, [6]National Institute for Agro-Environmental Sciences, Tsukuba, Japan, [7]Kyushu University, Fukuoka, Japan

Introduction: Galling insects have remarkable abilities to manipulate plant tissues physiologically and morphologically for their own benefit. Here we report that *Contarinia* sp. (Diptera: Cecidomyiidae), which induces leaf galls on *Styrax japonica* (Styracaceae), shows a striking ability to regulate the survival, growth, and proliferation of host-plant cells even after shedding of the gall-bearing leaves

Methods: We examined the number and size of plant cells in galled tissues, and analyzed chlorophyll fluorescence, carbon fixation, C:N ratio, and water content of the galls on intact and shed leaves in autumn, when the first instars of *Contarinia* sp. started molting into second and then third instars.

Results: Concurrently with the larval development, flat galls started to grow into a globular shape even on shed leaves. The number and size of gall-tissue cells increased significantly on the shed leaves during the larval developmental period. Even when the ungalled portion of shed leaves had already died, the galled portion was fresh until the larvae left the galls. Galls on the shed leaves exhibited only weak photosynthesis activity. The nitrogen concentration of galls was higher than that of ungalled tissues, and the water content of galls increased during the gall growth. Tracer experiments using tritium water demonstrated that galls were able to actively absorb water from the environment.

Conclusions: We demonstrated that *Contarinia* sp. is able to regulate the survival, growth, and proliferation of galls on shed leaves. The growth of the galls on such leaves is probably sustained by utilizing residue nutrients in the galled leaves and by absorbing water from the environment.

The *ipm*PIPE: Focus on the Other I in IPM

James VanKirk[1], Julie Golod[2], Scott Isard[2]

[1]Southern Region IPM Center, Raleigh, NC, United States, [2]Pennsylvania State University, State College, PA, United States

The *ipm*PIPE , a coordinated framework initiated to address the arrival of Asian soybean rust (ASR) in the United States, offers utility in management of many pests that migrate seasonally. It already has evolved to address several other pests and for use across international borders.

Information management, integration, and model development has been led to date by Dr. Scott Isard of Penn State University. Crop and pest information collected in the field is correlated with diagnostic information from a separate data system. Modeling integrates weather and climate data from a variety of sources with all other pertinent information to provide predictions of pest movement, population development and crop risk.

An unrestricted website provides timely information including reports of pest presence and development; crop development; and expert advice on risk and management options. A map-based interface enables users to focus on a particular region, state, or county. The calendar-based function provides access to all information from inception in 2005 to the present. A restricted site provides models outputs and other in-depth information for qualified experts.

Success derives in part from the extensive communication, coordination, and education efforts integral to this approach. Another critical contributor is the strong collaborative approach to all aspects of the framework of diverse stakeholder groups including producers and grower organizations, government agencies of several nations, agribusiness, and others.

Visual learning of a landmark sequence in wood ants, *Formica rufa*

Natalie Hempel de Ibarra[1], Olena Riabinina[2], Thomas S. Collett[2]

[1]University of Exeter, Exeter, United Kingdom, [2]University of Sussex, Brighton, United Kingdom

Introduction: Ants are known to travel long distances to a food source and back home. Field experiments performed on desert ants Cataglyphis and Melophorus suggest that ants are able to memorise and retrieve certain features of their idiosyncratic routes. However, it is not entirely clear if the animals are able to prime one memory of a visual stimulus by another visual stimulus, i.e. if they are able to learn a sequence of patterns.

Methods: We have designed a set of experiments with wood ants *Formica rufa* to investigate their ability to learn a visual sequence. First we selected four stimuli discriminated by the ants (horizontally or vertically oriented stripes (H and V) or green and UV colours (G and UV).

Results: We presented the ants with either stimulus H or V on the surrounding background walls while offering a choice between G and U in a Y-maze. In this paradigm G was rewarded if the context was set by H, and the same for U and V. Ants were able to learn this task quickly. Also the ants learned to perform right or left turns in the context of H and V, respectively. Finally, the ants encountered H or V first in a Y-maze, and later had to choose between G and U. The ants found this last task difficult.

Conclusions: We conclude that whereas these ants are very good at linking stimuli together when they are presented simultaneously, they are not adept at sequential binding i.e. linking stimuli that are separated in time.

Developing novel pesticide applications for vector control with US military funding

Graham White

University of Florida, Gainesville, Florida, United States

Since 2004, the US Armed Forces Pest Management Board supports research efforts to find and develop new pesticides and better application methods against mosquitoes and other biting flies. Primarily designed for protection of military personnel against vector-borne diseases, these products have wider potential for controlling pests and vectors of public health and veterinary importance. With $5m/year budget, this initiative called “Deployed WarFighter Protection (DWFP) against disease-carrying arthropods” already yielded >100 refereed publications, posters and presentations, from USDA Agricultural Research Service units dealing with medical and veterinary entomology, plus 30 competitive awards to academics, industry, CDC, and military entomologists. Leading product developments will be highlighted, with explanation of arrangements (via USDA project IR-4 for minor use registrations) to expedite EPA regulatory approvals.

New vector control tools from the US armed forces pest management board

Graham White

University of Florida, Gainesville, Florida, United States

Faced with dwindling availability of effective public health pesticides, in 2004 the US Armed Forces Pest Management Board launched an initiative to boost the discovery, development and registration of new insecticides and application methods for vector control and personal protection against arthropods of medical importance. Known as the R&D program for Deployed WarFighter Protection (DWFP) against disease-carrying arthropods, with $5m annual budget, efforts focus on new adulticide formulations and application methods to combat mosquitoes, phlebotomine sand flies and muscoid flies. Projects include screening chemical libraries from commercial partners, finding compounds with new modes of action, computational chemistry, synthesis and assays (QSAR) for optimization of candidate compounds, reformulating agricultural insecticides suitable for vector control, design and improvement of spraying systems, field demonstrations of vector control tools and strategies. Based on reviving collaboration with USDA-ARS National Program for Veterinary, Urban and Medical Entomology, the DWFP program also awards grants of up to $250K for 3 years to competitive proposals from academics, industry, military entomologists and other government agencies, not restricted to the USA. Some of the most productive DWFP projects will be showcased.

Phylogeny and biology of the Tineoidea: a review of current research on the 'basal' families of Ditrysia

Donald Davis

Smithsonian Institution, Washington, DC, United States

The superfamily Tineoidea is recognized generally to be the most plesiomorphic group of ditrysian Lepidoptera; until 1988 the superfamily included the groups now assigned to the Gracillarioidea or even Gelechioidea. Molecular work in progress reconfirms the basal position for the Tineoidea, as well as the closer association of the Gracillarioidea with Yponomeutoidea. Currently five families are included within Tineoidea, with their interrelationships appearing as Tineidae + (Eriocottidae + (Psychidae + Arrhenophanidae) + Acrolophidae))). The principal autapomorphy of the Tineoidea is the presence within A10 of most females of a slender pair of ventral pseudapophyses, whose development is associated typically with an unusually elongated, telescopic oviscapt. Other characteristics useful in distinguishing Tineoidea from Gracillarioidea and most ditrysian Lepidoptera are the presence of erect scales on the frons, labial palpi with lateral bristles, and haustellum with short, disassociated galeae. Tympanal organs are absent except on S2 of Harmacloninae (Tineidae). Possible synapomorphies of the non-tineid families are the strong tendency of the antennae to bipectination, reduction of the maxillary palpi, forewing with Rs4 terminating on the termen rather than on the costa, and female frenulum with more than 4 bristles. A general overview of the biology, subfamily diversity, and morphology of each family will be presented, emphasizing major discoveries over the last decade as well as of work now in progress.

Buruli ulcer disease in Africa: The potential role of aquatic insects in transmission

Richard W. Merritt[1], Mark E. Benbow[1], Heather Williamson[2], Ryan K. Kimbirauskas[1], Mollie D. McIntosh[1], Rebecca Kolar[1], Pamela Small[2], Daniel Boakye[3]

[1]Michigan State Univesity, East Lansing, MI 48824, United States, [2]University of Tennessee, Knoxville, TN 37996, United States, [3]Noguchi Memorial Institute for Medical Research, Univ. of Ghana, East Legon, Ghana

Buruli ulcer is the third most frequent mycobacterial disease in humans, next to tuberculosis and leprosy, often causing serious skin ulcerations, bone deformities, and disability. Buruli ulcer has emerged dramatically since the 1980's, with increasing numbers of cases being reported from at least 31 countries, mostly in tropical and subtropical areas, including Africa. Although poorly understood, the epidemiology of Buruli ulcer associates the resurgence with people who live and/or work close to wetlands, especially slow flowing (riverine) or stagnant water bodies (marshes, swamps), often created as a result of some human environmental disturbance. The disease is not known to be contagious between humans, and epidemiological studies have not yet established natural reservoirs or modes of transmission. Laboratory studies suggest possible transmission via aquatic biting insects; however, no field studies have tested this hypothesis. Our study represented the first field examination of biting water bugs (Hemiptera: Naucoridae, Belostomatidae, Nepidae) in disease endemic and non-endemic areas of Ghana, Africa. From collections of 22,832 invertebrates we compared composition, abundance and associated *M. ulcerans* positivity between 15 endemic and 12 non-endemic sites. Biting hemipterans were rare and represented a small percentage (usually < 2%) of invertebrate communities. There were no significant differences in hemipteran abundance or pathogen positivity between endemic and non-endemic sites, and there were no correlations between biting hemipteran abundance and *M. ulcerans* positivity. Therefore, while it is possible for infection through insect bites, there is little field evidence to support biting hemipterans as primary vectors of *M. ulcerans*.

Phylogeny of the heelwalkers (Insecta: Mantophasmatodea) based on mtDNA sequences, with evidence for additional taxa in South Africa

Jakob Damgaard, Klaus-Dieter Klass, Mike D. Picker, Gerda Buder

Natural History Museum of Denmark, Copenhagen, Denmark

Introduction: Less than a decade after the description of Mantophasmatodea, a considerable amount of material has been collected from various places in southern Africa. The material shows a striking diversity, not only in overall morphology, but also in reproductive organs, as far as such information is available. Since the sister group to Mantophasmatodea is uncertain, few such characters are directly comparable among insect orders, and a molecular phylogeny is established in order to make the taxonomy reflect the evolutionary relationships within the order.

Methods: A parsimony analysis on app. 1300 bp of mitochondrial DNA sequence data (COI + 16S) was performed on a selection of mantophasmatodeans including multiple specimens from eight described and four undescribed species of Austrophasmatidae; three specimens of *Sclerophasma paresisense* (Mantophasmatidae); and two specimens of *Praedatophasma maraisi* and one of *Tyrannophasma gladiator* (not yet convincingly assigned to any family). For outgroup comparison a broad selection of taxa from hemi-metabolous insect orders was included.

Results: Equally weighted parsimony analyses of the combined data sets supported Austrophasmatidae and all species and genera of Mantophasmatodea as being monophyletic. Most species were highly supported, but *Karoophasma biedouwense* had only moderate support and *Austrophasma caledonense* low support. Mantophasmatodea, Austrophasmatidae, and a *Tyrannophasma gladiator* + *Praedatophasma maraisi* were all strongly supported, while relationships among the two latter clades and Mantophasmatidae remain ambiguous. Concerning the relationships among genera of Austrophasmatidae, support values are moderately high for some nodes, but not significant for others.

Conclusions: COI and 16S are highly congruent at the species level as well as at the base of Mantophasmatodea, but congruence is poor for most intergeneric relationships. In forthcoming studies, deeper relationships in the order will be additionally explored by nuclear genes for a reduced sample of specimens.

Entomological experiences for rural youth in Oregon through university partnerships

Sujaya Rao

Oregon State University, Corvallis, Oregon, United States

Children have an innate curiosity about insects but, as they grow older, the 'entomologist' in children is lost due to perceptions that bugs are 'yucky', scary, and not 'cool', or due to lack of encouragement from parents and teachers who may themselves be intimidated by insects. The innate curiosity about insects can be fostered if children are provided rewarding entomological experiences, as it is well recognized that 'experience' is the greatest teacher. At Oregon State University, through partnerships with K-12 schools, students in rural Oregon schools have been engaged in entomological activities formally in the classrooms and informally during public events. One formal and one informal example will be presented: 1) A new innovative 'Bees and Pollination' unit that was implemented through which university researchers engaged students in four rural communities in an ongoing research project while providing them with a typical scientist's experience. Students developed hypotheses, conducted experiments, collected data and made inferences. They presented their results through oral and poster presentations during a 'Discovering Partners in Nature' conference organized at the university. 2) Family Bug Nights that were organized in rural schools to increase awareness about insects in children, their parents and community members. These evening events, organized by Oregon State University's undergraduate club, BugZoo, in collaboration with teachers in the schools, drew over 250 rural community members per night. Both programs and their impacts will be discussed.

Understanding the invasive potential of the khapra beetle, *Trogoderma granarium* Everts, in the Australian grain storage system using the established warehouse beetle, *T. variabile* Ballion as a model

Katarina Mikac

University of Canberra, Canberra, ACT, Australia

Introduction: The invasive warehouse beetle *Trogoderma variabile* (Coleoptera: Dermestidae) is an international pest of grain storage structures, packed goods and stored grain. Individuals were first documented in eastern Australia in 1977 and later Western Australia in 1979. Recent *T. variabile* distribution surveys indicate that its abundance has doubled in Australia during the period 1990-2000. The increased abundance of *T. variabile* is of serious concern as it is often confused with the destructive khapra beetle *T. granarium*, a visually indistinguishable sister species of *T. variabile*, currently not found in Australia. In this study the genetic structure, gene flow and dispersal patterns among *T. variabile* populations in eastern and Western Australia were investigated and the findings used as a model to understand the invasive potential of *T. granarium*.

Methods: The mitochondrial gene *Cytochrome Oxidase I* (COI) was used to estimate the genetic structure, gene flow and dispersal of eight *T. variabile* individuals from 20 populations in eastern and Western Australia.

Results: Moderate to low levels of genetic structure was found among populations. No pattern of isolation by distance was found. There is evidence to suggest that individual *T. variabile* from eastern Australia founded populations in Western Australia, indicating dispersal over large distances.

Conclusions: Preliminary results indicate that a single introduction of *T. variabile* in eastern Australia was possibly responsible for the subsequent spread and introduction of *T. variabile* to Western Australia. It is assumed that like *T. variabile*, *T. granarium* has the potential to disperse over large distances should it accidently be introduced to Australia.

Ejaculation strategies of *Ephestia kuehniella* Zeller (Lepidoptera: Pyralidae) males in relation to potential remating and female age

Jin Xu, Qiao Wang, Xiong Zhao He

Institute of Natural Resources, Massey University, Palmerston North, New Zealand

Introduction: Sperm and other material associated with ejaculates are limited resources. Thus in the polygamous mating system males are expected to allocate ejaculates strategically depending on the quality of their mates and their opportunity to remate. The Mediterranean flour moth, *Ephestia kuehniella*, is a polygamous species. During copulation *E. kuehniella* males transfer gelatinous secretions and a spermatophore containing accessory gland secretions and dimorphic sperm, eupyrene and apyrene sperm, to females. Here we investigated whether and how *E. kuehniella* males adjusted their ejaculation size in the presence/absence of rival males or other potential partners, and in response to the age of their partners.

Methods: Mating trials were performed in different sex ratio, density and female age. Spermatophore and associated ejaculated material were dissected and weighed immediately after mating. The number of eupyrene and apyrene sperm was counted.

Results: In the presence of other potential partners a male transferred significantly smaller spermatophore size with fewer number of eupyrene and apyrene sperm to his partner than in the absence of other potential partners. The presence of rival males had no effect on spermatophore size and number of sperm. The male ejaculated a significantly smaller spermatophore with fewer number of sperm to the old than to the young female.

Conclusions: Males allocate smaller ejaculates when they mate with older partners or when they have immediate opportunity to inseminate other mates. The presence of rival males does not appear to affect the amount of ejaculates males transfer.

Induction of self-superparasitism by the presence of a conspecific in the infanticidal parasitoid *Echthrodelphax fairchildii* (Hymenoptera: Dryinidae)

Emi Ito, Yoshihiro Yamada

Graduate School of Bioresources, Mie University, Tsu, Mie, Japan

Introduction: Van Alphen and Visser (1990) suggested that self-superparasitism is likely to be adaptive when conspecifics are present. Ito and Yamada (2005, 2007) disclosed the adaptiveness of self-superparasitism in the parasitoid *Echthrodelphax fairchildii* when conspecifics are present. They indicated that the total fitness performance of the first and second progenies on triple-parasitized hosts is larger than the fitness performance of the first progeny on double-parasitized hosts when the first-to-second oviposition interval is short. Moreover, they suggested that the probing for infanticide of earlier-coming progenies is less profitable when conspecifics are present than when they are not. In the present study we examined whether the presence of a conspecific induces self-superparasitism and hesitation in infanticidal probing. Results on self- and conspecific superparasitism when a conspecific was present were compared with those on self- and conspecific superparasitism when conspecifics are not present

Methods: After placing two parasitoids of *E. fairchildii* in a small vial for one hour one of the two was allowed to perform self- or conspecific superparasitism with different oviposition intervals. By observing superparasitism bouts we recorded the occurrence of superparasitism and infanticidal probing, and the sex of eggs laid based on the movement of the genitalia (Yamada & Imai, 2000).

Results: The self-superparasitism rate was higher when a conspecific was present than when it was not, when the oviposition interval was 8 h or shorter, in particular, less than 0.5 h. However, the presence of a conspecific did not change the superparasitism rate when the oviposition interval was 24 h or longer, and when superparasitism was conspecific. The presence of a conspecific did not change either the probing rate or the sex ratio of eggs laid irrespective of whether superparasitism was self- or conspecific. The probing rate was mostly less than 20% when the oviposition interval was 8 h or shorter under both self- and conspecific superparasitism, while it was mostly more than 40% when the oviposition interval was 24 h or longer. The eggs laid were almost always female.

Conclusion: The presence of a conspecific induced self-superparasitism when the oviposition interval was short.

Do queenless colonies of *Apis mellifera* and *A. florea* attract more drifted workers than colonies with a queen?

Nadine Chapman[1], Piyamas Nanork[2], Julianne Lim[3], Wandee Wattanachaiyingcharoen[4], Madeleine Beekman[1], Benjamin Oldroyd[1]

[1]University of Sydney, Sydney, NSW 2006, Australia, [2]Mahasarakham University, Mahasarakham 44150, Thailand, [3]University of Queensland, St Lucia, QLD 4072, Australia, [4]Naresuan University, Phitsanulok 65000, Thailand

When a honey bee (*Apis*) colony becomes queenless and broodless its only reproductive option is for some of its workers to produce sons before the colony perishes. However, for this to be possible the policing of worker-laid eggs must be curtailed and this provides the opportunity for queenless colonies to be reproductively parasitized by workers from other nests. Queenless colonies of the open nesting *A. florea* are heavily parasitized by non-natal workers, whereas the cavity nesting species *A. mellifera* and *A. cerana* are less heavily parasitised. Genetic analysis of worker populations has demonstrated that the proportion of non-natal workers present in *A. mellifera* colonies declines after a colony is made queenless, where as the proportion of non-natal workers increases in queenless *A. florea* colonies. We compared the rate of drift between queenless and queenright colonies of *A. florea* and *A. mellifera.* Here we show that workers from queenless *A. florea* colonies are more likely to leave their nest and join another colony compared with workers from queenright colonies and these drifted workers are much more likely to join another unrelated queenless colony than a colony with a queen. In contrast, no pattern was detected during drift of workers between queenless and queeright *A. mellifera* colonies.

RATS! *Rattus rattus* and *Rattus exulans* are eating rare Hawaiian arthropods

Francis Howarth

Bishop Museum, Honolulu, Hawaii, United States

Introduction: Although circumstantial evidence implicates rat predation as threatening native arthropods, few data demonstrating their impacts are available. To begin filling this lacuna, rats were collected during a multidisciplinary study of the ecology of Kipahulu Valley, a wilderness area on Maui Island managed by the US National Park Service.

Methods: Stomach contents from 160 *Rattus rattus* and 174 *Rattus exulans* were analyzed. The sexes were about equally represented. Arthropod remains were separated, mounted on slides and identified. Arthropod surface micro-sculpture proved valuable for associating individual macerated fragments into identifiable composites.

Results: Highly sclerotized exoskeletons (beetles, true bugs, legs and claws) were over represented compared to softer tissues, but even soft chitin fragments, such as moth larval skins, could be recognized and associated with other pieces by their micro-sculpturing. Arthropod remains were found in all but one *R. exulans* stomach, and all but five *R. rattus* stomachs. *R. exulans* stomachs contained 9.2 morpho-species/rat, whereas *R. rattus* stomachs contained significantly fewer (5.0 morpho-species/rat). Lepidoptera larvae were the most abundant food item occurring in 91% of *R. exulans* stomachs and 82% of *R. rattus*. Beetles were next in frequency, 77% of *R. exulans* and 40% of *R. rattus*, followed by spiders, true bugs and crickets. Several rare insects were eaten including some that remain only known from rat stomachs, such as remarkable new species of crickets, beetles, and lacewings.

Conclusion: These data corroborate the conjecture that rat predation is a major factor in the rarity of many native arthropod species.

Development of host range testing for a potential *Uraba lugens* biological control agent

Lisa Berndt, Toni Withers

Scion (New Zealand Forest Research Institute Ltd), Rotorua, New Zealand

Uraba lugens (Lepidoptera: Nolidae) is an invasive pest of *Eucalyptus* from Australia, recently established in New Zealand. Although it is currently causing damage mainly in urban amenity trees, it continues to spread, and is predicted to establish throughout eucalypt growing regions of the country. Development of biological control is currently underway for this pest. Host range testing has begun on *Cotesia urabae* (Hymenoptera: Braconidae), a solitary larval endoparasitoid presumably specific to *U. lugens* in Australia.

Sequential no-choice small arena tests were used initially to determine physiological host range, followed by choice tests at a larger scale to examine host finding abilities. Initial results have shown that this parasitoid is willing to attack a number of non-target species, one of which may be a suitable physiological host. Here we discuss options for further experimentation to best clarify the status of this parasitoid as suitable candidate for *U. lugens* biological control.

Management strategy of *Helicoverpa armigera* resistance to Bt cotton in China

Kongming Wu

Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing, China

Transgenic cotton expressing the Cry1Ac toxin from *Bacillus thuringiensis* has been widely planted in China since 1998. Susceptibility of *H. armigera* field populations to the Bt insecticidal protein Cry1Ac was monitored from 1997 to 2007. The results indicated that the field populations sampled were still susceptible to Cry1Ac protein and that a shift toward resistance among *H. armigera* populations was not apparent. The evaluations on natural refuges showed that a planting system consisting of wheat, soybean (peanut), corn, and Bt cotton could supply refuges for cotton bollworm throughout the year. Adequate provision of refuges on an area-wide basis, and successful production of susceptible insects could increase the probability that a rare resistant homozygote mated with a susceptible individual to produce heterozygous progeny susceptible to Cry1Ac. This strategy has been recommended for areas where farmers exclusively grow cotton without natural refugia from other crops.

Cellular level examination of a bark beetle-fungus interaction

Cetin Yuceer[1], Olga Pechanova[1], Kier Klepzig[2]

[1]Mississippi State University, Department of Forestry, Mississippi State, MS, United States, [2]USDA Forest Service, Southern Research Station, Pineville, LA, United States

Introduction: The southern pine beetle, *Dendroctonus frontalis* Zimmermann (Coleoptera: Scolytidae), harbors fungal symbionts in its mycangium. These fungi grown within the host tree provide necessary nutrition to developing beetles and compete with a pathogenic bluestain fungus. Secretions from the mycangial gland cells appear to regulate the species composition of and provide nourishment for these symbiotic fungi. However, the mechanisms (e.g., secreted antibiotic chemicals or nutrients, proteins or pathways) by which this relationship is maintained are not known.

Methods: We conducted qualitative and quantitative proteomics experiments to identify proteins using pronotal tissues from both sexes of SPB.

Results: We identified a number of proteins that are involved in metabolism, cell structure, contractile apparati, and defense, using information from the red flour beetle (*Tribolium castaneum*) genome sequence.

Conclusions: Although we currently don't have direct evidence that the more abundant proteins in the female SPB pronotum are involved in the synthesis/secretion of chemicals/nutrients, their possible roles should not be dismissed. These proteins could be parts of pathways regulating fungal growth and/or reproduction or be involved in selection against non-symbiotic fungi. They may also be expressed as a part of mycangial self-maintenance.

Developing an integrated pest management (IPM) strategy for the legume pod borer (*Maruca vitrata*)

R. Srinivasan[1], Song-Tay Lee[2], Mei-Ying Lin[1], Ching-Yi Lee[2], Chun-Chu Huang[1], Yun-Che Hsu[1], Fu-Cheng Su[1]

[1]AVRDC-The World Vegetable Center, Shanhua, Tainan, Taiwan, [2]Southern Taiwan University of Technology, Yung-Kang City, Tainan, Taiwan

Introduction: The legume pod-borer (LPB), *Maruca vitrata* is most serious on legumes in Asia and Africa. Alternative pest management strategies are warranted based on economic, social and environmental issues due to pesticide abuse.

Methods: Field explorations were made to identify potential natural enemies. Mass-culturing techniques were established for two promising parasitoids. A nucleopolyhedrovirus (NPV) was isolated, characterized, formulated as a potential bio-pesticide and field evaluated.

Results: *Nemorilla maculosa* (Tachinidae) and *Apanteles taragamae* (Braconidae) were the two most promising parasitoids on LPB in Taiwan. *N. maculosa* preferred the fifth instar larvae, and one female parasitized about five larvae. The maximum parasitism occurred at 20-35℃. *A. taragamae* preferred the first instar larvae. A single female parasitized about 30 larvae. The maximum parasitism occurred at 30℃. A NPV infecting LPB (MaviMNPV) was characterized based on ultra-structural morphology, REN patterns and sequences of the coding region of the *Polh* gene. The effectiveness of MaviMNPV was tested alone and in combination with neem and *Bacillus thuringiensis*. The efficiency of the MaviMNPV formulation containing lignin as a UV protectant was significantly higher (84.44%). However, the other formulation that contained optical brightener performed better in reducing LPB damage (14.77%) in yard-long bean. The pod damage in hyacinth bean was significantly reduced by both formulations (8.38 and 9.79% as against 18.29% in control).

Conclusions: An IPM strategy based on parasitoids and bio-pesticides is being validated. Additional parasitoids will be explored from the Southeast Asian region, which is supposed to be the origin of LPB, to broaden the sustainability of this IPM strategy.

Functionally-linked ultrastructural changes in the water vapour absorptive epithelium of the firebrat, *Thermobia domestica* (Packard), during development and the moulting cycle

John Noble-Nesbitt

School of Biological Sciences,, Norwich, United Kingdom

Sustained active water vapour absorption (WVA) from relative humidities down to as low as 43% is essential for the growth, development and survival of the firebrat in hot, dry environments where liquid drinking water is lacking. WVA starts falteringly during the second nymphal instar and reaches its mass-specific peak in the late-third and fourth instars.

The water vapour absorptive epithelium, in the posterior rectal (anal) sacs, boasts the highest known concentration of elongated mitochondria densely packed in hexagonal array alongside deep pleated infolds of the enormously hypertrophied, portasome-studded apical plasma membrane (apm). This apical complex comprises some 80% of the cell volume. It arises post-embryonically and reaches fully functional maturity just as WVA peaks in the third instar.

Early in the short-lived first instar, rapid mitochondrial biogenesis occurs in 'mitochondrial factory cells'. These cells become densely packed with mitochondria which are shared out amongst the daughter cells during mitoses. The mitochondria subsequently elongate alongside apm infolds, creating the apical complex.

During each moult WVA temporarily ceases. Despite the considerable investment represented by the apical complex, it regresses fully as a new cuticle overlying the epithelium is secreted. Portasome-studded apm rafts form and remain sequestered within the cells. Mitochondria round off and multiply. Cells divide. Mitochondria and rafts pass to the daughter cells. At the end of the moult, the rafts rapidly re-coalesce into deep-pleated infolds alongside elongating mitochondria, re-forming the apical complex. WVA resumes immediately after ecdysis.

Investigations on biology and host range of *Urentius* spp. (Hemiptera: Tingidae) in Sudan

Abdalla A. Satti

Environment and Natural Resources Research Institute, National Centre for Research, Khartoum, Khartoum State, Sudan

Introduction: *Urentius hystricellus* and *U. euonymus* are major pests of eggplant and pigeon pea, respectively. Several alternative hosts were also reported for each pest species, but some hosts were believed to be infested by the two pests. Actually, a lot of confusion has been found between these pests and their host plants. Accordingly, this work aimed to differentiate between such species and to verify their biology and host range in Sudan.

Methods: Host plants for both *Urentius* spp. were thoroughly surveyed throughout the year concentrating mainly at Khartoum State, but some areas in central and northern Sudan were also observed. The surveys also included other wild and cultivated plants in search for new hosts. Morph metrical studies were done for insects collected from each host. The life cycles were performed during autumn and winter seasons for the two pests, each on two (cultivated and wild) of its major hosts. Moreover, *U. euonymus* collected from pigeon pea and a wild host (*Abutilon* sp.) were reared on caged eggplant to confirm the differentiation between the two pests.

Results: The results showed clear morphological and biological differences between *U. hystricellus* and *U. euonymus*. The durations of pre-imaginal stages of the latter pest were longer than those of the former, but each exhibited similar durations on their respective hosts. Each pest has its own host range, and no single host was found infested by the two pests together, as believed. Some mistaken hosts for each pest were corrected and new hosts were added. However, among three hosts indicated for *U. hystricellus*, *Solanum incanum* was a new record. On the other hand, five hosts were indicated for *U. euonymus*, two of which (viz. *Chrozophora plicata and Rhynchosia memnonia*) were new records. Insects collected from the two hosts of *U. euonymus* didn't breed and died within 3-5 days when confined to eggplant in cages, thus ensured their difference from eggplant tingid bug.

Conclusions: This study verify the presence of both *U. hystricellus* and *U. euonymus* as different pest species infesting different host plants in Sudan, with mistaken hosts being corrected and new hosts added.

Quantitative food webs in space: herbivore-parasitoid communities on pedunculate oak *Quercus robur*

Riikka Kaartinen, Tomas Roslin

University of Helsinki, Helsinki, Finland

Introduction: While quantitative food webs provide accurate information about community structure and relationships between species, they have rarely been used to compare multiple local communities. In this study, we construct quantitative food webs of insects for tens of host trees, and thereby examine the impact of landscape context on the relative frequency and strength of interspecific interactions.

Methods: In 2006 and 2007, we sampled 30 oak trees in south-western Finland. 22 of these trees were located within a 5 km^2 island, where the spatial location of all oak individuals has been mapped. Eight additional trees were sampled elsewhere, within particularly dense oak stands or especially far from all other oak individuals. We sampled each tree twice both years by cutting down 30 c. half metre branches. All leaf mines and galls were collected for rearing.

Results: In 2006 we collected 33 800 leaf mines and galls of which 13 300 were reared, and in 2007 we collected a further 28 800 individuals of which 15 900 were reared. Preliminary analyses suggest that both the species composition of local communities and the type and frequency of host-parasitoid interactions within them may vary with the spatial context and the local abundance of host plants.

Conclusions: Once completed, we expect this study to offer the first quantitative insight into he effect of habitat fragmentation on herbivore-parasitoid food web structure.

Bioecology of the invasive B biotype compared to the indigenous Ms biotype of *Bemisia tabaci* on tomato

Bernard Reynaud[1], Helene Delatte[1], Pierre- François Duyck[4], Aurélie Triboire[1], Nathalie Becker[3], Patrice David[2]

[1]CIRAD UMR PVBMT, Saint Pierre, La Réunion, France, [2]CEFE CNRS UMR 5175, Montpellier, France, [3]MNHN CNRS UMR 5202, Paris, France, [4]University of California, Davis, CA, United States

Studies on success or failures of biological invasions by different insect biotypes are scarce and could provide interesting insights into the traits that determine greater or lower ability to invade. Life history traits of invasive whiteflies *Bemisia tabaci* of the B biotype (known as a worldwide invasive biotype) and of the indigenous biotype Ms (not known as an invader anywhere in the world), both from the island of La Réunion (Indian Ocean), were compared for this purpose. In our study we demonstrated that within a cultivated host plant (tomato), the B biotype differs from the Ms by a combination of several life-history traits. This combination gives the invasive biotype an advantage over the resident both in terms of rapid demographic growth (increased intrinsic rate of increase and associated traits such as short developmental times and high fecundity) and in terms of competition (large adult and offspring sizes), without any recorded trade off. However, in the field the resident biotype remains dominant on non-cultivated hosts (weeds) and in a particular climate (high humidity). This suggests that invasive biotypes are characterized by physiological, morphological and biological adaptations to a relatively uniform environment created by anthropic activities at different places in the world, while resident biotypes may persist in less altered habitats.

The aquatic and semi-aquatic Heteroptera of Madagascar: faunal affinities and patterns of intra-island endemism

John T. Polhemus[1], Dan A. Polhemus[2]

[1]Colorado Entomological Instititute, Englewood, Colorado 80113, United States, [2]Bishop Museum, Honolulu, Hawaii 96817, United States

Madagascar represents a significant area of endemism for the infraorders Leptopodomorpha, Gerromorpha, and Nepomorpha.On a world basis these infraorders contain a documented 23 families, 343 genera and 4799 species . Of these, 18 families, 57 genera and 161 species are currently recorded from Madagascar. Although this biota represents only 3% of the described world fauna, it exhibits extreme species level endemism (80%), and contains 12 specialized endemic genera. All the remaining non-endemic genera are shared with Africa. Despite its predominantly African affinities, certain elements that occur elsewhere only in tropical Asia, such as the gerrid subfamily Ptilomerinae and certain Microveliinae, provide evidence of a former connection between Madagascar and India prior to Cretaceous rifting. At the species level, at least 35 new species remain to be described, all of them Madagascar endemics These new species are concentrated in the families Veliidae (Microveliinae, Rhagovelia), Aphelocheiridae (Aphelocheirus) and Naucoridae (Temnocoris). The intraisland distributions of Malagasy water bugs define four major internal biogeographic regions: the eastern wet forest, the central plateau, the western dry forests, and the northern volcanic massifs, with many genera exhibiting localized endemic speciation among these regions. Collections of Madagascar water bugs have been sporadic, with the last major survey in the mid-1980s. Certain key areas remain to be collected, notably Mt. Tsaratanana, the Masoala Peninsula, the Isalo Massif, the Mt. Andringitra massif, and the mountains west of Ft. Dauphin.

Pupal parasitoids of grape berry moth *Lobesia botrana* (Denis & Schiff.) (Lepidoptera:Tortricidae) and their role in an IPM program in vineyards

Gholamali Akbarzadeh Shoukat, Klaus Horstmann, Ebrahim Ebrahimi

[1]1Agricultural and Natural Resources Research Center, Orumieh, Islamic Republic of Iran, [2]Lehrstuhl Zoologie 3 Biozentrum, Am Hubland, Wuerzburg, Germany, [3]Plant Protection Research Institute, Tehran, Islamic Republic of Iran

Introduction: In order to alleviate growing public concerns regarding the effects of pesticides on human health and environment impact much attention has been given to biological control using parasitoids in recent decades. Since grape berry moth *Lobesia botrana* (Denis & Schiff.) was known as the key pest of grapes in Orumieh, Iran therefore this study was conducted to determine pupal parasitoids of the pest and to assess their potential for natural control during 2005-2007.

Methods: Pupae of GBM were collected under loosen barks of unsprayed vineyards form early December until mid April and were reared in containers at room condition with 15-20 days interval. Emerged parasitoid adults were counted and classified to different families then each group were studied and identified by related specialists. Average of parasitism and its trend was discussed according two years data.

Results: Seven parasitoid species were reared from grape berry moth pupae including: *Itoplectis tunetana* (Schmiedeknecht), *Pimpla aracadica* Kasparian, *Pimpla ?confinis* Kasparyan, *Dicaelotus inflexus* Thomson, *Labiinae* sp. belonging to Ichneumonidae family as well *Pteromalus puparum*(L.) and *Homoporus* sp. belonging to Pteromalidae. The occurrence of these parasitoids on grape berry moth pupa are reported for the first time. Pupal parasitism ranged from 12 to 48% with an average of 21%. Parasitism rates were increased toward initiation of the growth season.

Conclusions: Parasitism was medium and it is likely that additional surveys in this area will yield new parasitoids for introduction into Iran.

Population ecology of *Scotinophara lurida* in rice fields in Korea: its spatial distribution and phenology model

Hunsung Kim, Joon-Ho Lee

Seoul National University, Seoul, Republic of Korea

Introduction: The spatio-temporal pattern of the rice black bug, *Scotinophara lurida* was studied in rice fields, and its phenology simulation model was developed for development of its management program.

Methods: Visual counts of *S. lurida* were conducted in rice fields, and its spatial patterns for egg, nymph and adult were examined with SADIE (Spatial analysis by Distance IndicEs). The components for the phenology simulation model were a degree-day immigration flight model of overwintered adults, temperature-dependent developmental model of each stage, survival rate of each stage and an adult oviposition model. To develop an immigration flight model of over-wintered adults, the cumulative percentage light trap capture data were fit to a Weibull function as a function of degree-days. Laboratory and greenhouse experiments were conducted to determine the effect of temperature on the development and survival of each stage and fecundity of female adults. A linear function was used to model the developmental rate of each stage. Distribution of developmental time for each stage was modelled against physiological age by a Weibull function. The oviposition model was developed incorporating the three components of average total fecundity, cumulative oviposition rate function, and survival rate function which were modelled using extreme value function, two-parameter Weibull function and sigmoid function, respectively. The phenology model was validated with the data collected over 2 years in a rice field.

Results: The distribution pattern of overwintered *S. lurida* and egg were random ($I_a = 1$) or uniform ($I_a < 1$) in rice field, while aggregated distribution pattern ($I_a > 1$) appeared to be common for nymphs and newly emerged adults. Overall, the simulation model predictions agreed with the observed pattern of each developmental stage of *S. lurida* in the field.

Conclusions: The spatial distribution pattern of *S. lurida* is temporally very stable and the distribution of immigrated overwintered adults strongly affected the spatial distribution of later developmental stages. The phenology simulation model predicted the time of peak occurrences of life stages of *S. lurida* well.

Phoretic mites on *Pityokteines curvidens* (Coleoptera: Curculionidae: Scolytinae) caught in pheromone traps

Milan Pernek[1], Stacy Blomquist[2], John Moser[2]

[1]Forest Research Institute, Jastrebarsko, Croatia, Croatia, [2]USDA Forest Service, Southern Research Station, Pineville, Louisiana, United States

Introduction: The species composition and abundance of phoretic mites of the bark beetles *Pityokteines curvidens*, caught in pheromone traps were investigated in Croatia. Mites, phoretic on bark beetles are involved in complex symbiotic interactions with bark beetles, fungi, including ophiostomatoid species and their host trees. This research may form the basis for further studies on the hitherto unknown interactions between *P. curvidens*, their phoretic mites and fungal associates.

Methods: Beetles were sampled by using "Curviwit" pheromones (composed of metilbutenol and ipsenol) in Theysohn traps placed at two localities in Croatia. *P. curvidens* beetles caught in the pheromone traps were weekly collected in 2006, placed into plastic cups with 70% ethanol. For mite inspection beetles were transferred to lactophenol for clearing and their accompanying mites were counted and plucked from their bodies.

Results: A total of 10 mite species were documented which included *Dendrolaelaps quadrisetus*, *Histiostoma piceae*, *Paraleius leontonychus*, *Pleuronectocelaeno barbara*, *Tarsonemus minimax*, *Trichouropoda lamellosa, Uroobovella ipidis, Schwiebia* sp., *Histiostoma* sp. and an unidentified species from the family Orimbatidae. *U. ipidis, P. leontonychus,* and *D. quadrisetus* were the most frequent mites. While *Pleuronectocelaeno japonica* and *Schizostethus simulatrix* were not found in this study as on beetles collected from logs in previous studies, four new mite species including *Schwiebia* sp., *Histiostoma* sp. *Pleuronectocelaeno barbara* and an unidentified mite from the family Oribatidae, were found as new mite associates of *P. curvidens*.

Conclusions: The records of mite species in this study increase the number of known mite associate of *P. curvidens* from 10 previously documented species to 14 species.

The genus *Carminator* (Hymenoptera: Megalyridae): geographic distribution and phylogeny

Toshiharu Mita[1], Kazuhiko Konishi[2]

[1]Kyushu University, Fukuoka-shi, Fukuoka-ken, Japan, [2]National Agricultural Research Center for Hokkaido Region, Sapporo-shi, Hokkaido, Japan

The family Megalyridae is a relatively rare group of parasitic wasps. They parasitize larvae of wood-boring beetles (Cerambycidae, Buprestidae, Bostrichidae) and mud-nesting wasps (Sphecidae) rarely (Shaw, 1990). Almost all other megalyrids are distributed in Southern Hemisphere, but a genus *Carminator* Shaw is the representative in Asia. This genus comprises the Cryptalyrini Shaw together with South American *Cryptalyra* Shaw (Shaw, 1990). Unlikely *Clyptalyra* or other genera, the *Carminator* has bizarre appearance by many unique characters like the shallow subantennal groove; the five-toothed and stout mandible; the prognathous head; and the strongly arching ovipositor (Shaw, 1988, 1990). Six species have been recorded from Japan, Southeast Asia, and Bismarck Archipelago (Shaw, 1988, Mita *et al*., 2007). All of them except for *C. ater* are monotypic, and no male has been reported. In the course of our study on the *Carminator*, two female specimens, which exhibited two additional undescribed species, and a male specimen, which could not be placed in any species yet, were found from Southeast Asia. In this presentation, we discuss the morphology of the species, analyze their phylogenetic relationships, and attempt to demonstrate the preliminary view of the dispersion pattern of the *Carminator*.

The role of immune defence in avian predation risk on a territorial damselfly

Markus Rantala, Johanna Honkavaara, Jukka Suhonen

University of Turku, Turku, Finland

Introduction: It has been commonly thought that predators prey more often on socially subordinate individuals that are in poor physiological condition, although empirical evidence supporting the hypothesis is scarce.

Methods: Here we tested whether the activation of immune system, or individual variation in immunity has any effect on survival and predation risk of the territorial banded demoiselle, *Calopteryx splendens*.

Results: We found that immune challenged males were less frequently territorial than control or sham-manipulated males. This suggests substantial fitness cost of the activation of immune system as territorial males had higher mating success than non-territorial males in damselflies. We also found that immune challenged males were more often predated by a small passerine bird (*Motacilla alba*), than control or sham-manipulated males. The overall survival of immune challenged males was reduced, supporting the prediction that the activation of immune system is costly. Interestingly, we also found that territorial males had lower predation risk than non-territorial males, suggesting that predation risk is condition dependent. Furthermore, males with weak immune defence had a higher predation risk than males with strong immune defence, supporting the hypothesis that predators prey upon individuals of inferior phenotypic quality.

Conclusion: In the light of these experiments it appears that predation risk is strongly associated with the immune system in the wild, may cause substantial selective pressure on immunity and may shape trade-offs between immunity and life history traits.

The maintenance of high ant diversity in tropical rain forest canopies: Empirical evidence for a lottery model with taxonomically limited competition.

Tom Fayle[1], William Foster[1], Paul Eggleton[2]

[1]University of Cambridge, Cambridge, Cambridgeshire, United Kingdom, [2]Natural History Museum, London, United Kingdom

One of the major questions facing ecologists today is that of how high diversity is maintained in tropical ecosystems. We investigate this question using the ant communities in epiphytic bird's nest ferns as a microcosm. Bird's nest ferns are widespread and abundant tropical epiphytes, which collect leaf litter and acquire nutrients from the ensuing decomposition. The resulting mass of decomposing material is an ideal habitat for arthropods in the canopy, being buffered against changes in microclimate. We surveyed 87 ferns and found 71 species of ant with colony centres within these ferns. Three factors were important in structuring these ant communities:

1. Species richness increased with fern size.

2. Species composition changed with fern size and with fern height in the canopy, although together these two variables explained only 8.1% of the total variation in species composition.

3. Conspecific colonies never co-occurred, and congeneric colonies did so less frequently than expected by chance.

We also carried out experimental invasions of ferns using a model invader (*Diacamma* sp.). Ferns contained either a conspecific colony, a congeneric colony, or a colony of a species from a different genus. We found that *Diacamma* could successfully invade only when there was no conspecific or congeneric colony present. We conclude that while fern size limits the number of species in the ant community, and fern size and height weakly affect community composition, the nature of that community is mainly controlled by interactions between congeneric species, which presumably have similar niches. Ants colonise the ferns more or less at random until the ferns are full, with the proviso that colonisation will be unsuccessful if there is a congeneric colony already present. This means that stochasticity will play a large role in determining the species composition of the ferns, allowing the high diversity in this canopy ecosystem to be maintained.

Beetles at our service

Olga Ameixa, Pavel Kindlmann

Department of Theoretical Ecology, Institute of Systems Biology and Ecology AS CR and Faculty of Natural Sciences of the University of South Bohemia, Ceske Budejovice, Czech Republic

Introduction: Simplification of local landscape mosaics and of landscape composition result in a decreased ability of agricultural landscapes to support natural ecosystem components and processes. With the dismantling of collective farms, agriculture in the Czech Republic is being restructured. Some conservative policies are being applied, like building new natural corridors. These structures help to maintain biological diversity, protect water resources, conserve soil and help to maintain functional habitats, which includes travel corridors for native wildlife, when they move from nests or burrows to areas where they hunt, feed, or breed. After joining the European Union, the pressure for yield has forced farmers in the Czech Republic to increase the amount of agrochemicals used and the expectation is for a further increase of these inputs to face of these new challenges. It is known that intensive production methods severely deplete the ability of the agricultural landscape to provide services, but the effects of these actions on the local biodiversity are still unknown.

Methods: Coleoptera individuals were collected (beating/sweep netting and pitfall traps) from natural and semi-natural habitats; individuals were identified to the species level.

Results: Here we characterize the Coleoptera (Coccinellidae and Carabidae) diversity in several types of habitats (natural and semi-natural). We discuss how agricultural practices and the use of natural corridors influence the “goods and services” supplied by Coleoptera. Differences between the species assemblages in the different habitats were observed.

Conclusions: The species assemblages in natural communities are influenced by agricultural intensification, the impact of corridors is unclear.

Forenseek: a simulation program of carrion-feeding insect's development dedicated to forensic entomology.

Damien Charabidze[1], Gildas Morvan[3], Didier Gosset[1], Benoit Bourel[2]

[1]Université Lille 2, Lille, France, [2]Faculté Libre des Sciences et Technologies, Lille, France, [3]Laboratoire de Génie Informatique et d'Automatique de l'Artois, Bethune, France

Introduction: Post-Mortem Interval (PMI) estimation and understanding of circumstances of death in forensic entomology are only based on the expert analysis. The expert exploits insect samples and many other important data, such as environment description, meteorological data, police investigation data or bibliography. The quality of diagnosis and information analysis depends on a rigorous scientific method as well as a strong experience and intuition of the expert. However, all the factors cannot obviously be taken into account. Nevertheless, in a forensic context, the conclusion must be absolutely explained and justified, and not any hypothesis can be disregarded.

Methods: ForenSeek is a computer based Decision Support System (DSS) dedicated to forensic entomology. The core part of the software program is a multiagent model of behaviour and development of necrophagous diptera larvae. This concept allows to model complex group behaviours from simple individual data, and thus is particularly well adapted to study insect populations. Moreover, results provided by this model are intended to be automatically computed to extract relevant information and then estimate PMI.

The aim of this project is 1: the PMI estimation after retrieving available parameters and field data, including their reliability degree; 2: the simulation of various situations and processes of colonisation from initial data and parameters.

Results: In fact, complexity of the matter brings us to divide the whole project in two sub-projects: a simulation system of the behaviour and development of insect larvae;
A DSS that analyses these simulations and estimate PMI

Conclusion: Together, these tools form a comprehensive software program, which should allow a clear increase of speed and accuracy of entomological forensic expertises.

Establishing a protocol for South African agriculture, based on new crop case studies

Vaughn Swart, Maitland Seaman, Schalk Louw

University of the Free State, Bloemfontein, South Africa

Introduction: The greatest threat to biodiversity in the past 50 years has been due to habitat destruction associated with agriculture. The sustainability of an agro-ecosystem depends on the conservation of its biodiversity, whilst, conversely, the agro-ecosystem affects the surrounding environment. The development of a robust methodology is thus necessary by implementing measures of biodiversity as mechanisms to indicate degree of disturbance of the environment.

Methods: Two sites with different crop and natural vegetation types, climate and agricultural practices were chosen as case studies, i.e. Green Valley Nuts, Prieska, Northern Cape, (with a pistachio crop) and Winterton, Kwazulu-Natal, (with a kenaf crop). At each site marked transects were sampled for insects and vegetation. At four different locations on site, three transects in the relevant crop and three in the surrounding environment were set 2, 10 and 50 metres from the crop border. Insects were used as indicator community since they are prevalent, have high species diversity, are easy to sample, are important in ecosystem function, provide early detection of ecological changes and respond to environmental changes faster than vertebrates. Insect morpho-species were categorised into functional feeding groups.

Results: After analysis, patterns of similarity in the biodiversity of each transect can be seen at the different locations, relative to the frequency and diversity of vegetation sampled.

Conclusions: Biodiversity should indicate a relationship between communities and is a sign of the level of ecosystem integrity. An early prototype version of the model design is suggested and further streamlining is planned for the future with the aid of a workshop.

Establishing a protocol for South African agriculture, based on new crop case studies

Vaughn Swart, Maitland Seaman, Schalk Louw

University of the Free State, Bloemfontein, South Africa

Introduction: The greatest threat to biodiversity in the past 50 years has been due to habitat destruction associated with agriculture. The sustainability of an agro-ecosystem depends on the conservation of its biodiversity, whilst, conversely, the agro-ecosystem affects the surrounding environment. The development of a robust methodology is thus necessary by implementing measures of biodiversity as mechanisms to indicate degree of disturbance of the environment.

Methods: Two sites with different crop and natural vegetation types, climate and agricultural practices were chosen as case studies, i.e. Green Valley Nuts, Prieska, Northern Cape, (with a pistachio crop) and Winterton, Kwazulu-Natal, (with a kenaf crop). At each site marked transects were sampled for insects and vegetation. At four different locations on site, three transects in the relevant crop and three in the surrounding environment were set 2, 10 and 50 metres from the crop border. Insects were used as indicator community since they are prevalent, have high species diversity, are easy to sample, are important in ecosystem function, provide early detection of ecological changes and respond to environmental changes faster than vertebrates. Insect morpho-species were categorised into functional feeding groups.

Results: After analysis, patterns of similarity in the biodiversity of each transect can be seen at the different locations, relative to the frequency and diversity of vegetation sampled. **Conclusions:** Biodiversity should indicate a relationship between communities and is a sign of the level of ecosystem integrity. An early prototype version of the model design is suggested and further streamlining is planned for the future with the aid of a workshop.

Tools to improve surveillance for insect plant biosecurity in Australia

James Ridsdill-Smith, Darryl Hardie, Rob Emery

Cooperative Research Centre for National Plant Biosecurity, Perth, Western Australia, Australia

When an invasive insect species becomes established in a new area/region/country populations are very low and hard to detect, however with every month that they remain undetected they will become harder and more expensive to eradicate. Australia with a coastline of 60,000 km requires sentinel trapping to detect key threats like Asian gypsy moth and fruit fly species. We are looking to improve trap design, including remote traps that wirelessly self-report as well as developing software for identification through shape and pattern recognition. Regularly serviced grids of traps are used for fruit flies to acquire measurable evidence of absence. Even when an incursion has occurred, many traps catch no flies. We are researching the use of fewer traps placed in strategic locations predicted from fly behaviour studies using new spatial statistical methods. The development of these new surveillance trends will produce massive amounts of biological and spatial data and the development of software tools on hand-held PDAs (Personal Digital Assistants) is a cost effective way to collect, audit and validate these biological and spatial data in the field. Spatial data from GPS can be used to navigate to traps and data can be ported to third party web applications like Google Earth for desktop validation. The CRCNPB brings together many organisations to develop a new generation of surveillance tools that can be used by regulatory authorities throughout Australia to detect incursions earlier, allowing eradication before they impose a major economic impact on industry and government.

Arbuscular mycorrhizal symbiosis triggers prey-mediated changes in the life history of the predatory mite *Phytoseiulus persimilis*

Daniela Hoffmann[1], Horst Vierheilig[2], Peter Schausberger[1]

[1]Institute of Plant Protection, Department of Applied Plant Sciences and Plant Biotechnology, University of Natural Resources and Applied Life Sciences, Vienna, Austria, [2]Departamento de Microbiología, Estación Experimental de Zaidín, CSIC, Granada, Spain

Soil organisms such as arbuscular mycorrhizal (AM) fungi may influence aboveground herbivores via shared host plants. Only a few studies examined whether these effects are passed on to higher trophic levels. We investigated the effects of AM symbiosis on selected life history parameters of the specialized predatory mite *Phytoseiulus persimilis* feeding on two-spotted spider mites *Tetranychus urticae*. Experiments were performed on plant and artificial substrates to distinguish between effects mediated by prey with and without direct influence of the host plant on the predator. The plant substrate were leaves of broad bean (*Phaseolus vulgaris*) that were either colonized by the AM fungus *Glomus mosseae* (+M) or not (-M). The artificial substrate were closed acrylic cages. On the leaf juvenile survival and development, and oviposition were assessed supplying prey in surplus. In the cage juvenile survival and development were assessed as a function of the predator feeding history (mothers feeding on prey reared on either +M or -M), prey feeding history (+M or –M) and quantity of prey supplied. Oviposition in the cage was also measured at limited prey availability. Juvenile survival in the cage with limited prey supply was significantly increased if prey or predator or both had a +M feeding history. Moreover, developmental time in the cage and on the leaf (for feeding stages) was significantly shorter for individuals feeding on +M prey. Minimum prey needed to oviposit was not affected by AM symbiosis. We discuss possible implications of our results for multi-trophic aboveground - belowground interactions.

Global change and IPM: the emblematic case of *Bemisia tabaci* in Mediterranean Europe

Olivier Bonato, Jacques Fargues, Frédéric Pellegrin

UMR CBGP, Montferrier/Lez, France

The impact of global change on Integrated Management of *Bemisia tabaci* in protected crop is assessed under predictive hypothesis of ambient air temperature increase. The increase of air temperature modifies temperature inside greenhouse. All the components of the agrosystem are affected by this change and particularly the biotic potential of both whitefly and natural enemies. Therefore the efficiency of integrated management strategies usually employed to control *B. tabaci* is questioned in a Mediterranean context of global change.

Ditrophic relationship of *Liriomyza* spp. with its potato host

Sunita Facknath

University of Mauritius, Reduit, Mauritius

The genus *Liriomyza* (Diptera : Agromyzidae), includes several species which are important pests of ornamentals and greenhouse crops. In *L.trifolii* (Burgess) and *L. huidobrensis* (Blanchard), age of potato leaves and trichome density had the strongest influence on host preference and performance.

Adult choice of host species had a pre-imaginal component, which could be reinforced by an imaginal component, while choice of plant variety operated at imaginal level and was not inherited. Intraplant preference was towards larger, older, lower leaves, although the middle leaves were superior for growth and development of young stages, i.e. oviposition preference–offspring performance hypothesis was not supported, but Hopkins' host selection principle operated at the level of host species, and to some extent at level of host variety, but at host age.

L. trifolii and *L. huidobrensis* were more attracted to conspecific- and heterospecific-infested plants and potato odour, than to uninfested plants/ odour. *L. trifolii* showed a lower preference for *L. huidobrensis*-infested plants than to conspecific-infested plants. *L. huidobrensis* attraction to conspecific-infested plants was due to increased amounts of E-4,8-dimethyl-1,3,7-nonatriene, methyl salicylate, germacrene D, germacrene-4-ol, and caryophyllene released by infested plants.

Liriomyza huidobrensis females were found to lay a greater number of eggs in a situation of inter-specific competition than in an intra-specific one. *L. huidobrensis* larvae consumed greater amounts of nutrients compared to *L. trifolii*, and exhibited interference and exploitative competition.

Plants grown under high nutrient levels were more attractive due to higher leaf nutrients and differential levels of phytovolatiles.

Handling of large numbers of names in Braconidae with Taxapad, exemplified by the revision of European Opiinae

Cornelis van Achterberg[1], Dicky Yu[2]

[1]Nationaal Natuurhistorisch Museum (Naturalis), Leiden, Netherlands, [2]University of Kentucky, Lexington, Wyoming, United States

The parasitoid family Braconidae (Hymenoptera) belongs to the Ichneumonoidea, which is one of the largest superfamilies in the animal kingdom. In total about 44,000 taxa (species and genera) are known, of which ca 43 % or 19,000 taxa belong to the Braconidae. These taxa are associated with numerous other spp. (e.g. as hosts) accounting in total for more than 221,000 taxa to be handled. It looks like a Sisyphean task but it can be accomplished with the interactive software "Taxapad" developed by the second author. How this is done, and how it can be used for a large revision, is exemplified by the European Opiinae with more than 300 valid species and many synonyms.

Data on the distribution, life-history and morphology of immature stages of *Eupales ulema* (Coleoptera: Chrysomelidae: Eumolpinae)

Károly Vig

Savaria Museum, Szombathely, Hungary

Introduction: *Eupales* is a monospecific eumolpine genus native to SE Europe, mostly to the Balkan Peninsula and Turkey. The northernmost known populations of *Eupales ulema* breed in southern parts of Hungary on the southern slopes of the Mecsek Hills, which are sub-Mediterranean in climate. The life-history and the morphology of the immatures stages of the species have still not been described, and the purpose was to obtain this information.

Results: Field observations so far find the adults appearing in mid-April. They feed exclusively on the cornelian cherry *(Cornus mas)*. Mating occurs on the food plant in the typical riding mode of leaf beetles. The eggs of the female are placed in the soil, where the larvae presumably feed on the roots of the food plant and pupation is also thought to occur. In Hungary, one generation develops each year. It proved possible to raise L1 larvae in the laboratory. The neonate larvae are yellowish white with developed legs. As with all the typical eumolpine species, the larvae are totally blind with no sign of stemmata on the head capsule. The last abdomen segment of the freshly hatched larvae do not carry a caudal abdominal shield. After hatching, the larvae bore into the ground and do not feed on cornelian cherry leaves offered to them. This presentation details the knowledge of species distribution and life-cycle acquired and sets out and illustrates the typical morphological features of the larva.

Evaluation of termite resistant plant attributes for their bioactivity against *Macrotermes* termites

Bekele Jembere, Gedion Yohannes, Mengistu Gemech, Ermias Dagne

Addis Ababa University, Addis Ababa, Ethiopia

Introduction: The monotypic genus *Hagenia abyssinica* (Rosaceae) commonly known as Kosso is most widely used to expel human tapeworm and the wood is resistant to termite. Attributes of the plant responsible for such effect sought investigation and hence this study was initiated.

Methods: Tests were conducted on toxicity, anti-feedant and repellent effects of the plant on *Macrotermes* termite workers under field and laboratory conditions. Different levels of aqueous extract of the plant's female flower powder was applied on filter papers to test toxicity effect. Repellency effect of polar and non polar extracts of the different parts of the plant was tested using Y tube olfactometer, while anti-feedant effect of the plant was tested by applying the different extracts on *Croton macrostachyus* (susceptible wood) stakes and providing them to the termites in mounds.

Results: The female flower extract killed the entire worker termites at all levels of extraction, while no repellency effect of any part of the plant was observed. However, susceptible wood stakes treated with different polar extracts of *H. abyssinica* saw dust were significantly protected. Phytochemical investigation of the koso plant resulted in the isolation of one compound partially characterized on the basis of spectroscopic data.

Conclusion: Results from the toxicity and anti-feedant tests indicate that the tree is resistant to termites for it ha s toxic and anti-feedant bioactive compounds.

Biological control of *Callosobruchus theobromae* (L.) (Coleoptera: Bruchidae), a seed pest of edible legumes

D.R. Thakur, H.S. Banyal

Department of Biosciences, Himachal Pradesh University, Shimla, Himachal Pradesh, India

Introduction: Class Insecta comprising largest fascinating fauna of the animal kingdom. Beetles, the insect order Coleoptera, are dominant form of life on earth and one of every five living species is a beetle. Insects belonging to the family Bruchidae (Coleoptera) are commonly called “pulse weevils” or bruchids or “Dhoras”. These bruchids are cosmopolitan in distribution and cause serious loss to legumes both in fields and stores worth million of rupees every year. Therefore, an increased attention towards non-chemical methods of stored product protection is the need of modern agriculture system, because chemical control is often not affordable for sustainable farming, whereas the chemicals available are health hazards. Therefore, simpler, environmentally innocuous, self-regulatory, long lasting and relatively inexpensive mode to retain pest population below economic injury level is by inoculating the stores and fields by their natural enemies. Thus main aim of the present study is to catalogue entomophagous diversity and assess their potential in regulating active population of *Callosobruchus theobromae* (L.) (Coleoptera: Bruchidae), a seed pest of different legume commodities.

Materials and Methods: Pods of *Dolichos lab lab* infested with *C. theobromae* were collected from different localities of Punjab and Himachal Pradesh, India and carried to laboratory in wire mess cages. Pods infested with bruchids were also carrying different stages of parasitoid on host insect. Culture was maintained to observe emergence both of host and parasitoid insects. Adults of *U. femoralis* also emerged in the culture from the eggs of host insects, which were already parasitized in the field. Females of *U. femoralis* were allowed to lay eggs by supplying different age host eggs. Numbers of eggs laid by a female parasitoid were observed microscopically. Development of parasitoid egg inside the host egg and their emergence as adult were recorded carefully. Similarly larval parasitoid emerged were also maintained in culture by supplying different old aged larvae of host insect. Behaviour of parasitoids, mating, egg laying and developmental duration etc. were also recorded at ordinary environmental conditions.

Results: Egg endoparasitoid, *Uscana femoralis* (Trichogrammatidae: Hymenoptera), a eupelmid and two pteromalids species have been identified as idiobiont and koinobiont parasitoids of *C. theobromae*. Egg parasitoid deposited its eggs inside the host eggs by puncturing chorion through its ovipositor. Host eggs of 0-84 hours old were accepted for parasitization. Parasitoid eggs hatched inside the host eggs and further development was completed inside at the cost of host egg ooplasm. Adult parasitoids came out after 9.4 ± 0.46 days by making a circular cut in eggshell of host insect.

Gravid females of koinobiont hymenopteran parasitoids felt the presence of host larvae inside the seeds with the help of their antennae and laid eggs on or inside the developing larvae. It has been observed that parasitoids deposited their eggs when larvae were either in 2^{nd} or 3^{rd} instar stages. The parasitized larvae developed at the usual rate up to the last instar or pupal stage but their after development was paralysed by developing parasitoid. An exist hole was excavated in the mid dorsal region of the host body to come out of it. Thus parasitoid larvae while coming out killed the host larvae in the operation and used their remains as a mat for further development. Parasitoid larvae pupate outside the host body but were still inside the seed of *D. lab lab*. Adult parasitoid came out by cutting a small irregular but circular hole in testa of seed and life cycle was completed in 16-24 days.

Conclusion: Parasitoids are fast developing and having inherent capacity to complete their development more quickly at the cost of host organisms. Synchronization of life cycle with developing stages of host insects is an ecological adaptation of parasitoids to ensure continues food supply and developmental mat to sustain their growth and development from sufficiently bigger size and long developmental duration hosts which are available in the vicinity for a brief time period.

High egg laying capacity, destruction of host eggs before they hatch into larvae and low developmental duration place the idiobiont parasitoids in the category of potential biocontrolling agents. However, larval parasitoid killed the host larvae when sufficient damage was done to legume seeds, but their role as bio-controlling agent even at that stage cannot be ignored, because killing of bruchid pest at any stage may check its out break in next generation. Thus induction of these hymenopteran parasitoids in the '**Integrated Pest Management**' strategy of bruchid is advocated through this research.

Bulb mite biocontrol in lilies

Izabela Lesna[1], Maurice Sabelis[1], Cor Conijn[2]

[1]University of Amsterdam, Amsterdam, Netherlands, [2]Applied Plant Research, Lisse, Netherlands

Introduction: Bulb mites (*Rhizoglyphus robini*) are a serious pest of many ornamental bulb crops, in particular cultivated lilies. We investigated possibilities for biological control with the soil-dwelling predatory mite, *Hypoaspis aculeifer*.

Methods and Results: Biocontrol of bulb mites was applied in three phases of lily bulb cultivation:
Bulb propagation phase (storage rooms): Experiments were carried out in closed plastic bags filled with lily bulb scales and vermiculite, as is common practice in lily bulb propagation. The results showed that *H. aculeifer* was able to suppress its prey to very low densities, when released in a ratio of 1 : 20 prey.
Flower production phase (greenhouse): Experiments in the greenhouse soil (peat, sand) showed that in absence of predatory mites populations of the bulb mite, on lily bulbs increased, whereas the release of predatory mites caused the bulb mite populations to decrease, when released in a ratio of 1 : 2 prey.
Bulb growth phase (field): Experiments in lily fields showed suppression of population growth of the bulb mites when the initial predator-to-prey ratio varied between 1 : 1 and 3 : 1 prey.

Conclusions: Our results are among the very few showing the feasibility of biological control of a below-ground plant pest. The method to control bulb mites is now available for lily growers (e.g. under the trade-name ENTOMITE) and recommended especially for application in the lily bulb propagation phase. Implementation in practice has been achieved via successful trials at 6 selected lily farms in the Netherlands.

Potential of repellents in the control of tsetse and other disease vectors

Rajinder Saini, Ahmed Hassanali

icipe-African Insect Science for Food and Health, Nairobi, Kenya

Repellents for the control/management of disease vectors like tsetse are being identified at *icipe* from synthetic sources or from natural blends of un-preferred animals, which are common in tsetse habitats but not fed upon.

The synthetic tsetse repellent 2-methoxy-4-methylphenol can provide substantial protection to cattle either in 'push' mode or when used in conjunction with baited traps in 'push-pull' strategy. Most livestock keepers prefer the repellent technology compared to other tsetse and trypanosomiasis control options due to the technology's simplicity and mobility. Toxicological assessment of the repellent indicates no adverse effect on the health of exposed animals. A major constraint of the technology, however, at the moment is the repellent collar prototype, which breaks easily and needs to be commercially produced.

The repellent blend responsible for making waterbuck refractory to tsetse has been identified as pentanoic acid, geranlyacetone, guiaiacol and δ-octalactone. This blend was as effective as the 15 component waterbuck repellent blend (WRB) that contributes to refractiveness to these animals. The WRB not only reduces number of flies (*G. pallidipes*) coming to an ox (>75%) but also the feeding efficiency by >90% indicating that WRB is a potent repellent. Dispensers for WRB are being developed.

Preference for feeding at specific on-host sites by the vector of East Coast Fever, *Rhipicephalus appendiculatus,* has also opened up the possibility of manipulating the behaviour of this tick by 'push' and 'push-pull' tactics and suggests that investigations of feeding preferences of other vectors may similarly yield useful tools and tactics for their control.

Molecular phylogenetics of the Vespoidea

Erik Pilgrim, James Pitts, Carol von Dohlen

Utah State University, Logan, UT, United States

The 24,000+ described species of Vespoidea include many well-known stinging wasps, such as paper wasps and hornets (Vespidae), velvet ants (Mutillidae), spider wasps (Pompilidae), and ants (Formicidae). Members of this family exhibit compelling behaviors associated with prey capture, nest construction and provisioning, and parental care, including complex social behaviors. Indeed, behaviors in Vespoidea have been instrumental in developing evolutionary theories positing stepwise transitions from simple to complex. Such theories necessarily depend on an understanding of evolutionary relationships among taxa exhibiting the putative transitional states, yet phylogenetic proposals for Vespoidea are conflicting, with no well-supported consensus emerging from morphology. We collected molecular data from four nuclear genes (elongation factor-1 F2 copy, long-wavelength rhodopsin, wingless, and the D2-D3 regions of the 28S ribosomal RNA (~3000 bp in total)). We analyzed molecular data under both maximum-parsimony and Bayesian inference methods. Bayesian inference returned a well-resolved consensus with posterior probabilities of over 95% for most nodes. We used this topology as the best estimate of phylogeny at the family and subfamily levels. Notable departures of our phylogeny from previous estimates include: 1) paraphyly of Vespoidea resulting from the nesting of Apoidea within a lineage comprising Formicidae, Scoliidae, and two subfamilies of Bradynobaenidae; 2) paraphyly of Bradynobaenidae, Mutillidae, and Tiphiidae; 3) a sister relationship between Rhopalosomatidae and Vespidae, 4) Rhopalosomatidae + Vespidae as sister to all other vespoids/apoids.

The Buzz and the Beat(les): insect inspiration for music throughout the ages

Frank Turpin

Purdue University, West Lafayette, Indiana, United States

Ecologically and metaphorically insects seemingly are everywhere. Including music created by humans. Insects and their behavior have not only inspired music lyrics and song titles but also names for musical groups. Insect-inspired songs include children's chants, folksongs, rock and roll and classical music. The first insect-related song to top the popular music charts in the United States was "Glowworm" recorded by the Mills Brothers in 1952. "Glowworm" is an adaptation of a 1908 song from the German operetta "Lysistrata." Butterflies are the most common insects referenced in music but insects from most major orders have also managed occasionally to "strike a chord" with songwriters over the years.

Micro-hotspot determination and buffer-zone value in the core of a global hotspot (Cape Floristic Region)

Paul B.C. Grant, Michael J. Samways

University of Stellenbosch, Stellenbosch, Western Cape, South Africa

Introduction: The Kogelberg Biosphere Reserve (KBR) is a buffered, second-order biodiversity hotspot within a first-order global biodiversity hotspot, the Cape Floristic Region, South Africa. The extraordinarily rich flora is matched by an extremely rich dragonfly (Odonata) fauna, which are excellent indicators of habitat type and environmental quality.

Methods: Number of individuals and species of male dragonflies, in addition to environmental variables, were recorded during 15-min observation periods in quadrats within the core, buffer and transition zones of the (KBR).

Results: Using this micro-distributional data on this special but vagile faunal component, it is shown that the KBR consists of distinct and localized hotspots of many nationally rare, endemic and Red Listed species exclusively within its protected core.

Conclusion: Determination of these local third-order hotspots is of critical importance from a reserve management point of view. They are important in conservation planning, prioritization of areas for alien vegetation removal and environmental monitoring. Presence of buffer zones, as well as transition areas, surrounding the core play a vital role in buffering edge effects and maintaining core patch quality. While these buffer and transition areas do not support high numbers of species, nor any endemic species they never the less provide habitat heterogeneity, which inevitably leads to overall increased species richness. The inclusion of these buffer and transition zones into the biosphere reserve is therefore highly recommended to protect core habitat and to boost species richness through habitat heterogeneity.

Temperature-dependent development of insects simulated with INSIM for MatLab

Lia Hemerik[1], Egbert van Nes[2]

[1]Wageningen University, Biometris, Department of Mathematical and Statistical Methods, Wageningen, Netherlands, [2]Wageningen University, Department of Aquatic Ecology and Water Quality Management, Wageningen, Netherlands

Introduction: For many practical purposes it is useful to be able to predict the development of a pest insect. Insect development is strongly influenced by temperature. Each species ceases to grow below a certain threshold temperature. Duration of the development of egg, larval and pupal stages of insects are mostly reported at constant temperatures. Measures to eradicate pest species in agricultural practice can only be taken at the right time, if the occurrence during the year of stages is known. We introduce a new version of the insect simulation model INSIM, that calculates the development of insects under different temperature regimes.

Methods: In INSIM for MatLab the development of insects is simulated based on daily minimum and maximum temperatures together with tables of relative mortality, development time and its standard deviation at different temperatures. The threshold value of development should be denoted and , if more than one generation is simulated, reproduction of adults should be known at different temperatures.

Results: We present simulation outcomes for one insect species with known temperature dependent developmental rates.

Conclusions: Advantages of INSIM for MatLab are that (1) temperature-dependent development and survival are easily provided to the program, (2) insects with egg to egg development times >1 year can be simulated, (3) different developmental thresholds can be set for different insect stages, (4) INSIM for MatLab is faster, more flexible and more user friendly than the original programme and (5) it is freely available from the internet.

Recent progress in insect telemetry

Wolfram Kutsch

Dept. of Biology, Konstanz, Germany

Recent technical developments enable to accumulate data in freely moving insects, too. Animals can be equipped with telemetric devices that are small enough not to impede normal behaviour. Momentarily there are two major trends: 1) Pursueing of the free-ranging insect, 2) telemetric transmission of physiological data. The latter aspect is of great relevance to understand processes underlying behavioural performances. Initially, the electrical activities of major muscles have been recorded which are involved in free flight of locusts. Recently it became possible also to record the activity of specific sense organs. The approach to record the activity of neuronal elements instantaneously offers the option to describe the participation of selected CNS parts and their interaction with sensory inputs. It is obvious that this approach wil be more fruitful compared to studies analyzing restricted animals.

Odor-mediated parasitoid-host interaction: A model study

Marjolein Lof, Lia Hemerik, Maarten de Gee

Biometris, Department of Mathematical and Statistical Methods, Wageningen University, Wageningen, Netherlands

Introduction: Parasitoids are efficient natural enemies. Once they found a patch parasitism rates can be very high. Moreover, some parasitoids are able to distinguish odors that are associated with their hosts. Our study system is the *Drosophila melanogaster* based food web. Fruit flies of the species *D. melanogaster* feed and breed on ephemeral resources like fermenting fruit. Chemical attraction towards infochemicals like fermentation products and an aggregation pheromone emitted by recently mated females, play a directive role in the localization of these resources. Aggregation of *D. melanogaster* on resources is the result of this process. The fruit fly's natural enemy, the larval parasitoid *Leptopilina heterotoma* is known to use the same odours to find its host. We studied how the ability to use odors affects the interaction between a parasitoid and its host.

Methods: We developed a spatially explicit model that incorporates odours dispersion and population responses in a heterogeneous environment. The interaction between host and parasitoid was modelled by a Holling type II functional response.

Results: We investigate the costs and benefits of the use of infochemicals by studying fruit fly population numbers and larval mortality due to Allee effect, competition and parasitism.

Conclusions: There is a balance between the effects of the three aforementioned processes, where in some cases parasitism just might tip the host population into extinction.

Laurel wilt in the southeastern United States, a new disease caused by a fungal symbiont of *Xyleborus glabratus*

Robert J. Rabaglia[1], Stephen W. Fraedrich[2], Thomas C. Harrington[3], Albert E. Mayfield, III[4]

[1]USDA Forest Service, Forest health Protection, Arlington, Virginia, United States, [2]USDA Forest Service, Southern Research Station, Athens, Georgia, United States, [3]Department of Plant Pathology, Iowas State University, Ames, Iowa, United States, [4]Florida Department of Agriculture and Consumer Service, Division of Forestry, Gainesville, Florida, United States

A non-native ambrosia beetle, *Xyleborus glabratus*, was first found in North America in 2002 near Savannah, Georgia, United States. Extensive mortality of redbay, *Persea borbonia*, has occurred in coastal Georgia and South Carolina since 2003, and northeastern Florida since 2005. The redbay mortality is due to a vascular wilt disease caused by an undescribed *Raffaelea* sp. that is the fungal symbiont of *X. glabratus*. The *Raffaelea* sp. has been isolated consistently from the mycangia of *X. glabratus*, and wilted redbay trees infested with the beetle. Redbay seedlings and trees inoculated with the fungus succumbed to the wilt within 5 to 12 weeks. Field studies have shown greater than 90% redbay mortality in plots in Florida within two years of initial disease detection. Additional lab and field studies have found that other members of the Lauraceae including sassafras, spicebush, pondberry, pondspice, avocado and California bay laurel are susceptible to the wilt caused by the *Raffaelea* sp.

Lessons from IPM successes in managing invasive pest species of horticultural crops in Asia

Peter Aun-Chuan Ooi

AVRDC-The World Vegetable Center, Bangkok, Thailand

As horticulture science advances and international trade in fruits and vegetables increases, so is the risk of inadvertently introducing exotic insect pests into tropical Asia. Two invasive species of interest in Asia are *Plutella xylostella* (L.) from the warm Mediterranean and *Liriomyza huidobrensis* (Blanchard) from South America. The introduction of *Diadegma semiclausum* (Hellen) effectively managed *P. xylostella* but the culture of dependence on chemical control by the growers has fostered the need for an Integrated Pest Management (IPM) approach led to farmer education to understand how an exotic parasitoid works and how to conserve them.

Studies conducted in Thailand showed that *Coenosia exigua* Stein, an indigenous predator, adapted to feed on *L. huidobrensis* and through a programme of breeding this predator in the field, *L. huidobrensis* was brought under control.

A common factor in the successful IPM of both invasive species has been the need to educate farmers about the role of natural enemies. It was important to educate farmers about how *D. semiclausum* attacks and keep populations of *P. xylostella* in check. This was initially challenging as farmers often do not know about parasitoids. However, experiences in Vietnam and Thailand showed that crucifer farmers can learn and appreciate the efficacy of parasitoids and help conserve them thereby reducing dependence on chemical control. In the case of the IPM of *L. huidobrensis*, promoting breeding of *C. exigua* resulted in reduction of pest populations and farmers were educated to adapt this technique to their own field conditions.

A problematic termite genus

Johanna Darlington, Charles Cook, Giselle Walker

University of Cambridge, Cambridge, United Kingdom

The genus *Odontotermes* (Isoptera, Termitidae, Macrotermitinae) is a large genus, with very many nominal species in it. It is characterised by the presence of one large tooth near the middle of the left mandible in the soldier caste. The genus has never been revised for Africa, there are no published keys, and identification of species is often difficult.

W.V. Harris (unpubl.) divided them in two, based on the morphology of the soldier head. Species in his "latericius" group have piriform head capsules (= tapering anteriorly) and either no teeth, or one small weakly defined tooth, near the middle of the right mandible. All others have sub-rectangular heads and one large tooth near the middle of the right mandible, often as large as that on the left mandible

To resolve this dichotomy and define the species present in East Africa, we have produced a partial molecular phylogeny for *Odontotermes* based on mitochondrial DNA. This shows that the residual morphological group is monophyletic (except for one species) while the "latericius" group is not.

The type of fungus comb built by different species fits exactly with the phylogeny. The residual group all build fungus combs of the sponge type (or modifications of it), except for the one species mentioned above. It and all the "latericius" group species build fungus combs of the fragile laminar type. Thus it appears that the architecture of the fungus comb is a more accurate indicator of relatedness than soldier morphology.

A problematic termite genus

Johanna Darlington, Charles Cook, Giselle Walker

University of Cambridge, Cambridge, United Kingdom

The genus Odontotermes (Isoptera, Termitidae, Macrotermitinae) is a large genus, with very many nominal species in it. It is characterised by the presence of one large tooth near the middle of the left mandible in the soldier caste. The genus has never been revised for Africa, there are no published keys, and identification of species is often difficult.

W.V. Harris (unpubl.) divided them in two, based on the morphology of the soldier head. Species in his "latericius" group have piriform head capsules (= tapering anteriorly) and either no teeth, or one small weakly defined tooth, near the middle of the right mandible. All others have sub-rectangular heads and one large tooth near the middle of the right mandible, often as large as that on the left mandible

To resolve this dichotomy and define the species present in East Africa, we have produced a partial molecular phylogeny for Odontotermes based on mitochondrial DNA. This shows that the residual morphological group is monophyletic (except for one species) while the "latericius" group is not.

The type of fungus comb built by different species fits exactly with the phylogeny. The residual group all build fungus combs of the sponge type (or modifications of it), except for the one species mentioned above. It and all the "latericius" group species build fungus combs of the fragile laminar type. Thus it appears that the architecture of the fungus comb is a more accurate indicator of relatedness than soldier morphology.

Local adaptations of life history traits of a *Drosophila* parasitoid, *Leptopilina boulardi*

Joffrey Moiroux, Cécile Le Lann, Jean-Sébastien Pierre, Philippe Vernon, Joan van Baaren, Jacques van Alphen

[1]*University of Rennes 1, Rennes, France,* [2]*Leiden University, Leiden, Netherlands*

Introduction: Local climate is an important source of selection on life history traits. Clinal variation in life history traits on a continental scale has been well documented for a number of insect species, but local adaptation to climate has not often been investigated. We have studied local adaptations to climate of a parasitoid, focusing on early reproduction.

Methods: Four populations of *Leptopilina boulardi,* a pro-ovogenic *Drosophila* parasitoid, originating from contrasting climates were sampled in the North of Iran, and cultured under standard conditions. We compared several life history traits of females (size, early reproduction, lipids content, activity, development time), and associated trade-offs.

Results: Discriminant analysis revealed that the four populations differed in one or more of the measured traits. Under very dry and hot desert conditions, large females with a rapid development are found - in contrast to the trade-off usually observed - whereas in the humid warm climate of the Caspian coast, females are smaller and invest more in early reproduction. We predicted that host distribution, which depends on climate, would explain the observed patterns better than abiotic climate itself. *Drosophila* hosts are more abundant during a longer season in the region with a humid climate allowing the parasitoids there to spend less energy and time in patch finding in comparison to wasps from desert populations. This results in selection for early reproduction traded off against a body size and longevity. In the hot and dry climate, a larger body size and smaller initial egg load allow dispersal and facilitate patch finding, while a short development time allows better tracking of the host populations that go through bust and boom periods. In addition a relatively high water content provides them with some protection against dessiccation.

Conclusions: Climate can exert a strong selection pressure on a local-scale for parasitoids, via spatial or temporal distribution of hosts.

Susceptibility of *Anopheles* mosquito larvae to some selected entomopathogenic fungi in the tropical climate of Nigeria

Funmilola Oluyemi Omoya, F. A. Akinyosoye, Bolanle Boboya

Federal University of Technology, Akure, Nigeria

Introduction: Malaria, a mosquito-borne and a potentially deadly disease in tropical African countries as well as the increasing level of insecticide resistance, has attained a global concern/attention. The ineffectiveness of chemical pesticides so far has lead to an intensive search for new control measures. Three types of entomopathogenic fungi were used in order to determine the larvicidal activity.

Methods: The susceptibility of *Anopheles* mosquito larvae *Varicosporium elodae, Trinacrium substile* and *Articulospora inflata* were isolated from the cricket and grasshopper species and investigated under laboratory conditions. The larvicidal activities on the anopheles mosquito larvae sampled from Akure, Western Nigeria, were analysed and observed for 72 h using different levels of concentrations, ranging from 1.1×10^5 spore/ml to 6.3×10^5 spore/ml on the third instars larvae of *Anopheles arabiensis.*

Results: Different values of mortality rates were observed among the investigated larvae with a range of 50%. *V.elodae* displayed the highest mortality rate of 80%, *T. substile* 50% and *A. inflata* 30% on the larvae of *Anopheles arabiensis.*

Conclusion: Among the fungi used in this study the larvicidal activity of *Varicosporium elodea* was most pronounced. This clearly indicates that it can be used as a bio-control agent for *Anopheles arabiensis,* thereby affording minimum disturbance within the tropical and temperate climate regions as compared to the chemical pesticides.

Modelling the attractivity of colours for aphids

Thomas Döring, Jim Hardie

Imperial College London, Ascot, Berkshire, United Kingdom

Introduction: In aphids and other Hemiptera, colours play an important role in the process of host finding. However, the mechanisms underlying the responses of these insects to colours in the field are still not fully understood.

Methods: Water traps (14 cm diameter) of 140 different colours (hues ranging from blue to green to yellow, with varied brightness) were set out in the field in spring 2007 in a completely randomised design. All caught aphids were identified to species level. Trap colours were measured with a spectrophotometer. Using information from previous electrophysiological work, the 'attractivity' of trap colours was modelled with two input variables, the photon catch G that a given trap spectrum produced in a green receptor (with a peak sensitivity at 530 nm), and B, the respective photon catch for a blue receptor peaking at 470 nm. The model was then applied to spectra of leaf colours to predict their relative attractivity for aphids.

Results: The trap catch, totalling 17383 winged aphids, was dominated by *Brevicoryne brassicae* and *Myzus persicae*. The best model for the attractivity y (ranging from 0 to 1) had the form $y=a*\log(G/B)+b$, for $G>B$, and $y=b$ else, with $a=1.92\pm0.055$ and $b=0.019\pm0.001$ (mean ± s.e., $r^2=0.89$, $n=140$). Red leaves were predicted to be less attractive than green leaves.

Conclusions: The model can accurately predict the response of aphids to coloured surfaces. The selection of appropriate non-attractive leaf colours may be used as a tool for aphid control.

Genomics and post-genomics of parasitoids

John Werren

University of Rochester, Rochester, NY, United States

The three species of *Nasonia* are the first parasitic hymenoptera to have their genomes sequenced. Here I describe the status of the genome project and its applications. The genome information greatly increases utility of *Nasonia* as a model genetic system, but more importantly will greatly enhance advancement of genetic and genomic studies of parasitic hymenoptera. Comparisons with honey bee and other insects reveal possible hymenopteran specific and chalcidoid specific gene sets. RNAi has been developed in *Nasonia*, providing a means to investigate function of these genes. Opportunities now exist to identify parasitoid genes involved in host preference, diapause, mate discrimination, pathogen resistance, sex ratio control, parthenogenesis, and many others of biological importance and implications to biological control. The possibility of directed genetic modification to produce “domesticated” parasitoids is no longer just an abstraction. In the long-term, such developments could reduce human dependence on chemical pesticides, with significant positive implications to human health and the environment. Therefore, research efforts into the genetics and genomics of parasitoids should be expanded and vigorously pursued.

Extinction debt of vascular plants and butterflies in five European countries

Jochen Krauss[1], Riccardo Bommarco[2], Ingolf Steffan-Dewenter[1]

[1]University of Bayreuth, Department of Animal Ecology I, Population Ecology, Bayreuth, Germany, [2]Swedish University of Agricultural Sciences, Department of Ecology, Uppsala, Sweden

Introduction: Time lags in species extinctions (extinction debt) are a rarely recognised threat for long-term species survival in fragmented habitats. Abandonment of extensive management practices and agricultural intensification lead to enormous landcover changes and loss of natural or semi-natural habitats within the last 50 years in Europe. However, especially long living species might be delayed in their extinction. Our project aimed to reveal the impact of historic habitat loss on current species richness and potential future extinction risks of vascular plants and butterflies in five European countries.

Methods: In the EU project COCONUT (Understanding effects of land use changes on ecosystems to halt loss of biodiversity, www.coconut-project.net) we recorded vascular plant and butterfly species richness in 30 fragmented semi-natural grassland sites in Finland, Sweden, Estonia, Germany and Spain. Within a 2km buffer around each study site we quantified actual habitat loss using current and historic aerial photographs. Species were categorized with respect to habitat specialization and dispersal ability to analyse trait-related differences.

Results: We recorded 180 – 370 vascular plant species and 50 – 80 butterfly species in the five countries. Historical habitat loss was 36 ± 4 % (range: 4 – 78 %) for Finland und is currently calculated for the other countries. The data will allow us to calculate expected future species loss due to historical land use change.

Conclusions: Time delayed extinction events might cause a severe reduction in species richness, even if conservation strategies manage to keep remaining habitat fragments at a constant quality.

The Offshore Pest Information System – early pest warning for US borders

Ronald Stinner, Karl Suiter

NSF Center for IPM, NCSU, Raleigh, NC, United States

International trade is rapidly expanding; the relevance of international borders is diminishing. With that expansion comes the risk of the spread of exotic plant pests. The Offshore Pest Information System (OPIS) is a secure, structured, risk-focused process designed to collect, synthesize/analyze, communicate and utilize relevant offshore pest information by USDA/APHIS officials. The system was developed cooperatively by USDA/APHIS and the NSF Center for IPM and is linked to other relevant sources of pest information.

Homeland Security inspectors at ports of entry need to be aware of pest situations abroad on a daily basis in order to focus their inspection activities. State plant regulatory agencies also need similar information for their pest surveys. APHIS risk assessors and trade managers need to know what pest threats exist offshore as they evaluate potential trade opportunities with countries that may harbor pests of concern to the USA. Producers and importers need current pest incidence information before they negotiate sale contracts to ensure that the products they purchase from Offshore will not be infested with plant pests and suffer quality loss or seizure upon arrival due to infestation/infection.

The timely collection, synthesis and communication of offshore pest information provides US safeguarding personnel with the tools necessary to focus their activities based on commodity and origin-based risk posed in a dynamically changing world.

This paper describes the technical aspects of OPIS, including how reporting is handled electronically, data sources, linkages with other database systems, and security issues involved.

Impacts of environmental alterations on the population dynamics and the gregarisation of the red locust in the Sofia basin (Madagascar)

Alex Franc[1], Gérard Duvallet[2], Annelise Tran[3], Valeria Soti[3], Jean-François Duranton[1]

[1]Locust Ecology & Control research unit, Agricultural Research Centre for International Development (CIRAD), Montpellier, France, [2]Centre for functional and evolution ecology, Paul Valery University, Montpellier, France, [3]Epidemiology Research Unit, CIRAD, Montpellier, France

The red locust *Nomadacris septemfasciata* (Serville, 1838) *Orthoptera*: *Acrididae* is found in southern Africa and on islands in the Indian Ocean. Although responsible for plagues in southern Africa, only a few local outbreaks have been reported in Madagascar. Yet, in 2002, locusts became gregarious in the Sofia basin, i.e., swarms and larval bands threatened the two main rice-producing basins of the country. The overall scope of this study is to explain this new gregarisation of the red locust in Madagascar.

Factors controlling the locust population dynamics were determined during a four year field monitoring program (2003 to 2007). The ecological requirements of this locust were assessed during the different periods of its life cycle. The evolution of the locust habitat was mapped using remotely sensed data (Spot satellite).

Our results show a close connection between red locust ecological requirements and environmental modification in the Sofia basin. First, the locust potential of each habitat at the eco-regional and macro-regional scale was quantified. Second, these habitats were mapped in 1986 and 2004. Satellite images revealed extensive deforestation thus providing new favourable breeding habitats for locusts. This environmental alteration also opened migration pathways between complementary ecological areas. The combination of both these factors allowed the red locust gregarisation to be possible. A red locust forecasting system is outlined within the scope of a preventive control strategy.

Arthropod Aloft: The new science of insect flight

Robert Dudley

University of California, Berkeley, CA, United States

Flying insects represent an abundant and diverse set of design solutions to the common biomechanical problem of creating and controlling aerodynamic forces. Hovering insects are stable yet highly maneuverable, long-distance migrants fly and navigate over thousands of kilometers, and major ecological themes of the terrestrial biosphere, such as pollination and tropical biodiversity, derive from adaptive radiations of the pterygote insects. Recent technological advances, ranging from quantitative flow visualization and unsteady force measurements on flapping wings to remote telemetry of free-flying insects, have substantially enhanced our abilities to capture and describe varied features of the flight envelope. Neurophysiological studies of sensory mechanisms and associated locomotor output have increasingly revealed sophisticated, integrated pathways for flight control. Ecological, allometric, and phylogenetic studies of aerodynamic performance, in turn, permit elucidation of the broader significance of particular flight behaviors and capacities. Although the insect analogue of *Archaeopteryx* has yet to be unearthed, recent demonstrations of controlled aerial behavior in the absence of wings have suggested new evolutionary trajectories for the initial origin and functional utility of protowings. Ongoing aerodynamic studies of flight performance in the modern insect fauna are suggesting enviable and perhaps even unattainable design specifications for the emerging technology of microair vehicles. This symposium presents diverse experimental studies within the exciting and technologically infused science of insect flight.

Some determinants of insect species distributions across spatial scales

Jorge Soberon, Joaquin Hortal

University of Kansas, Lawrence, Kansas, United States

There are many factors that affect the distribution of a species, and they act with different strengths at different spatial and temporal scales. At coarse scales (large extent, low resolution), bioclimatic modeling has proven to be very predictive of the broad features of distributions of many species. Physiological tolerance, movement capacities and historical factors are predictors of these broad features, and can be statistically modeled using the suites of techniques known as “Ecological Niche Modeling”. However, the fine grained details of distributions are determined by different processes, related to habitat selection and availability, species interactions, and resource consumption. In this presentation I will discuss one conceptual approach to integrate several processes acting at different scales. I will highlight some theoretical and practical problems to an integrative, multiscale estimation of species distributions. Using the example of *Baronia brevicornis* (Lepidoptera: Papilionidae) I will illustrate the possibilities and limitations of the method.

Role and evolution of viral cystatins in an insect host-parasitoid interaction

Céline Serbielle[1], Shafinaz Chowdhury[2], Jean-Michel Drezen[1], Elisabeth Huguet[1]

[1]Institut de Recherche sur la Biologie de l'Insecte, Université François Rabelais, Tours, France, [2]National Research Council Canada, Biotechnology Research Institute, Montreal, Canada

Introduction: Parasitoid wasps have developed amazing strategies to parasitize their insect hosts. One of the most effective involves the domestication of polydnaviruses which are injected in the host. Expression of viral genes inside the insect host alters its immune response and developmental program resulting in the emergence of adult parasitoid wasps. We are interested in characterizing the role and evolution in the host-parasitoid interaction of a viral gene family encoding cystatins which are inhibitors of cysteine proteases.

Methods: We performed functional studies which consisted in determining expression levels and biochemical activity of viral cystatins. To understand the constraints imposed on polydnavirus evolution, we measured selection pressures acting on cystatin genes. By homology modelling we obtained the 3D structure of a viral cystatin which enabled us to precisely map selected sites.

Results: Viral cystatins are expressed at an early stage and reach very high levels of expression during parasitism. The purification of a recombinant form of one viral cystatin (cystatin1) revealed that this cystatin is functional having potent inhibitory activity towards human and insect cysteine proteases. Furthermore, we demonstrate strong adaptive evolution acting on cystatin genes. The model of the 3D structure of cystatin1 provides a framework to position the positively selected residues and reveals that they are situated in key sites which are important for the interaction with target proteases.

Conclusions: The combination of physiological and evolutionary approaches emphasizes the potential role of cystatins as pathogenic factors and suggests that cystatins coevolve with host cysteine proteases.

CO_2 as a floral scent: When "primary" metabolites have "secondary" functions

Robert Raguso

Cornell University, Ithaca, NY, United States

Introduction: Fragrance plays diverse roles in plant-pollinator interactions, and its information content depends upon the sensory milieu in which it is perceived. Flowers emit CO_2 in different contexts, including thermogenesis. Could CO_2 function as a pollinator attractant? CO_2 was studied in rewarding and deceptive flowers with phylogenetic and allometric controls.

Methods: CO_2 was measured with a LI-COR 840 CO_2/H_2O analyzer and normalized per floral mass from hawkmoth-pollinated *Oenothera, Nicotiana, Ipomoea* and *Mirabilis* species and their bird-, bee- and self-pollinated relatives. Similar data were collected from *Asimina* and *Trillium* species with red, fermented-smelling flowers and their white-flowered, non-sapromyophilous relatives. Flower-naïve hawkmoths were tested in a laminar flow wind tunnel using artificial, scented flowers with or without above-ambient CO_2 emissions.

Results: Hawkmoth pollinated flowers from all lineages opened explosively, emitting a burst of CO_2 that persisted for the first hour after anthesis, when nectar was available. *Manduca sexta* moths utilized CO_2 as a redundant scent for tracking flowers from a distance, but preferred flowers with scent and CO_2 to those with scent alone in choice assays. Red-flowered *Asimina* and *Trillium* species had no nectar but emitted yeasty or carrion odors; high CO_2 emissions from these flowers may complement visual and olfactory signals mimicking microbial decay. White-flowered *Asimina* and *Trillium* species emitted less floral CO_2 than their deceptive relatives.

Conclusions: Floral CO_2 is prevalent in nectar-rich or deceptive flowers and should be sought in those harboring nectar yeasts.

Reliability, quality and cost: The basic challenges of commercial natural enemy production

Karel J.F. Bolckmans

Koppert BV, Berkel en Rodenrijs, Netherlands

The reliability and cost-effectiveness of production techniques for natural enemies and the quality of the end-product are important for both the farmer (customer) as well as for the producer of natural enemies.

Farmers need to have access to sufficient numbers of high quality natural enemies at the right moment and at an acceptable cost. If the natural enemies are of high quality, lower numbers of natural enemies will be needed to achieve good pest control, and the cost to the grower will therefore be lower.

Reliable and cost-effective production systems and supplying high quality products can give a producer a very important competitive advantage in the market. Substantially decreasing the cost of natural enemies allows entering into new crops and other geographic areas. The use of invertebrate biological control agents for augmentative biological control is expanding rapidly. As the opportunities for biological control increase also the challenges and economic risks for producers of natural enemies increase. Different approaches are needed for mass-rearing large quantities of beneficial insects and mites.

Reliability, quality and cost are key challenges of all manufacturers of goods, not only for producers of beneficial insects and mites. Organizing and rethinking current production practices around these 3 key challenges will allow the biological control industry to further professionalize and to prepare for the future.

Ecosocial implications of cattle health improvement based on adaptive management of arthropod transmitted diseases

Gianni Gilioli[1], Getachew Tikubet[2], Andrea Sciarretta[3], Pasquale Trematerra[3], Andrew Paul Gutierrez[4], Johann Baumgärtner[5]

[1]Università Mediterranea di Reggio Calabria, Dipartimento di Gestione dei Sistemi Agrari e Forestali, Reggio Calabria, Italy, [2]ICIPE, Regional Office Addis Ababa, Addis Ababa, Ethiopia, [3]Università degli Studi del Molise, Dipartimento di Scienze Animali, Vegetali e dell'Ambiente, Campobasso, Italy, [4]University of California Berkeley, Department of Environmental Science, Policy and Management, Berkeley, California, United States, [5]Università degli Studi di Milano, Istituto di Entomologia agraria, Milano, Italy

Introduction: Bovine trypanosomiasis is a key constraint in the development of many East African agro-pastoral communities. Suppression of tsetse fly (*Glossina* spp.) and control of trypanosomiasis were carried out in a community-based project at Luke, South-western Ethiopia, from 1995 to 2006.

Methods: The control system relied primarily on drug administration and tsetse vector suppression based on odour baited trap technology. Geostatistical analysis was used in trap deployment and precision-target vector management operations. Impact was assessed by monitoring vector abundance and disease prevalence and by survey based changes in cattle husbandry, land management and community socioeconomics. A bioeconomic model was used to interpret ecological, economic and social changes.

Results: On the positive side, tsetse populations fell to very low levels, disease incidence decreased to about 10% greatly increasing cattle and oxen densities and productivity, oxen availability increased land cultivation, and revenue increased allowing purchases of more cattle and the establishment of a school. Negative effects include: tsetse control will lead to overstocking and intensified agriculture and land degradation that will require land use planning to achieve sustainability. The bioeconomic model predicts the positive and negative outcomes and provides bio-economic decision support to stakeholders in interpretative dimensions.

Conclusions: Trypanosomiasis control is possible by implementing available technology in an adaptive management framework. However, new social structures and responses are required to cope with the eco-social changes on system sustainability and resilience.

Assessing the risk posed by the invasion of *Harmonia axyridis* on European ladybirds. 2. Consequence of encounter

Remy Ware[1], Michael Majerus[1], Renate Zindel[2], Rene Eschen[2], Marc Kenis[2]

[1]Department of Genetics, University of Cambridge, Cambridge, United Kingdom, [2]CABI Europe-Switzerland, Delémont, Switzerland

Introduction: The risk posed to native European coccinellids by *Harmonia axyridis* can be considered in terms of the likelihood of encounter between *H. axyridis* and a given species, and the consequence of this encounter, which could be competition or predation. The likelihood of encounter was reviewed in the previous presentation. Here we assess the impact of competition, based on published information on the dietary requirements of different species, and the impact of predation, based on field observations and empirical laboratory studies.

Methods: The impact of competition between *H. axyridis* and a given European species is assigned to a numerical scale based on the degree of dietary overlap between them, and the ability of a species to revert to specialist habitats following the encroachment of a competitor. The impact of predation by *H. axyridis* is also applied to a quantitative scale, which takes into account any chemical, physical and behavioural defensive strategies. Where possible, we utilise our own experimental data on predatory interactions in this assessment, but for species where such data is lacking, we make informed extrapolations based on field observations and published information. For each species, the product of likelihood of encounter with *H. axyridis*, and the impact of competition is calculated, and added to the product of likelihood of encounter and impact of predation. This gives a total risk index score which can be compared across species.

Results: From this assessment, *Adalia 2-punctata* emerges as the species most at risk from the establishment of *H. axyridis*. This is attributable to its high degree of habitat overlap, its shared diet, its suspected inability to shift to an optimal habitat, and the vulnerability of its immature stages to intraguild predation. In contrast, the host-plant restricted phytophage *Epilachna argus* is considered least at risk due to its unusual dietary and host plant requirements.

Conclusions: This procedure has allowed us to identify species that may be particularly threatened by *H. axyridis*, and thereby provides the impetus for conservation strategies. In addition, it raises issues over the adequacy of previous risk assessment procedures when introducing species outside their native range for the purpose of biological control.

Indirect interactions: Competition among fungal mutualists from sympatric and allopatric bark beetle populations

Thomas Seth Davis[1], Richard Hofstetter[1], Kier Klepzig[2]

[1]Northern Arizona University, Flagstaff, Arizona, United States, [2]USDA Forest Service, Pineville, Louisiana, United States

Introduction: The role of interspecific interactions can have implications for population dynamics, endemic-epidemic transitions and plant-insect interactions. Several *Dendroctonus* species maintain strong relationships with mutualist fungi, which they transport between hosts in mycangia and developing larvae feed upon. Mycangial fungi play an important role in mediating the fitness of emerging adult beetles by providing nutritional supplement to larvae, interactions among mutualist fungi in the gallery environment of host trees may have consequences for beetle population dynamics.

Methods: We isolated 20 strains of mycangial fungi from two bark beetle species (*D. frontalis* and *D. brevicomis*) in Arizona, 9 from *D. frontalis* in Mississippi, and 10 from *D. brevicomis* in California. We performed a total of 1144 pairwise competition assays among sympatric fungi (Arizona) and between allopatric fungi (Arizona, Mississippi, and California). We also determined the rate of growth for all fungal strains at six temperatures. We also report the results of replacement series experiment of beetles in live trees.

Results and Conclusions: We demonstrate that fungal performance varies with respect to evolutionary history, beetle host, and fungal species. Fungal species with an evolutionary history of competition were the strongest competitors overall. We used temperature and competitive performance both independently and in combination. Results in the discriminate function analysis were strongest when both environmental (temperature) and ecological (competitions) interactions were included. Also, our analysis is the first to demonstrate that interactions among fungal species can be used to delineate competitive communities in ordination space.

Indirect interactions: Competition among fungal mutualists from sympatric and allopatric bark beetle populations

Thomas Seth Davis[1], Richard Hofstetter[1], Kier Klepzig[2]

[1]Northern Arizona University, Flagstaff, Arizona, United States, [2]USDA Forest Service, Pineville, Louisiana, United States

Introduction: The role of interspecific interactions can have implications for population dynamics, endemic-epidemic transitions and plant-insect interactions. Several *Dendroctonus* species maintain strong relationships with mutualist fungi, which they transport between hosts in mycangia and developing larvae feed upon. Mycangial fungi play an important role in mediating the fitness of emerging adult beetles by providing nutritional supplement to larvae, interactions among mutualist fungi in the gallery environment of host trees may have consequences for beetle population dynamics.

Methods: We isolated 20 strains of mycangial fungi from two bark beetle species (*D. frontalis* and *D. brevicomis*) in Arizona, 9 from *D. frontalis* in Mississippi, and 10 from *D. brevicomis* in California. We performed a total of 1144 pairwise competition assays among sympatric fungi (Arizona) and between allopatric fungi (Arizona, Mississippi, and California). We also determined the rate of growth for all fungal strains at six temperatures. We also report the results of replacement series experiment of beetles in live trees.

Results and Conclusions: We demonstrate that fungal performance varies with respect to evolutionary history, beetle host, and fungal species. Fungal species with an evolutionary history of competition were the strongest competitors overall. We used temperature and competitive performance both independently and in combination. Results in the discriminate function analysis were strongest when both environmental (temperature) and ecological (competitions) interactions were included. Also, our analysis is the first to demonstrate that interactions among fungal species can be used to delineate competitive communities in ordination space.

Genetic variability of *Ixodes ricinus* ticks and diversity in prevalence and genospecies of *Borrelia burgdorferi s. l.* in Lithuania and Norway

Algimantas Paulauskas[1], Daiva Ambrasiene[1], Jana Radzijevskaja[1], 0lav Rosef[2], Jurga Turcinaviciene[3]

[1]Department of Biology, Vytautas Magnus University, Kaunas, Lithuania, [2]Department of Environmental and Health Studies, Telemark University College, Bø i Telemark, Norway, [3]Department of Zoology, Vilnius University, Vilnius, Lithuania

Introduction: In the last decade northward expansion and density of *I. ricinus* tick in Fennoscandia was increased. Genetic variability of ticks and the prevalence of *B. burgdorferi* s.l and Borrelia genospecies in *I. ricinus* ticks were analyzed in different biotopes of Lithuania and Norway.

Methods: RAPD markers were used to measure the genetic diversity of ticks collected from 6 populations. Ticks collected in different landscapes were tested for the presence of the *Borrelia* using *fla* and *OspA* genes of *B. burgdorferi* s.l. PCR.

Results: The high level of diversity of RAPD markers in *I. ricinus* populations was detected. The number of fragments and the amount of intraspecies polymorphism varied between the primers, the sites and the countries. The overall prevalence of *Borrelia* infection was 14% in Lithuania, and 5.6% in Norway. The highest prevalence of *Borrelia* (20%; 21.2%) was found in deciduous and mixed forests; a lower prevalence (7.4%) in pine forests and in the coastal zone coastal (4.7%), and the least prevalence (2.4%; 0.6% in Lithuania and Norway, accordingly) in grasslands. In Lithuania, *B. afzelii* genotype was found in 76% of infected ticks, *B.garinii* in 10%, and *B. burgdorferi* s.s. in 7%. Double infections were observed in 1% of infected ticks. *B. afzelii* was found in 59.4%, *B.garinii* - in 18.8%, and *B. burgdorferi* s.s. - in 9.4% of Norwegian infected ticks.

Conclusions: The occurring genetic variation in ticks populations might be explained by aggregation of migratory birds in places situated on the main birds migratory rout during the spring and the autumn.

The causes and consequences of multiple mating in the social wasp *Vespula maculifrons*

Michael Goodisman[1], Jennifer Kovacs[1], Eric Hoffman[2]

[1]Georgia Institute of Technology, Atlanta, Georgia, United States, [2]University of Central Florida, Orlando, Florida, United States

Introduction: The evolution of insect societies depended on high relatedness among interacting group members. Thus it is surprising that some social insect queens mate with multiple males (polyandry), because polyandry decreases relatedness among colony members relative to cases where the queen mates singly. The fact that some social insect queens are polyandrous suggests that multiple mating may provide benefits that counteract the perceived relatedness costs. However, few studies have demonstrated benefits to polyandry in social insect species.

Methods: We used molecular genetic markers to dissect the breeding system of the social wasp *V. maculifrons*. We assessed colony fitness by counting the number worker and queen cells that colonies produced. Statistical methods were then used to determine if levels of polyandry were associated with increased production of cells within colonies.

Results: Our results indicated that *V. maculifrons* colonies were always headed by a single, multiply-mated queen. We also found that queen mate number was directly, strongly, and significantly correlated with the number of queen cells produced by colonies. Because *V. maculifrons* queens are necessarily reared in queen cells, our results demonstrated that queens that mated with many males headed colonies capable of producing many new queens.

Conclusions: Our data revealed that multiple mating by *V. maculifrons* queens may be associated with increased reproductive success. Thus this research provides a rare example of an association between multiple mating and fitness in a natural social insect population and helps explain why some social insect queens mate multiply.

Effects of adjacent pasture and forest land uses on leafhoppers vectors of *Xylella fastidiosa*, causal agent of Crespera disease in coffee

Nilsa Bosque-Perez[1], Mariangie Ramos[2]

[1]Department of Plant, Soil and Entomological Sciences, University of Idaho, Moscow, ID, United States, [2]Joint PhD Program, University of Idaho and Tropical Agricultural Research and Higher Education Center (CATIE), Turrialba, Costa Rica

Introduction: Leafhoppers in the subfamily Cicadellinae are potential vectors of *Xylella fastidiosa*, the bacterial causal agent of Crespera disease of coffee in Costa Rica. Cicadellinid leafhoppers (sharpshooters) are generalist xylem-sap feeders, and are known to move between habitat types in the landscape, potentially seeking complementary resources. The effects of adjacent forest and pasture land uses on coffee leafhopper communities and *X. fastidiosa* presence were studied in Turrialba, Costa Rica.

Methods: Leafhoppers were sampled bimonthly in 2006 in three conventional coffee farms. Migration Malaise traps were placed in the center of the farm and along farm edges neighboring forest and pasture. Yellow sticky cards were placed at the same farm locations, in addition to adjacent forest fragments and pasture lands. In each farm, eight coffee plants per site (edge with forest, edge with pasture, and farm center) were collected and tested for *X. fastidiosa* presence.

Results: Sixty-one leafhopper species were collected. Leafhopper communities in coffee farms had greater similarity to pasture than to forest communities. Leafhopper abundance was higher at the farm edge with pasture than with forest. Leafhoppers moved equally to pasture and coffee at the farm edge with pasture, but unidirectionally to coffee from forest. Leafhopper patterns of abundance could not be related to *X. fastidiosa* presence.

Conclusions: Leafhoppers appear to use complementary pasture and coffee resources. Forests appear to be sources of leafhoppers in these landscapes.

Multiple lines of evidence reveal the earliest radiations of true flies (Insecta: Diptera)

Brian Wiegmann

North Carolina State University, Raleigh NC, United States

Introduction: Resolution of the earliest lineages of true flies (Diptera) is a major goal of the US NSF-funded Assembling the Tree of Life project, FLYTREE. This international collaborative project has assembled data from nuclear and mitochondrial genomes, morphology, and the fossil record to reconstruct the history of diversification within this major insect order.

Methods: Fourteen nuclear genes, full mitochondrial genomes, and over 400 morphological characters from all life stages were assembled for a comprehensive sample of dipteran taxa. Parsimony, Bayesian, and maximum likelihood methods are used to estimate relationships. Nucleotide data, together with key fossils, are used to estimate divergence times for dipteran infraorders and superfamilial clades.

Results: Diptera originated in the Permian approximately 270 mya and all of the major extant dipteran infraorders originated before 250 mya. This rapid proliferation of fly clades, morphologies, and life histories has made it difficult to establish a stable classification. Individual data types yield radically different scenarios for the pattern and timing fly diversification. Combining multiple genes, genomic data, and morphology provides the clearest picture to date of this rapid expansion of fly lineages. We compare alternative statistical methods for investigating the strength of support for hypotheses based on individual genes or data partitions.

Conclusions: The earliest lineages of Diptera radiated in parallel in aquatic and semi aquatic habitats followed by impressive later expansions of lineages that use flowering plants as primary or secondary food resources.

The roles of PKC in mediating 20E-induced gene expression in salivary glands of Drosophila melanogaster

Qisheng Song, Yaning Sun, Shiheng An

University of Missouri, Columbia, Missouri, United States

Ecdysone receptor (EcR) and its heterodimeric partner, Ultraspiracle protein (USP), are nuclear receptors that mediate the action of the insect molting hormone, 20-hydroxyecdysone (20E). There is evidence that the activity of both receptors is affected by phosphorylation. Using molecular and proteomic approaches, we have shown that protein kinase C (PKC) activity is necessary for mediating 20E-induced expression of a specific set of genes, including 11 novel ones, and is also responsible for the intracellular localization of EcR and USP in larval salivary glands of *Drosophila melanogaster*. Inhibition of PKC activity resulted in alternation of EcR and USP subcellular localization and reduced 20E-dependent transcriptional activity of some of the newly identified genes rapidly, raising the possibility that these are direct gene targets of EcR and USP. We also investigated the effect of RNAi disruption of PKC isoforms on 20E-induced gene expression in the larval salivary glands. The composite data suggest that PKC plays an important role in mediating 20E-induced gene expression.

Effects of local and landscape context on leafhopper communities in coffee farms of Costa Rica

Mariangie Ramos[1], Nilsa Bosque-Perez[2], Luko Hilje[3], Sanford Eigenbrode[2]

[1]Joint Ph.D. Program, University of Idaho and Tropical Agricultural Research and Higher Education Center, Moscow, ID, United States, [2]Department of Plant, Soil and Entomological Sciences, University of Idaho, Moscow, ID, United States, [3]Department of Agriculture and Agroforestry, Tropical Agricultural Research and Higher Education Center (CATIE), Turrialba, Costa Rica

Introduction: Cicadellinid leafhoppers are potential vectors of *Xylella fastidiosa*, the bacterial causal agent of coffee Crespera disease. Little is known about *X. fastidiosa* vector ecology in Costa Rica. We examined effects of local (shade, management, weed cover) and landscape (surrounding area in coffee, forest, pastures, and fallows) factors on leafhopper abundance and richness in coffee agroecosystems.

Methods: We monitored leafhoppers seven times from 2005 to 2006 using yellow sticky traps in four farm treatments: a) organic two-strata systems with *Erythrina poeppigiana* shade trees, b) organic three-strata with *Cordia alliodora-Musa-E. poeppigiana* shade trees, c) conventional two-strata with *E. poeppigiana* shade trees, and d) conventional three-strata with *C. alliodora-Musa-E. poeppigiana* shade trees. Shade percentage and weed cover data were collected during each sampling. Landscape context was characterized by determining land use (coffee, pasture, forest, and fallow) percentage within two different radii (100 and 500m) around each farm.

Results: Principal Components Analysis demonstrated different leafhopper species assemblages were associated with each farm treatment, but no significant differences in overall leafhopper abundance or species richness were observed among treatments. However, some leafhopper species were significantly more abundant in conventional two-strata systems than in other systems examined. Shade was a key local variable, negatively affecting leafhopper abundance. Proportion of land in fallow was positively correlated with leafhopper species richness at 100m and 500m radii, but other land cover types had no effect.

Conclusions Leafhopper assemblages and some individual species differed among coffee shade systems, but landscape variables had a weak effect on overall leafhopper abundance.

Do the crazy-ants *Paratrechina fulva* Mayr, 1862 (Hymenoptera: Formicidae) control the passage of foods inside their bodies?

Carlos Massuretti de Jesus, Daniel Russ Solis, Odair Correa Bueno

Departamento de Biologia, Centro de Estudos de Insetos Sociais, Universidade Estadual Paulista – UNESP, Rio Claro, São Paulo, Brazil

Introduction: Over evolution ants developed distinct strategies to find, consume and use food resources. Studies about feeding in ants are important as they allow us to identify where storage, digestion and absorption of foods occur in their body. The present investigation aimed at analyzing the passage of food through the digestive system of the crazy-ant *Paratrechina fulva*.

Methods: Water-soluble dye Rodamin B and the lipid-soluble dye Sudan Black were added to 3 different diets as tracers. The solid food was prepared by mixing equal parts of dehydrated bovine liver, Pullman® sponge-cake, peanut oil with Sudan Black (0.1%) and aqueous honey solution (1:1) with Rodamin B (0.2%). Two liquid foods were also used: aqueous honey solution (1:1) with Rodamin B (0.2%), and peanut oil with Sudan Black (0.1%). The foods were then offered to laboratory colonies of crazy-ants. We collected 80 workers which had ingested food, and past set periods of time they were dissected under a stereomicroscope. The ingested quantity of tracers was measured in the infrabucal pocket, postpharingeal glands, crop and ventriculus of each ant.

Results: Solid foods were retained in the infrabucal pockets and were later eliminated as small pellets; only liquid substances were actually ingested. Water-soluble tracers were found in infrabucal pockets, crops and ventriculi, while lipid-soluble tracers were found in infrabucal pockets, postpharingeal glands and crops.

Conclusions: Our results suggest workers can control the passage of foods through their digestive systems. We also think lipids ingested might be stored and metabolized in the postpharingeal glands.

Effects of forest insect invasions on forest succession

Andrew Liebhold

USDA Forest Service Northern Research Station, Morgantown, WV, United States

Given the trend of escalating globalization, increased numbers of alien insects are inevitable and can be expected to be one of the dominant influences in the world's forest ecosystems over the next century. When considering the likely impacts of these invaders, it is necessary to consider more than just effects on forests as they currently exist but to regard forests as dynamic systems and evaluate the role that invaders play in altering long-term forest succession processes. In some cases we can observe that invaders may cause spectacular short-term impacts (e.g., high levels of tree mortality), but if these effects mimic disturbances caused by pre-existing, natural disturbance agents then their effect on long-term patterns of forest dynamics may be minimal. In contrast, other alien species may induce changes to forest ecosystems, unlike any pre-existing disturbance agents and these impacts may destabilize natural cycles of forest dynamics, ultimately leading to drastic changes in ecosystem properties and ecosystem services. We illustrate these varying roles played by alien invaders using examples from eastern N. America.

Interaction rate and task allocation in harvester ants

Deborah M Gordon

Stanford University, Stanford, CA, United States

Introduction: Ant colonies operate without central control. Task allocation is the process that adjusts the numbers of workers performing each task, according to the current situation. A long-term study of a population of about 300 colonies of the red harvester ant *Pogonomyrmex barbatus*, in the southwestern US, shows that the rate of brief antennal contact informs task decisions.

Methods: Small glass beads treated with task-specific cuticular hydrocarbon extract were used as artificial ants to manipulate interaction rate.

Results: Ants respond to contact with beads treated with cuticular hydrocarbon extract, demonstrating that ants use task specific cuticular hydrocarbon extract to assess the task of the ants they meet. Foraging is initiated by interaction with returning patrollers. Interaction must occur at a rate of one per 10 sec to stimulate the onset of foraging. Once foraging begins, the intensity of foraging is regulated by interaction with returning successful foragers. Since the duration of a foraging trip depends mostly on the amount of time spent searching, the rate at which foragers return with food is a measure of current food availability. Foraging intensity responds very quickly to changes in the rate at which foragers return. This may be due to the limited interval over which an ant can remember an interaction.

Conclusions: Task allocation depends on a dynamical network of brief antennal contacts, during which one ant evaluates the task-specific cuticular hydrocarbon profile of the other.

Education in quality assurance for rearing insects

Norman Leppla, Frank Davis

University of Florida, Gainesville, Florida, United States

Introduction: The purpose for education and training in quality assurance for insect rearing is to maintain consistent, reliable production of high quality insects that meet established standards at the lowest possible cost.

Methods: Education in insect rearing and quality assurance can be gained from courses at Mississippi State University, Department of Entomology and Plant Pathology and Insect Diet and Rearing Research, LLC; working in an established insect rearing facility; and by studying available literature (http://www.amrqc.org, proceedings and http://www-naweb.iaea.org/nafa/ipc/index.html, publications). Studies focus on generic procedures, such as measuring and monitoring life history and performance characteristics, and on developing site-specific tests indicative of quality. Quality Assurance tests have been developed for many mass- reared insects, including major pest species and certain predators and parasitoids used in biological control.

Results: Education and training in quality assurance helps to make insect rearing more productive because entire systems are involved. Optimization of each step in the insect rearing processes affects the others in a system, e.g., egg quality and quantity results in a certain density of developing larvae per rearing unit and this affects the size of pupae and performance of adults. Students learn about the additive effects of environmental factors on rates of development and survival of successive insect growth stages. Quality assurance then becomes a matter of managing environments (production control) to satisfy the needs of the insects (product control).

Conclusions: Quality assurance in insect rearing requires knowledge of all aspects of the physical rearing system relative to the biology of the insect.

Global population genetics of the *Wolbachia* pandemic in arthropods and implications of *Wolbachia*-insect lateral gene transfers to arthropod evolution

John Werren

University of Rochester, Rochester, United States

Wolbachia are among the most abundant intracellular parasites on the planet, infecting upwards of 65% of insects, as well as many other arthropods and filarial nematodes. The implications of these bacteria to arthropod cell biology, ecology and evolution are potentially profound, but still remain controversial. In particular, a key question is whether *Wolbachia* accelerate adaptive evolution and speciation in their hosts. Here I present recent data showing that lateral gene transfers from *Wolbachia* to animal genomes are common and widespread. In one case, the nearly entire genome of *Wolbachia* has been incorporated into that of the fly *Drosophila ananassae*. The potential fitness consequences and possibilities for acquisition of novel gene function are discussed. Studies of the global diversity and distribution of Wolbachia among arthropods are also presented. These studies reveal extensive global movement of some strains, taxon associations of others, and genetic exchanges among members of the global *Wolbachia* metapopulation.

Regional effects of exotic forest pests in eastern North America

Andrew Liebhold[1], Randall Morin[2], Kurt Gottschalk[1]

[1]USDA Forest Service Northeastern Research Station, Morgantown, WV, United States, [2]USDA Forest Service Northern Research Station, New Town Square, PA, United States

Given trends of ever-increasing levels of global trade and travel, non-indigenous forest insects and diseases are becoming increasingly common throughout the world. While most of these species remain sparse and their effects on forests remain unnoticed, a few of these species cause wide-spread dieback and mortality of forest tree species. Eastern North America has experienced a particularly large number of invasions by destructive forest pests. While many studies have been conducted to measure the effect of these pests in individual stands, little or no information is available to assess their impacts over large regions. Here, we present analyses of the regional impacts of three alien forest pests, the gypsy moth (*Lymantria dispar*), hemlock woolly adelgid (*Adelges tsugae*) and beech scale, (*Cryptococcus fagisuga*) on a regional scale across the eastern USA. These analyses were conducted by comparing the historical ranges of these species with forest inventory data collected at thousands of points. Results indicate that while impacts on tree mortality may be particularly high in some locations, these impacts tend to be diluted over large areas and more difficult to detect. Based upon these results suggestions are made for how to go about quantifying regional impacts in the future.

Translocation tools for New Zealand weta

Corinne Watts, Ian Stringer, Greg Sherley, George Gibbs, Chris Green

[1]Landcare Research, Hamilton, New Zealand, [2]Department of Conversation, Wellington, New Zealand, [3]Department of Conversation, Auckland, New Zealand, [4]Victoria University, Wellington, New Zealand

Examples of transfers involving three species of New Zealand weta (Orthoptera: Anostostomatidae) are used to illustrate improvements in transferring and monitoring these insects. Weta are large, nocturnal insects that occupy a similar niche to small rodents elsewhere in the world. Some are locally extinct where introduced mammals occur and many transfers were done for species recovery and/or restoration purposes. The initial transfer method, simply collecting and releasing, and their subsequent irregular monitoring is illustrated using Mahoenui weta (*Deinacrida mahoenui*). The first improvements using artificial retreats to both release and monitor tree weta (*Hemideina thoracica*) took advantage of this species' roosting behaviour. In one case, both the donor and released populations were monitored. Transfers of the very rare tusked weta, *Motuweta isolata*, illustrate further improvements including captive rearing, monitoring the released insects and their progeny with artificial objects and exploring other monitoring methods including the use of harmonic radar and transmitters. An example of using a transfer for further research is provided with the Cook Strait giant weta (*D. rugosa*) where transmitters were used to follow their dispersal after release. Future directions and research are briefly discussed followed by a plea to follow release protocols and, in particular, fully document any releases.

The importance of Allee effects in predicting and managing insect pest invasions

Andrew Liebhold, Patrick Tobin

US Forest Service Northern Research Station, Morgantown, WV, United States

The Allee effect refers to decreasing net population growth with decreasing density; under strong Allee effects there exists a threshold below which low-density populations are driven toward extinction. They may arise from a variety of factors such as failure to find mates, failure to saturate predators and inability to utilize hosts through cooperative feeding. Though Allee effects have historically been applied to species conservation, there has been recent recognition of their importance in low-density populations during biological invasions. Given the importance of Allee dynamics during the establishment and spread of invading species, Allee effects create powerful opportunities for managing invasions. Specifically, by strengthening Allee effects, low-density populations of invaders can be driven to extinction without further management intervention, defying the notion that eradication can only be achieved by killing all individuals. Here we briefly review Allee effects with specific attention to their role in biological invasions and outline current management techniques, such as mating disruption and the sterile insect technique, from the context of their manipulation of the Allee threshold to manage invasions. We also suggest new approaches for manipulation of Allee effects that could be used to manage invading species; these approaches include natural enemy augmentation and other methods that affect population growth and consequently alter the Allee threshold. Finally, we discuss how variation in life history traits influence the strength of Allee effects and how this information can be used to predict invasions success among different pest species.

Evolutionary genetics using the *Nasonia* species complex

John Werren

University of Rochester, Rochester, NY, United States

Nasonia is a complex of four closely related species that is rapidly emerging as a model for evolutionary genetics and the genetics of complex traits. It has several features that make it an excellent genetic system. These include ease of handling, short generation time, male haploidy, interfertile species, visible and molecular markers, and a wealth of phenotypes of biological relevance. The form of sex determination, called haplodiploidy, makes *Nasonia* particularly suited for genetic studies. Females are diploid and develop from fertilized eggs, whereas males are haploid and develop parthenogenetically from unfertilized eggs. This allows geneticists to exploit many of the advantages of haploid genetics in an otherwise complex eukaryotic organism. *Nasonia* readily inbreeds, permitting production of isogenic lines, and the four species in the genus are inter-fertile (after removal of the endosymbiont *Wolbachia*), facilitating movement of genes between the species for efficient positional cloning of quantitative trait loci (QTL). Full (6X) genome sequencing of *N. vitripennis* and partial (1X) sequencing of the interfertile species *N. giraulti* and *N. longicornis* is now completed. This genome project provides a wealth of interspecies polymorphisms (SNPs, indels, microsatellites) to facilitate positional cloning of genes involved in species differences in behavior, morphology and development. Here we report the cloning of genes involved in sex specific wing size differences between sibling species of *Nasonia*. These represent the recent micro-evolution of gene networks affecting sex specific development. We also report studies of the genetic basis of interspecies hybrid breakdown, which involves genes encoding nuclear and mitochondrial components of the electron transport chain. The system shows great promise for dissecting the genetic basis of speciation and species differences in development and behavior.

Life history responses to nutritional deprivation in aphidophagous Coccinellidae

Mpho Phoofolo[1], Kris Giles[1], Norm Elliott[2]

[1]Oklahoma State University, Stillwater, Oklahoma, United States, [2]United States Department of Agriculture, Agricultural Research Service, Stillwater, Oklahoma, United States

Introduction: Preference for aphids by coccinellids makes them particularly susceptible to nutritional stress caused by within-season food scarcity because aphid populations are both spatially and temporally ephemeral (exhibit 'boom-and-bust' dynamics over short intervals) in nature. This study examined the ability of coccinellid larvae to cope with unpredictable food resources.

Methods: We studied life history responses of three species, *Coleomegilla maculata*, *Hippodamia convergens*, and *Harmonia axyridis*, when deprived of aphids for different periods of time during the 4th stadium.

Results: For larvae fed only on day 1 of the stadium, *H. convergens* had the highest starvation resistance, followed by *H. axyridis*, then *C. maculata*. Both *C. maculata* and *H. axyridis* lost significantly more weight than *H. convergens* when starved throughout the 4th stadium. Access to aphids for ≥1 day was required for pupation in all three species, with 35.7% pupation success in *H. convergens*, 14.3% in *C. maculata*, and 5.9% in *H. axyridis* when fed for 1 day. The weight of 4th instars and adults declined in an accelerating pattern as food deprivation period increased. However, food deprivation period had no significant effect on pupal development time for any of the three species or on larval development time for *C. maculata* and *H. convergens*. The increase in *H. axyridis* larval development time as a result of an increase in food deprivation period was curvilinear.

Conclusions: Based on this study, it would appear that *H. convergens* is better able to cope with acute nutritional stress than either *C. maculata* or *H. axyridis*.

Odor evoked neural oscillations in Drosophila

Nobuaki Tanaka[1], Kei Ito[2], Mark Stopfer[1]

[1]NICHD, Bethesda, Maryland, United States, [2]IMCB, The University of Tokyo, Tokyo, Japan, Japan

Odor elicited neural oscillatory synchronization has been observed in a very wide and diverge range of species. In two intensively studied insects, honeybee and locust, such oscillations have been shown to contribute to the encoding and decoding of odor quality. Yet there is no evidence for such oscillations in Drosophila, a preparation that offers many genetic tools for the analysis of olfactory pathways.

To study odor elicited temporal patterns of neural activity in Drosophila, we developed a way to do intracellular recording with sharp electrodes. We succeeded in recording from various antennal lobe neurons under odor stimulation for up to 30 min. After recording, we confirmed which neurons were recorded by injecting a neuronal tracer, neurobiotin. In addition, we also succeeded in recording odor-elicited local field potential (LFP) oscillations from the mushroom body: presentations of common, diluted odorants elicited ~10 Hz oscillations. Paired intracellular and LFP recordings showed spikes and subthreshold membrane potential oscillations in antennal lobe neurons were strongly phase locked to the LFP, suggesting that oscillations arise from antennal lobe circuitry.

Characterizing the mechanism underlying the neural oscillations, we found picrotoxin, antagonist for the GABAA receptor, can reversibly block the oscillatory activity. To isolate circuit elements responsible for the oscillations, we are now using the GAL4-UAS system to express shibire, a temperature sensitive dynamin mutant gene, in specific populations of antennal lobe neurons. This system will allow us to conditionally and transiently block chemical synaptic transmission from targeted neurons, revealing precise mechanisms underlying neural coding.

Reproduction in fire ant (*Solenopsis invicta* Buren) queens: vitellogenin receptor biology

Patricia Pietrantonio, Hsiao-Ling Lu, Mei-Er Chen

Texas A&M University, College Station, TX, United States

Introduction: In social insects, control of reproduction is a complex and poorly understood process. The red imported fire ant, *Solenopsis invicta* Buren (Hymenoptera: Formicidae) is an invasive, aggressive pest with high reproductive ability. To aid in population management, knowledge is needed on the effector proteins and the regulatory pathways involved in reproductive control. The vitellogenin receptor (VgR) is responsible for the receptor-mediated endocytosis of vitellogenin (Vg) for egg formation and embryonic development. Understanding VgR biology may be useful to elucidate mechanisms leading to high reproductive capacity in queens. Other hormone receptors, such as the short neuropeptide F receptor from fire ants, are being investigated as potentially involved in reproductive control.

Methods and results: We cloned the fire ant VgR (*Si*VgR), characterized the transcriptional expression pattern in virgin queens and demonstrated that methoprene increases transcript abundance, suggesting JH is involved in VgR regulation. An antibody specific against *Si*VgR was developed. Caste and tissue specific expression of *Si*VgR was studied through western blot analysis. A *Si*VgR protein of 202 kDa was detected in both virgin (alate) and mated (dealate) queen ovaries. Immunohistochemistry of ovarioles of virgin and mated queens showed differential VgR distribution in early and late stage oocytes. This is the first report on the spatial and temporal expression profile of a hymenopteran VgR.

Conclusion: The specific antibody against fire ant VgR is a powerful tool to test hypothesis of VgR regulatory gene networks. This study may contribute to understand the regulation of VgR in other hymenopteran species.

Ants, scales, and ladybeetles: complex interactions and natural pest control in a coffee agroecosystem in Mexico

Heidi Liere, Ivette Perfecto, John Vandermeer

University of Michigan, Ann Arbor, Mi, United States

We study the mutualism between an important coffee pest, the green scale (*Coccus viridis,* Hemiptera: Coccidae) and an aggressive tree-nesting ant, *Azteca instabilis* (Hymenoptera: Formicidae) in a coffee agroecosystem in Chiapas, Mexico. One part of our research project focuses on the interaction between this mutualism and a voracious scale predator, the ladybeetle *Azya orbigera* (Coleoptera: Coccinellidae). While adult ladybeetles feeding on the scales suffer from constant attack by the ants, the larvae have waxy filaments that render them immune to ant attacks and thus are able to prey freely upon ant-tended scales. Furthermore, the ants indirectly benefit the ladybeetle larvae by providing them enemy-free space. Consequently, we hypothesized that the distribution of the ladybeetles is closely linked to that of the ants. To test this hypothesis we established a 45-ha plot, marked all *A. instabilis* nests, and conducted a two-year long ladybeetle survey. We found significantly more ladybeetle larvae and adults in sites with ant nests. Furthermore, we found a significant relationship between the occupancy and persistence of the ladybeetle populations and the clustering of ant nests. The more ant nests within 20 m of the sampled site, the higher the probability the site was occupied by ladybeetles and the higher the probability that it remained occupied for longer. Our results suggest that the presence of this tree-nesting ant in the coffee plantation plays a key role in the persistence of ladybeetle populations, which in turn may play an important role in maintaining the scale populations below levels that may be damaging to the coffee plantation.

Climate change, forest disturbance and feedbacks: the mountain pine beetle in western North America

Allan Carroll[1], Werner Kurz[1], Caren Dymond[1], Graham Stinson[1], Greg Rampley[1], Eric Neilson[1], Tim Ebata[2]

[1]Natural Resources Canada, Canadian Forest Service, Pacific Forestry Centre, Victoria, BC, Canada, [2]British Columbia Ministry of Forests and Range, Victoria, BC, Canada

The mountain pine beetle is native to the pine forests of western North America where it normally exists at very low densities, infesting only weakened or damaged trees. Under conditions conducive to survival, populations may erupt and spread over landscapes causing the mortality of large numbers of healthy trees. While there have been 4 such eruptions during the past century in western North America, the ongoing epidemic is unprecedented in its size and severity – causing the mortality of mature lodgepole pines over approximately 14 million hectares in Canada alone. In addition to the direct ecological and economic impacts of such widespread tree mortality, the loss of carbon uptake and the increased emissions from decaying trees has converted the forests of western Canada from a small net carbon sink to a large net carbon source. Indeed, during the peak year of beetle impacts, emissions were similar in magnitude to the average annual direct emissions from forest fires for all of Canada. Moreover, through reductions to net primary productivity and increases in heterotrophic respiration, beetle impacts have negated any potential gains in carbon sequestration associated with climate warming, elevated atmospheric CO2 concentrations and nitrogen deposition. Significant warming has already allowed the mountain pine beetle to expand its range into formerly climatically unsuitable habitats. Additional warming could facilitate further range expansion, including invasion of the boreal forest, and lead to significant positive feedback to the global climate system.

Phenology of apple leaf-curling midge (Diptera: Cecidomyiidae) and its parasitoid *Platygaster demades* Walker (Hymenoptera: Platygastridae) in the field

Xiong Zhao He[1], Qiao Wang[1], Jim T. S. Walker[2], Dave J. Rogers[2], Peter L. Lo[2]

[1]*Institute of Natural Resources, Massey University, Palmerston North, New Zealand,* [2]*HortResearch, Havelock North, New Zealand*

Introduction: Apple leaf-curling midge (ALCM), *Dasineura mali* Kieffer, is a pest of apple in many countries in the world, and *Platygaster demades* is an important parasitoid that attacks ALCM eggs and larvae. Here we report our findings on the phenology of both species in Palmerston North (40.3° S, 175.6° E), New Zealand, in 2006-2007.

Methods: Shoots infested by ALCM were sampled every three days, and ALCM mature larvae were buried fortnightly. Emergence of buried insects was monitored daily and their development examined weekly.

Results: Both species had four generations. ALCM populations in the 2nd and 3rd generations were higher than in other two generations. The parasitism rate by *P. demades* was 44.5, 69.4, 78.6 and 86.9% for the 1st, 2nd, 3rd and 4th generations, respectively. All unparasitised 1st and 2nd and some unparasitised 3rd generation ALCM emerged in the same growing season. All unparasitised 4th generation and most unparasitised 3rd generation ALCM overwintered as cocooned larvae. *P. demades* entered aestivation as eggs between mid-November and late February, with mean aestivation rate being 6.3, 65.6 and 18.1% for the 1st, 2nd and 3rd generations, respectively. Aestivated *P. demades* eggs in the 2nd and 3rd generations and non-aestivated eggs in the 3rd and 4th generations hatched by early June and overwintered as larvae.

Conclusions: ALCM overwintered as mature cocooned larvae while *P. emades* aestivated as eggs and overwintered as larvae. Results suggest that vast majority of ALCM cocoons found on apple fruit are parasitized by *P. demades*.

Stoichiometric constraints within and across trophic levels

Pedro Barbosa, Astrid Caldas, Eric Lind

University of Maryland, College Park, MD, United States

No abstract was submitted, or incorrect abstract submitted, or submitted in an inaccessible format.

Residual toxicity of spinosad to predatory mites and their effectiveness against western flower thrips, *Frankliniella occidentalis* Pergande (Thysanoptera: Thripidae) in strawberry, *Fragaria ananassa* (Rosaceae)

Touhidur Rahman[1], Helen Spafford[1], Sonya Broughton[2]

[1]*School of Animal Biology, The University of Western Australia, Crawley, Western Australia, Australia,* [2]*Department of Agriculture & Food Western Australia, South Perth, Western Australia, Australia*

Introduction: Western flower thrips (*Frankliniella occidentalis*) has become a major horticultural pest throughout Australia following its first detection in 1993. Spinosad (trade name Success™) is the only insecticide currently registered in Australia that is both efficacious against *F. occidentalis* and regarded to be compatible with integrated pest management. To determine whether spinosad can be integrated with innudative biological control, we evaluated the interaction between spinosad and three predatory mite species *Typhlodromips montdorensis*, *Neoseiulus cucumeris*, *Hypoaspis miles*, available in Australia for control of *F. occidentalis*.

Methods: In the glasshouse, three strawberry cultivars (Albion, Camarosa and Camino Real) were sprayed once with water (control) or spinosad (120g/L). Adult thrips were released 24 h after spraying and predatory mites released 6 days later. Mites were released as single species, two species or three species combinations.

Results: Spinosad significantly reduced thrips numbers ($p < 0.05$) compared to the control. Interestingly spinosad had no effect on predatory mites as their numbers (*T. montdorensis* and *N. cucumeris*) gradually increased. Mites releases in combination with spinosad applications were generally more effective at reducing *F. occidentalis* numbers than spinosad application alone, with *T. montdorensis* and *H. miles* the most effective two species combination. No significant differences ($p > 0.05$) were found between releases of *T. montdorensis* and *H. miles* or *T. montdorensis*, *N. cucumeris* and *H. miles* in combination.

Conclusion: These results suggest that spinosad applications can be used to initially reduce *F. occidentalis* numbers, followed by combined releases of predatory mites.

Disruption of Argentine ant trail integrity using pheromone

David Suckling, Robert Peck, Lee-Anne Manning, Lloyd Stringer, Justin Cappadonna, Ashraf El-Sayed

HortResearch, Lincoln, New Zealand

Introduction: Argentine ants are considered one of the 100 most invasive species worldwide, because they can significantly reduce biodiversity, affect horticultural production, and cause a nuisance in urban situations, including hospitals. Currently, poison baiting systems are widely used against Argentine ants and many other important invasive ants. More environmentally-friendly control tactics are urgently needed for management and eradication of these invasive ants. This work investigates the possibility of using trail pheromone to disrupt trail following behaviour of the Argentine ants.

Methods: The trail pheromone (Z9-hexadecenal) was formulated for slow release in order to test whether trail following behaviour could be disrupted. Ant walking behaviour was recorded and digitized using video tracking before and after presentation of the trail pheromone.

Results: Disruption of Argentine ant trail following behaviours and reduced foraging success was achieved after presentation of an oversupply of trail pheromone, Z9-hexadecenal. Ants following trails showed a unimodal distribution of walking angles, but after presentation of the trail pheromone, there was no clear peak in the distribution of the walking angles. Ants showed initial high trail integrity, defined as the correlation statistic r^2, on a range of untreated substrates from painted walls to wooden or concrete floors, but this behaviour was significantly reduced by presentation of a point source of pheromone. The number of ants in the pheromone-treated area also increased over time, as recruitment from both directions apparently exceeded departures. Ant counts at bait cards were significantly reduced compared to the controls on the day of treatment, but trails recovered by two days after treatment due to rapid pheromone loss from the first formulation. Disruption effects lasted for several days. In larger plots, significant reductions in ant foraging to bait cards and reductions in trail formation were seen for up to two days from this formulation, and longer for a prototype micro-encapsulated formulation.

Conclusions: These results show that disruption of the trail following behaviour of Argentine ants may be possible using trail pheromone.

Rate of colonisation of *Bemisia tabaci* and its parasitoid *Eretmocerus hayati* : The role of landscape composition

Nancy Schellhorn

CSIRO, Indooroopilly, QLD, Australia

Introduction: Biological control is most effective when the control agent arrives in the crop at the same time or shortly after the pest. We investigated how the landscape composition (number, size and spatial arrangement of source populations) influences the process of colonisation of a pest, silverleaf whitefly, *B. tabaci*, and its parasitoid, *E. hayati*.

Methods: Sentinel melon seedlings (half infested with *B. tabaci* and half un-infested "clean") were placed in six cane trash fields either adjacent ($\leq$ 100 m) or far ($\geq$ 300 m) from host crops in two landscapes. They were arranged in a 100 m x 75 m 20 point grid and left for four days, removed and replaced three times.

Results: We found that the pest and parasitoid colonise seedlings within four days, and repeatedly. In landscapes with many sources of *B. tabaci,* colonisation of the new seedlings can be explained by the number of sources at the scale of kilometres, while in landscapes with limited production colonisation can be explained by the number of sources of *B. tabaci* within 100m. *Eretmocerus hayati* is also highly mobile, and colonisation can be explained by the density of the parasitoid at a scale of 2kms and being adjacent to a host crop of *B. tabaci*.

Conclusions: In landscapes with intensive cropping a combination of an area-wide approach, plus on farm management is necessary to control *B. tabaci*. Refuges of *E. hayati* within 2kms of the target crop allow for fast colonisation and may lead to better *B. tabaci* control.

Potential of entomopathogenic nematodes as biological control agents of stored product insects

James Campbell, Olgaly Ramos-Rodriguez

USDA ARS GMPRC, Manhattan, KS, United States

Entomopathogenic nematodes at first appear poorly adapted for use as biological control agents against insects that infest grain and processed grain-based products. However, the population structure and movement patterns of stored product insects indicate that in many environments pests originating from food material that accumulates in hidden refugia -- such as cracks or crevices in structures, empty grain bins, spillage outside facilities -- and subsequent movement into stored commodities can be important factors in product infestation. Biological control in general, and entomopathogenic nematodes in particular, may be an effective component of an IPM program when targeted at these refugia populations. We evaluated the efficacy of three *Steinernema* spp. against a range of stored product pest species and stages under laboratory conditions and found many pest species were susceptible. Tests of *S. riobrave* pathogenicity as a biopesticide under simulated field conditions, suggested that nematodes applied in a manner similar to some conventional chemical pesticides had a sufficient window of time to find and infect insects. Further research to enhance efficacy, evaluate range of field situations where nematodes might be used, and determine the impact of refugia treatments on overall pest population levels is still needed.

Assessment of structural fumigation efficacy in food processing facilities

James Campbell

USDA ARS GMPRC, Manhattan, KS, United States

Structural treatments such as heat or fumigation are sometimes needed to eliminate pest populations hidden in the buildings and equipment. Historically, methyl bromide has been widely used in food processing facilities such as flour mills for the suppression of stored-product insect pests; primarily the red flour beetle *Tribolium castaneum*. Use of this fumigant is being phased out and development and adoption of alternative control tactics, such as sulfuryl fluoride or heat, has been made more difficult due to the extremely limited published field data on action thresholds, efficacy, and rate of population rebound. Here, we evaluate the impact of multiple fumigations with methyl bromide or sulfuryl fluoride on red flour beetle populations in multiple flour mills. Red flour beetle population levels were assessed using either direct counts of insects from product samples, direct counts of insects sieved from the product stream (i.e., tailings samples), or from pheromone baited trap captures. From this data, average levels at time of treatment, percent decrease in number following treatment, and rate of rebound were determined. Influence of season, pest density and IPM tactics on efficacy and rebound were also evaluated. From the compilation of this type of monitoring data we can begin to develop a better understanding of the impact of fumigation on pest populations and improve the selection, timing and application of pest suppression tactics in flour mills.

Semiochemicals for managing storage pests: monitoring, mating disruption and precision-targeted pest control

Thomas Phillips[1], Manuel Campos[1], Rizana Mahroof[2], Kishan Sambaraju[1]

[1]Kansas State University, Manhattan, KS, United States, [2]South Carolina State University, Orangeburg, SC, United States

Pheromones and other semiochemicals have been identified for over 40 species of stored product insect pests. Monitoring programs are now well-established for key moth and beetle pests. Research on host volatiles has led to increased activity of aggregation and sex pheromones in monitoring programs for tenebrionid flour beetles, anobiid beetle pests, and moths. Mating disruption of pyralid moth pests has been demonstrated in commercial settings and the technology is being registered for commercial use world-wide. Semiochemical-based pest management methods provide reduced input or chemical free methods to suppress populations below action levels.

Documenting biodiversity: No end in sight in Staphyliniformia (Coleoptera)?

Alfred Newton, Margaret Thayer

Zoology Department, Museum of Natural History, 1400 South Lake Shore Drive, Chicago, Illinois 60605, United States

Known diversity of the beetle group Staphyliniformia (11 families placed in 2-3 superfamilies) is reviewed based on a recently completed world catalog in database form of all species-group names in a current classification. Preparation of this catalog (soon to be web-accessible) was greatly facilitated by the recent publication of modern printed catalogs of world species for all or significant parts of the largest families, and for all Palearctic species.

Through 2007, more than 87,700 species-group names have been proposed for 69,246 currently recognized species and 1,676 subspecies worldwide, of which 466 species (0.7%) are known only as fossils and 1,456 (2.1%) are also or only known in the larval stage.

Analysis of the description of new species by decade from Linnaeus 1758 to the present shows that the discovery rate in this group is accelerating dramatically, not tapering off. The numbers of active authors and total publications have roughly doubled in the past four decades and are more geographically dispersed now than ever before. From 1998-2007, a total of 370 authors in 1750 publications described on average more than 850 new species per year, all of these being much higher numbers than in any of the previous 24 decades since Linnaeus. Factors probably contributing to this increased taxonomic activity include dramatically improved sampling methods and access to systematic resources, and increased collaboration among systematists. This accelerated rate hinders estimation of actual species numbers using trend curves and similar historical methods because our species inventory is obviously very incomplete.

Ensuring high mortality of locusts and grasshoppers treated with Green Guard® (*Metarhizium anisopliae* var. *acridum)*

David Hunter

125 William Webb Drive,, McKellar ACT 2617, Australia

A critical part of ensuring that a biological control agent will cause high mortality, and at a reasonable price, is the initial choice of the isolate. Green Guard®, used in the control of locusts and grasshoppers, consists of an oil formulation of spores of the Australian isolate FI-985 of *Metarhizium anisopliae* var. *acridum.* The FI-985 isolate has high yield during production (100-120g spores per Kg of rice substrate), is virulent against target pest locusts and grasshoppers, and survives moderately well under UV light: the resulting combination of high yield, high virulence and good survival after application means that Green Guard® causes high mortality at a minimal dose, substantially reducing costs. Equally important in ensuring high mortality is proper formulation and application of the product. Dry spores can be stored for several years at cool temperatures and can be quickly formulated when required, essential in the highly variable market for locust and grasshopper control. However, for transport, Green Guard® is formulated as a spore concentrate in oil to limit temperature increases in the product during transport in the very hot summer conditions typical of regions infested with locusts and some species of grasshopper. Spores are transported in corn oil, which is thick enough to reduce settling during transport and storage, though settling is not eliminated completely. Just before use, the concentrate is mixed with a locally available light oil and applied using readily available equipment. In Australia, Green Guard® ULV has been applied to over 70 000 ha, mostly at a dose of 25g spores in 500 mL oil/ha. When it is very hot (maximum temperatures 35-42^{o}C), there is >90% mortality in 7-10 days, though mortality takes longer during the milder temperatures of spring. Similar high mortalities have been obtained in China, East Timor and Mexico, but when vegetation was dense and/or the spray equipment was of less consistent quality, alterations in the dose of spores and types and amounts of oil were required to ensure high mortality.

Royal manipulation of G-protein coupled receptors in the brain of the bee: impacts on brain function and behaviour

Alison Mercer, Kyle Beggs

University of Otago, Dunedin, New Zealand

Honey bee queens produce a pheromone that blocks aversive olfactory learning in young workers, but leaves appetitive learning intact (Vergoz et al., 2007, *Science*, 314, 384-386). Evidence suggests that the effects on aversive learning occur a consequence of pheromone-induced changes in dopamine signalling in the brain (Beggs et al., 2007, *PNAS*, 104: 2460-2464). Queen mandibular pheromone (QMP) reduces brain dopamine levels in young worker bees, selectively alters the expression of dopamine receptor genes, and changes the responsiveness of brain tissues to dopamine. We have found in addition that one of the key components of QMP, homovanillyl alcohol, has direct effects on the function of at least one of the GPCRs that mediates dopamine's actions in the brain. The selectivity of QMP's effects provides important clues about dopamine's role in the formation of associative olfactory memories in the bee.

Towards an integrated diversity and pest management (IDPM) of termites in an oil palm agroecosystem

Faszly Rahim[1], Idris Ghani[1], Ahmad Said Sajap[2]

[1]Universiti Kebangsaan Malaysia, Bangi, Selangor, Malaysia, [2]Universiti Putra Malaysia, Serdang, Selangor, Malaysia

Introduction: The emergence of termite as pest in oil palm agroecosystem on peat was alarming, which called for a multivariate ecological community study to identify the contributing factors and point of emergence. The results from the study was formulated towards an integrated management programme.

Methods: Factors contributing to the changes in community structure were extracted using the nonmetric multidimensional scaling (NMDS). A time-series analysis was then performed on the community data across a putative synthetic gradient of oil palm intensification.

Results: The NMDS ordination identified termite communities to be structured by the geographical position, history, and fragmentation of oil palm agroecosystem. Distinct communities were separated by latitudinal and longitudinal gradient. Lower diversity was found to be historical (age dependant), but more strongly influenced by total cover area and distance to forest patches. Changes in termite community structure along oil palm intensification gradient fitted the decreasing trend function, signalling that a decline in diversity resulted in pest emergence through time. The pest was found generally suppressed by high diversity of species interactions within the communities. However, improper control intentions had greatly reduces the strength of competition of spaces and resources, hence, pest infestation aggravated through time.

Conclusion: Termite management in the oil palm agroecosystem must consider also conservation and utilisations of termite as ecosystem engineers and the “do-nothing strategy”, to reduce treatment cost, is the central for pest management towards a new concept of Integrated Diversity and Pest Management (IDPM).

Molecular characterization of phosphine (fumigant) resistance in grain insect pests using the red flour beetle, *Tribolium castaneum* (Herbst.) as a model organism

Rajeswaran Jagadeesan[1], Paul Ebert[1], Patrick J. Collins[2], David Schlipalius[2]

[1]University of Queensland, St.Lucia, Queensland, Australia, [2]2Queensland Department of Primary Industries and Fisheries, Indooroopilly, Queensland, Australia

Introduction: Understanding the evolution of phosphine resistance in an insect genetic model and grain pest, *T. castaneum*, may assist with effective management of the major problem of phosphine resistance.

Methods: Inheritance of phosphine resistance was determined by dose-mortality response bioassays using genetic crosses of resistant (QTC931) and sensitive (QTC4) strains and the results were tested statistically for monogenic or polygenic inheritance. To determine genomic regions linked to resistance, phosphine-resistant F4 progeny were selected from a single-pair intercross (QTC4XQTC931) and bulk-segregant analysis was performed using RAF (Random Amplified DNA Fingerprinting). DNA markers putatively linked to phosphine resistance genes were cloned, sequenced and located within the *Tribolium* genome assembly. Nearby markers of known sequence (micro-satellites) were then used to confirm the genomic regions containing resistance genes.

Results: Backcross experiments revealed that the mode of inheritance of phosphine resistance genes is autosomal and incompletely recessive with two or more genes controlling high-level resistance. These results are corroborated by RAF bioassay which indicated the possibility of two or more loci involved in high-level resistance. Fine scale mapping of the genomic regions associated with phosphine resistance is currently underway.

Future Directions: Candidate genes identified by fine scale mapping will be characterized by gene expression and systematic gene disruption studies using RT-PCR, Micro-array and RNA interference techniques. This study will lead to diagnostic markers for resistance in a new species, enabling us to monitor the effectiveness of resistance management strategies and identify factors that cause phosphine resistance in the field.

The utilization of biomasses and returned benefits of termites in an oil palm agroecosystem

Faszly Rahim[1], Ahmad Said Sajap[2], Idris Ghani[1]

[1]Universiti Kebangsaan Malaysia, Bangi, Selangor, Malaysia, [2]Universiti Putra Malaysia, Serdang, Selangor, Malaysia

Introduction: Termites are important decomposer communities. However, in oil palm agroecosystem, termites functional benefits have yet to be appreciated. The significant contributions of termites utilization of biomasses in oil palm are quantified through niche and resource analysis to highlight their significant contributions.

Methods: Termite encounters on every resources in oil palm agroecosystem with variable management practices were used as the measure of frequency in a standardized transect sampling protocol. Niche-resource analysis was performed on the data to identify community preferences. Spatial pattern analysis was performed using SADIE to identify the correlation between community aggregation and environmental factors.

Results: Termites were found utilizing fragments of forest biomasses (timber stumps, trunks and chunks), predominantly wood chunks, as well as oil palm biomasses (stand and frond heaps) in the fields. The utilization of biomasses in oil palm were for food as well as nesting and breeding sites. No significant overlapping of niches were found indicating the specialization of the termite functional in resource preferences. Aggregation of communities across field blocks were found influenced by the partitioning of resources as well as levels of oil palm intensification. A shift in wood feeder to soil feeders; and from utilization of forest resources to oil palm biomasses, was noted as a successional response of communities through time.

Conclusion: Termites are important decomposer of the biomasses in oil palm agroecosystem that directly reincorporates the nutrients back to oil palm, however, the rates will be influenced by levels of intensification, which determines the availability of resources.

Area-wide spatial and successive mapping of termite infestation in an oil palm agroecosystem

Faszly Rahim[1], Ahmad Said Sajap[2], Idris Ghani[1]

[1]Universiti Kebangsaan Malaysia, Bangi, Selangor, Malaysia, [2]Universiti Putra Malaysia, Bangi, Selangor, Malaysia

Introduction: The termite *Coptotermes curvignathus* infestation is rampant in oil palm agroecosystem on peat. However, a complete mapping of infestation in any plantation had never been attempted that this study was initiated.

Methods: An area-wide mapping project was conducted through census on oil palm stands with cooperation of the management of an oil palm plantation. Spatial analysis using the SADIE method and mapping by Surfer surface mapping software was made on the grided field data. Rubber wood bait plots intensified within an infestation cluster was successively monitored for a period of a year.

Results: Infestation pattern significantly clustered into patches in an area-wide scale, suggesting mirror of the initial colonies distribution in the forest and environmental affinities, most importantly compartmentalization by drainage system. Generally, fields with high infestation showed clusters of very high local index of aggregation (suggested as hotspots) that emerges as isolated small patches as well as contiguous patches from fusion of several small patches. In contrast, fields with low infestation showed distinct hotspots with low intensity. The infestation pattern also showed the possible orientated infestation and dispersions proposed to be geomagnetism. Significant annual rhythm in the pest activity dynamics, suggested the circannual rhythm synchronizations with environmental and competing species.

Conclusion: The area-wide and successive mapping should be a future in pest surveillance and population ecology of the pest, as an improvement for targeted pest management strategy.

Biting patterns of *Anopheles minimus* (Diptera: Culicidae) in experimental huts treated with DDT and deltamethrin

Theeraphap Chareonviriyaphap[1], Pisit Poolprasert[1], Wannapa Suwondkerd[2]

[1]Kasetsart University, Bangkok 10900, Thailand, [2]Ministry of Public Health, Nontaburi 10100, Thailand

Movement patterns of natural population of *Anopheles minimus* females into experimental huts treated with DDT and deltamethrin were carried out at Pu Teuy Village, Sai Yok District, Kanchanaburi Province, west Thailand. Two experimental huts, control and treatment, were constructed in the fashion of local Thai homes. Under unsprayed conditions, peak biting activity of *An. minimus* females occurred at 1900-2200 hr. After one hut was sprayed with DDT, a significant reduction in number of *An. minimus* females biting in the treated hut was observed ($P < 0.05$). In addition, biting activity almost disappeared from the DDT treated hut before sunrise (0300-0600 hr). Apart from DDT, we also observed a significan reduction in biting of *An. minimus* females in the hut treated with deltamethrin ($P < 0.05$). However, *An. minimus* females continued to enter the deltamethrin treated hut and maintained significantly high levels of biting after 2100 hr and through the remainder of the night ($P < 0.05$). Overall comparisons with matched control, huts there was a greater proportion of *An. minimus* females biting in the hut treated with deltamethrin than in the hut treated with DDT. We conclude that DDT exhibited a stronger excito-repellent impact than deltamethrin on natural populations of *An. minimus*, an important vector of malaria in Thailand.

Wasp diversity ‘down under’: systematics and biogeography of Australian Rhopalosomatidae (Hymenoptera: Apocrita)

Lars Krogmann, Andrew D. Austin

[1]Staatliches Museum für Naturkunde Stuttgart, Stuttgart, Germany, [2]Australian Centre for Evolutionary Biology and Biodiversity, School of Earth and Environmental Sciences, The University of Adelaide, Adelaide, Australia

Introduction: The wasp family Rhopalosomatidae is represented in Australia solely by the genus *Olixon* Cameron, comprising 2 of the 11 known world species. *Olixon* species are wing-reduced, solitary, ectoparasitoids of crickets. Based on new material from intensive surveys we here record 17 species from Australia, 15 of which are new, thus more than doubling the number of world species of *Olixon*. We also discuss the distribution of the new species and present the results of cladistic analyses to evaluate the biogeography of the Australian fauna.

Material & Methods: Cladistic analyses of the world species of *Olixon* based on 47 morphological characters and 24 ingroup species were conducted in TNT under equal and implied weighting.

Results and discussion: The Australian rhopalosomatid fauna is much more species-rich than previously thought, but many species are restricted to fragmented forest patches in the south-west of the continent and are likely to be of significant conservation value. The results of the cladistic analyses indicate that 1) the Australian species of *Olixon* are polyphyletic, 2) about three-quarters of the Australian species form a monophyletic group, and 3) a South American *Olixon* is sister to all other species.

Reducing the chemical footprint when managing chrysomelid leaf beetles in eucalypt plantations: lethal trap trees

Jane Elek[1], Geoff Allen[2]

[1]Forestry Tasmania, Hobart, Tasmania, Australia, [2]CRC for Forestry, Hobart, Tasmania, Australia

Defoliation by native chrysomelid leaf beetles, *Paropsisterna bimaculata,* can cause economic losses of wood volume at harvest in *Eucalyptus nitens* plantations in Australia. Defoliation late in the summer is predicted have double the impact of defoliation that occurs earlier. Current populations are controlled using an IPM program where egg and larval populations are monitored and, if over an economic threshold, are aerially spraying with a synthetic pyrethroid. We explored alternative methods of managing defoliation that do not rely on spraying broad-spectrum insecticides using five criteria. Preferred landscape methods of management were: genetic selection of resistance to insects, promote habitats of beneficial insects by increasing plant diversity and silvicultural management. New options for managing outbreaks were: attract and kill traps, lethal trap trees and using softer chemicals. The easiest, short-term option would appear to be replacing a broad-spectrum insecticide with softer chemicals. However, implementation in the field has been disappointing. The softer chemicals are more expensive, more difficult to use logistically because of their shorter window of activity and they do not control the adult beetles that cause the higher impact damage at the end of the summer.

Therefore we are developing the option of lethal trap trees for outbreak management. The native forest species, *E. regnans* and *E. delegatensis*, have been identified as being more attractive to *P. bimaculata* for feeding and oviposition than plantation *E. nitens* and *E. globulus.* However, these trees were ineffective when planted as unprotected trap trees because they grew so poorly, due to repeated defoliation, that they were no longer sufficiently attractive to the beetles. Infusion of the trap trees with systemic insecticide, rendering the foliage lethal to beetles, would not only protect the trees but also reduce the population pressure of leaf beetles. Trials have been established to test the concept of lethal trap trees, and the nicotinoid insecticides, imidacloprid and clothianidin, are being evaluated for the best application method and dose that would provide at least three months of protection for the lethal trap trees.

For the longer term, we are working towards identifying kairomones or pheromones that could be used in attract-and-kill traps.

Spatial distributions and development of sampling methods for *Aphis gossypii* in commercial greenhouse cucumbers

Taek-Jun Kang[1], Heung-Yong Jeon[1], Seung-Ryong Cheong[1], Joon-Ho Lee[2]

[1]National Horticultural Research Institute, RDA, Suwon, Kyunggi-Do; [2]Department of Agricultural Biotechnology, Seoul National University, Seoul, Republic of Korea

Introduction: Cucumber, *Cucumis sativus* L, is major horticultural crop in Korea and cotton aphid, *Aphis gossypii* Glover, is one of the serious insect pests in commercial greenhouse cucumbers. So, spatial distribution and occurrence of *A. gossypii* were investigated in commercial greenhouse cucumbers during 2001 and 2005.

Methods: By investigating densities of *A. gossypii* within and between cucumber plants, we analyzed population dynamics and distributions of *A. gossypii*. Taylor's power law and geostatistical variogram model (SPATIALSTATS module) were used for analyzing spatial distribution patterns of *A. gossypii*, and developed economic sampling methods of *A. gossypii* in commercial greenhouse cucumbers.

Results: Most of *A. gossypii* were distributed in lower parts of leaves within plants (about 70% of total *A. gossypii* were between 1st and 7th leaves) and also highly clumped between plants (TPL b > 1) during all investigating periods. We developed stratified sampling plans within plants and could get a good estimation of *A. gossypii* by counting in lower 3rd and 6th cucumber leaves. By the results of variogram models (spherical, exponential, Gaussian model), distances which represent average degree of similarity between samples were about 18, 22, 17m respectively. Spatial distribution patterns of *A. gossypii* by ordinary kriging were similar with real distributions of *A. gossypii* in commercial greenhouse cucumbers.

Conclusions: Detailed studies of *A. gossypii* in cucumber greenhouses will provide insights into spatial distributions of *A. gossypii* in greenhouse cucumbers, which could lead to the development of economic sampling methods for *A. gossypii*.

The basis for floral specialization in a guild of wasp-pollinated plants

Adam Shuttleworth[1], Florian Schiestl[2], Steven D. Johnson[1]

[1]University of KwaZulu-Natal, Pietermaritzburg, KwaZulu-Natal, South Africa, [2]University of Zürich, Zürich, Switzerland

The basis for specialization in plants with exposed nectar is still poorly understood. Our research has revealed a guild of plants with exposed, concentrated nectar which are specialized for pollination by *Hemipepsis* pompilid wasps. We test the hypothesis that these plants use cryptic colouring, toxic nectar and selectively attractive floral volatiles to filter non-pollinating insects and achieve specialization. Reflectance spectrometry revealed that pompilid-pollinated flowers are typically dull-coloured and have similar spectra to the background vegetation. Choice tests with nectar from two species and sugar solutions showed that the nectars (which are consumed by *Hemipepsis* wasps) are unpalatable to honeybees. Choice experiments in the field and in the laboratory (using a Y-maze) revealed that pompilid wasps are attracted primarily by floral scent. Gas chromatography-mass spectrometry (GC-MS) and Gas Chromatography-Electro Antennagram Detection (GC-EAD) were used to analyze the floral volatiles produced by pompilid-pollinated flowers and to identify physiologically active compounds which function to attract *Hemipepsis* wasps. We conclude that pompilid-pollinated plants achieve specialization through crypsis, toxic nectar and selective pollinator attraction (through specific volatiles).

Circadian clocks regulate insect response to pesticides

Jadwiga Giebultowicz, Shawn Butcher, Louisa Hooven

Oregon State University, Corvallis, Oregon, United States

Introduction: Circadian clocks allow organisms to adapt biochemical and physiological processes to their environment in rhythms entrained by the solar day. There is emerging evidence that the toxicological response varies with time of day in many insect species. We use the model insect, *Drosophila melanogaster*, to investigate the role of genes encoding clock components in modulating susceptibility to pesticides at the physiological and molecular levels.

Methods: *D. melanogaster* used in these studies were either wild type or mutants in specific clock genes. Flies were exposed to several classes of pesticides at different times of day and LD-50 was calculated. Expression of genes involved in pesticide detoxification was investigated by RT-PCR. Enzyme activity of P-450, esterases and GST enzymes was assayed in different fly genotypes.

Results: By monitoring mortality of *D. melanogaster* exposed to selected pesticides at different times of day, we uncovered daily rhythms in susceptibility to several pyrethroids, fipronil, and malathion. A substantial decrease in permethrin resistance was observed in flies deficient in the gene *Clock* (*Clk*) and *cycle* (*cyc*) which encode positive elements of circadian feedback loop. A similar decrease was noted in flies deficient in the gene *Pdp1*, which is under transcriptional control of *Clk*/*cyc* complex.

Conclusions: We began to decipher the pathways that may govern the varying response of insects to pesticides at different times of day. Similar mechanisms may exist in insect pest species and assessment of putative daily rhythms of susceptibility should become an integral part of IPM practices.

Pyrethroid resistance in the redlegged earth mite: current situation and prospects for the future

Paul Umina, Ary Hoffmann

The University of Melbourne, Parkville, Australia

The redlegged earth mite (*Halotydeus destructor* Tucker) is an important pest of field crops and pastures in Australia, New Zealand and South Africa. Control of this pest relies heavily on chemicals, with few genuine alternatives presently available. Pesticide responses of *H. destructor* from the field which had reported chemical control failures were compared with mites from susceptible 'control' populations. Toxicology bioassays were conducted on adult mites across multiple generations. Very high levels of resistance to two synthetic pyrethroids, bifenthrin and alpha-cypermethrin, were detected in this species for the first time. This resistance was shown to be heritable, persisting after several generations of culturing. There was no evidence that resistance to organophosphorous chemicals had evolved, although low levels of tolerance have been detected in a previous study. Resistance to pyrethroids appears to be spreading and has the potential to become a widespread problem in Australia and elsewhere. These results highlight the need for more judicious management decisions in order to control pest species in a sustainable manner. Future research and management of the redlegged earth mite should be shifted away from broad-spectrum chemicals to cultural control, biological control, host plant resistance and the use of more selective pesticides.

The functional organization of a tropical insect society

Raghavendra Gadagkar

[1]Centre for Ecological Sciences, Indian Institute of Science, Bangalore, Karnataka, India, [2]Evolutionary and Organismal Biology Unit, Jawaharlal Nehru Centre for Advanced Scientific Research, Jakkur, Bangalore, Karnataka, India

Insect societies such as those of ants, bees, wasps and termites are characterised by reproductive division of labour and cooperative brood care. Thus these societies consists of one or a small number of reproductives (usually only queens but also kings in the case of termites) and a large number of sterile or nearly sterile workers. While the queens engage in laying eggs, all the tasks required for nest building, acquisition and processing of food, and brood care are performed by the workers. The functional organization of such insect societies that leads to efficient division of labour is a topic of obvious interest. In this lecture I will describe experiments designed to understand the functional organization of one such insect society. I have chosen the primitively eusocial wasp *Ropalidia marginata* for these investigations. *Ropalidia marginata* is abundantly distributed in peninsular India and serves as an excellent model system. An important feature of this species is that queens and workers are morphologically identical and physiologically nearly so. How does an individual become a queen? How does the queen suppress worker reproduction? How does the queen regulate the non-reproductive activities of the workers? What is the function of aggression shown by different individuals? How and when is the queen's heir decided? I will show how such questions can be experimentally investigated and discuss what the answers to these questions tell us about the functional organization of this primitive insect society and what they tell us about the evolution of insect sociality.

Antimicrobial production by fungus-growing ants: phenotype, genotype and an abrupt evolutionary transition in the host-parasite interaction

William Hughes[1], Jacobus Boomsma[2]

[1]University of Leeds, Leeds, United Kingdom, [2]University of Copenhagen, Copenhagen, Denmark

The metapleural gland of ants is an ancestral structure that is a key first-line defence against parasites. The paired glands located at the posterior of the thorax produce a broad spectrum of antimicrobial compounds that spread over the cuticle passively or by active grooming. The glands are fixed in size in adults, making them potentially useful for comparing investment in disease defence within and between taxa because the size of the glands is not confounded by factors such as age or health. The fungus-growing ants are particularly useful group for such comparisons because they are a monophyletic tribe in which taxa differ in several factors likely to affect their relationship with parasites. Furthermore, the two most derived genera, the leaf-cutting ants, have a diversity of phenotypes (castes) that may also differ in their host-parasite interactions. Here I will examine how the size of the metapleural gland differs between leaf-cutting ant castes and whether there is genetic variation for this key fitness-determining trait. I will also compare the size of the metapleural glands of leaf-cutting ants with those of the other fungus-growing ants and discuss the insights this provides into the relative parasite pressure experienced by the different taxa.

Rates of larval parasitism of false codling moth, *Thaumatotibia leucotreta* (Meyrick) (Lepidoptera: Tortricidae), on citrus in South Africa

Kierryn Keeton[1], Nomahlubi Sishuba[1], Sean Moore[2], Martin Villet[1]

[1]Rhodes University, Grahamstown, South Africa, [2]Citrus Research International, Port Elizabeth, South Africa

Thaumatotibia leucotreta is a major pest of citrus in South Africa. Due to problems associated with pesticides, alternative methods, such as the use of parasitoids, are becoming an increasingly attractive means of control of crop pests. However, it has been hypothesised that larvae of *T. leucotreta* are protected from parasitoids by their fruit-tunneling habits, and that because of this they will show low rates of parasitism that militate against using parasitoids against them as biological control agents. A six-month survey at two sites in the summer and winter rainfall regions of South Africa found only one specimen of parasitoid. In the equinoctial rainfall region, *Agathis bishopi* (Nixon) (Hymenoptera: Braconidae) was reared from two sites with rates of parasitism of 2.5%-37%. In the field, rate of parasitism was inversely related to age of the host larva, and in laboratory experiments female wasps showed a preference for ovipositing on second- and third-instar larvae and took 23-50 days to develop from egg to adulthood at 27°C. This suggests that this koinobiont preferentially attacks younger larvae, not because it is poorly adapted to the tunneling behaviour of its host and cannot reach older larvae, but because it requires younger larvae to allow it sufficient time to complete its development. Suggestions are made for incorporating these findings into integrated pest management programmes.

Pollinator food-webs on granite outcrops – diversity, specificity and a fly story

Caroline Gross, Wendy Waters

The University of New England, Armidale, NSW, Australia

Introduction: Granite outcrops often hold unique vegetation communities that function as island-refuges for biodiversity. Richness is high with 16-20 plant species in a 10 m^2 area. We tested a corollary that these communities have highly specialized floral systems and pollination mutualisms with the aim to determine the structure of pollinator food webs.

Methods: In Spring 2007, we studied plants and pollinators for 24 plant species and their insect visitors across three granite outcrop sites in eastern Australia. We resolved plant breeding systems for six key-plant species using bagging and hand–pollinations. We determined diversity and fidelity of visitors through observation periods, videoing and insect swabs (c. 110 hours of observations).

Results: Key plant species were mostly self–compatible. Pollinator specificity was low with most species sharing floral visitors. We detected 30 species of insect that we classified as abundant floral visitors. Flies were dominant followed by bees including the introduced honeybee. Most fly and native-bee species carried pollen and came into contact with anthers and stigmas in the observation flowers. Flies were more active early in the season than bees.

Conclusion: This is the first community level study of plant-pollinator interactions in Australia. High plant-species diversity was matched by high levels of diversity in floral-visitors. No single plant-pollinator partnerships were found. Some plant species were visited predominantly by flies and others by bees. We conclude that the granite habitats provide an oasis for many pollinators as the surrounding landscape has a simplified structure devoid of many understory components.

The conservation ecology of the endangered brackish water damselfly, *Mortonagrion hirosei*: Planning to establish a new habitat for mitigation

Mamoru Watanabe

University of Tsukuba, Tsukuba, Ibaraki, Japan

Introduction: In 1998, a tiny habitat of the brackish water damselfly, *Mortonagrion hirosei*, which is an endangered species in Japan was discovered in Ise, Mie Pref. It was a dense reed community on the brackish water, from which had been going to be reclaimed under the construction of sewage plant. The government of Mie Prefecture decided to preserve the local population.

Mitigation Project: The mitigation project started, because the habitat was too small to maintain the local population, and because surroundings of the habitat would become unavailable vegetation for the damselfly due to the plant development. In those days, however, there were few reports on the biology of the species. Therefore, we had to start to clarify quantitatively the population parameters of larvae and adults, behaviour, flight habit, body colour change for adults, saline tolerance of larvae as well as to measure abiotic environment, such as saline, water depth, water temperature and relative light intensity in the original habitat. Based on the accumulation of such information, the design for a newly established habitat was proposed.

Results: In early spring of 2003, huge number of reed rhizomes were transplanted for establishing the new habitat. Artificial brackish water was continuously supplied throughout the year. The artificial reed community has developed year after year and nearly completed to the dense community, though a lot of problems for the mitigation appeared during 2003-2007. Consequently, the adult population has increased in both the original and the established habitat. The mitigation project has now proved successful.

Dolichopodid species number in the North and South of West Palearctic (Diptera): Explanation of differences and forecast

Igor Grichanov

All-Russian Institute of Plant Protection, St. Petersburg, Pushkin, Russian Federation

West Palearctic as a whole is one of the best studied regions, but being investigated rather spotty regarding dolichopodids. The author has generalized their fauna for North Europe (NE) and East Mediterranean (EM) in form of species lists and keys (Grichanov, 2006, 2007). About 400 species are registered in NE and 520 in EM with many more EM species waiting descriptions.

Ten countries or territories with the biggest species lists (between 60 and 330) have been selected in each part of the Palearctic. The species number has been compared with the total area and ecological features of countries.

Sweden has the longest species list (330) in NE (followed by Finland, Leningrad Region and Norway), while Romania (263) in EM (followed by Krasnodar Territory and Ukraine). Taking into consideration country areas, we see other countries at top. Denmark, Estonia and Latvia have the highest index (12.20 to 5.77 species per 1000 sq.km) in NE, while Israel and Caucasian republics Karachai-Cherkessia and Kabardino-Balkaria are the most diverse EM territories (10.85 to 4.64).

There are subjective and objective reasons for this difference. Number of expeditions and enthusiastic dipterists in a country is the main subjective reason. A gradual decrease of biodiversity per unit area northward and eastward is an objective trend in NE. In EM the greatest biodiversity is observed in montane regions, such as the Caucasus, that is supported by data on Dolichopodidae. If a country has large area of flat lands in addition to mountains, then the species index is low.

Coarse woody debris and saproxylic beetles in a managed forest landscape in boreal Sweden

Barbara Ekbom, Martin Schroeder, Thomas Ranius, Stig Larsson

Dept. of Ecology, Swedish University of Agricultural Sciences, Uppsala, Sweden

Saproxylic beetles constitute a significant proportion of boreal forest biodiversity. However, the long history of timber production in Fennoscandia has significantly reduced the availability of dead wood and is considered a threat to the conservation of saproxylic beetle assemblages. Therefore, since the mid-1990s dead wood retention in harvested stands has formed an integral part of silvicultural practices. However, the contribution of this biodiversity-orientated management approach to conserving saproxylic beetle assemblages in boreal forest landscapes that include production forestry remains largely untested. Few studies have attempted to analyze the occurrence of CWD at the landscape level. We studied the occurrence of CWD in stands of different ages and management background in a boreal forest landscape in central Sweden. We examined differences in resident saproxylic beetle assemblages among stands under different management in the same boreal forest landscape, and in particular stands managed according to new conservation-orientated practices. We also investigated the relationship between beetle diversity and forest stand characteristics. The active creation of coarse woody debris (CWD) has been suggested as a measure to preserve and restore biodiversity in managed forests. A common practice in Sweden is to create high stumps at final cutting. Using the same boreal forest landscape we also evaluated the importance of high stumps for saproxylic (wood-dependent) beetles. The consequences of these results for biodiversity-oriented forest management are discussed

Novel mariner-like elements (MLE), Pmmar1, 2 and 3, isolated from the big-headed ant, *Pheidole megacephala*, inhabiting Okinawa, and their phylogenetic analyses

Yuichi Kawanishi, Hitoshi Ohnishi, Akito Kasahara, Kazuki Tsuji, Hideaki Maekawa, Yumiko Nakajima

University of Ryukyus, Nishihara-cho, Okinawa, Japan

Three types of *mariner*-like elements (MLE), named *Pmmar1*, *Pmmar2* and *Pmmar3*, were isolated. *Pmmar1* and *Pmmar2* are defective type elements in their ORFs encoding the transposase whereas *Pmmar3* inserted into *Pmmar1*, was an intact MLE element with inverted terminal repeats and a complete ORF. Sequence comparative analysis revealed that they show highly conserved homology one another and belong to the *mauritiana* subfamily of MLE. *Pmmar1* and *Pmmar2* are closely related to *Myrmar2* from red ant, *Myrmica ruginodis*, and *Botmar1* from bumble bee, *Bombus terrestris*. *Pmmar3* has the highest identity with *Mboumar* from harvester ant, *Messor bouvieri*. Novel MLEs from this big-headed ant in Okinawa were quite homologous to the ant inhabiting in Reunion island of French territory between Madagascar and Mauritius. This means the same population as in Reunion island but not in Libreville, Gabon, west coast of central area of Africa had been transported into Okinawa few hundreds years ago. Micro-satellite DNA analyses data also supported this situation.

Termite species inventory across an oil palm agroecosystem with variable scales of sampling

Faszly Rahim[1], Idris Ghani[1], Ahmad Said Sajap[2]

[1]Universiti Kebangsaan Malaysia, Bangi, Selangor, Malaysia, [2]Universiti Putra Malaysia, Serdang, Selangor, Malaysia

Introduction: No single sampling method has been found to significantly retrieve the species of termite communities across sites, which calls for an integrated sampling scheme. An inventory across oil palm agroecosystem on peat in Peninsular Malaysia was made to monitor termite diversity using sampling methodologies with variable scales as a proposed integrated sampling scheme.

Methods: The inventory was conducted from 2001 to 2005 using 16 units of 100 m x 2 m belt transects, 44 units of successively monitored 500 m^2 rubber wood bait plots, and various hectares of oil palm stand scouting. Community structure was extracted using hierarchical clustering and variations amongst community composition across sites were analysed using the multi response permutation procedure (MRPP).

Results: A total of 46 species of termites from three families, and 17 genera were collected during the inventory. These were collections of 36 species from the transects, 12 species attracted to rubber wood bait, 20 species from stand scouting, and some additional species from the casual samplings. Species-area curves indicated ample effort in retrieving species. This is the first known extended list of termite in oil palm as well as peat soil ecosystem. Hierarchical clustering extracted distinct communities existing in the oil palm agroecosystem on peat. The variations between communities across sites depended on the management history of fields rather than site and peat type alone.

Conclusion: Integrated sampling scheme is a practical method for inventory in retrieving termite species richness across agroecosystem as well as identifying community structures.

Yellow coloration in gregarious desert locusts: function and regulation

Jurgen Huybrechts, Filip Sas, Marisa Geens, Tim Vandersmissen, Arnold De Loof, Liliane Schoofs

K.U.Leuven, Leuven, Belgium

In adult insects, the colour of the cuticle changes rarely once the hardening has been completed. Even more so when colour changes are gender-specific and coincide with sexual maturation. Adult males of the desert locust *Schistocerca gregaria* turn yellow about 10 days after adult molt, but only if they live in crowded (gregarious) conditions. Isolated-reared (solitarious) males do not turn yellow, neither do females. Upon regrouping, yellowing is quickly induced, but again, only in males. All this suggests the existence of a gender-specific control mechanism, perhaps hormonal in nature. Juvenile hormone is known since long to play a role, but the gender-specificity of its effect on yellowing suggests that other factors are involved as well. The discovery that yellowing is due to the deposition in the already hardened cuticle of a carotene-binding 'yellow protein' has facilitated the analysis of the yellowing process. The results of our behavioral observations favor the view that the yellow color does not act as sexual attractant but rather as a signalling colour to discourage other males from mounting a male instead of a female.

Intraguild predation involving *Harmonia axyridis*: a threat to native biodiversity and ecosystem function?

Judith Pell[1], Jason Baverstock[1], Remy Ware[2], Michael Majerus[2], Helen Roy[3]

[1]Rothamsted Research, Harpenden, Hertfordshire, United Kingdom, [2]University of Cambridge, Cambridge, Cambridgeshire, United Kingdom, [3]NERC Centre for Ecology and Hydrology, Abbots Ripton, Cambridgeshire, United Kingdom

As an effective generalist predator of aphids and other hemipteran pests, *H. axyridis* has been a successful biological control agent. However, the very functional traits that have contributed to its success also implicate it as an intraguild predator that not only threatens the diversity of other natural enemies of Hemiptera (and their associated ecosystem services), but biodiversity more widely. A review of existing data on intraguild predation involving *H. axyridis* concludes that niche complementarity is almost certainly the mechanism by which *H. axyridis* remains in equilibrium with its co-evolved native guild of predators. In its alien range, the guild of predators are co-evolved with each other but not with *H. axyridis* and as such come into direct competition with *H. axyridis*. This has significant implications for predator diversity, biodiversity *per se* and also ecosystem services. Pest management strategies, aimed at maintaining predator diversity through habitat manipulation and the diversification of our agricultural landscapes, could help counter declines in predator diversity associated with the arrival of *H. axyridis*. Although implications for biodiversity in natural habitats are of grave concern, it is perhaps through the manipulation of managed land that we have the greatest chance of optimising the environment to favour our native diversity in the presence of *H. axyridis*, thereby also protecting diversity in natural habitats. To achieve this we need robust research data to fill gaps in knowledge and develop mitigation strategies.

Genetic relationship of *Diadegma semiclausum* populations of Taiwan and Syria by means of mitochondrial and nuclear DNA sequences

Kadirvel Palchamy, Robert de la Pena, Srinivasan Ramasamy

The World Vegetable Center, Shanhua, Tainan, Taiwan

Introduction: *Diadegma semiclausum* (Hellen) (Hymenoptera: Ichneumonidae) is an effective larval parasitoid for diamondback moth, *Plutella xylostella* L. (Lepidoptera: Plutellidae), and has been successfully introduced as a biological control agent in many parts of the world. In Taiwan *D. semiclausum* is adapted to low temperatures; in Syria, it is adapted to high temperatures. To explain the possible bases for this adaptation of *D. semiclausum* populations in Taiwan and Syria, it becomes necessary to examine if there is any species-level difference between the populations.

Methods: Using at least 10 insects each from Taiwan and Syria, the mitochondrial gene *cytochrome oxidase I* (COI) of *D. semiclausum* was amplified using the primer pair (UEA3: TATAGCATTCCCACGAATAAATAA and UEA8: AAAAATGTTGAGGGAAAAATGTTA) and partial sequences were obtained.

Results: Sequence alignments and further editing identified a consensus sequence of 707 bp in all the samples. Alignment of sequences of the Taiwan and Syria samples, based on the consensus sequence, did not reveal any difference between them. A high level of sequence similarity was also observed across the COI sequences of *D. semiclausum* insects from various countries available in the database.

Conclusion: Our initial results suggest that the *D. semiclausum* population in Syria does not differ from the population in Taiwan. However, we are in the process of confirming the species identity of the *D. semiclausum* populations of Taiwan and Syria using additional mitochondrial and nuclear genomic regions.

Discovering potent tsetse repellents from odours of refractory hosts and structure and blend optimization studies

Ahmed Hassanali, Rajinder Saini, Mathew Bett

icipe-African Insect Science for Food and Health, Nairobi, Kenya

Two approaches to discovering potent tsetse repellents will be highlighted. One has involved (i) initial GC-MS identification and wind-tunnel evaluation of EAG-active odour constituents specific to a wild animal (waterbuck) that is refractory to savannah tsetse, followed by (ii) field assays (against wild populations of *Glossina pallidipes*) of each group of candidate compounds, individually and in combinations, and successive subtraction assays that compared the relative repellencies of different blends with one of each of the constituents in different groups missing. The process showed that a blend of 4 constituents belonging to different classes of compounds reproduced the repellent activity of the original blend of 15 electrophysiologically-active repellent candidates identified from the host odours. The second approach has involved hypothesis-led wind-tunnel assays of a series of analogues of a known mild repellent of savannah tsetse (2-methoxyphenol) followed by detailed field evaluation of one of the promising candidates. A small modification of the known mild repellent enhanced significantly the repellency of the resulting compound against wild populations of *Glossina pallidipes* in Kenya. Performance of the two repellents in field experiments and their potential in tsetse management will be highlighted.

Ecological metabolomics of plant-insect interactions

Mirka Macel, Nicole M. van Dam, Wim H. van der Putten

Netherlands Institute of Ecology, Heteren, Netherlands

Traditionally the role of plant defense compounds in plant – insect interaction has been investigated using targeted analysis. By doing so, the effects of specific groups of compounds such as glucosinolates and alkaloids on insect herbivores and higher trophic levels have been extensively assessed. However, plants produce a wealth of different compounds and key compounds in plant – insect interactions could be overlooked by taking a targeted approach. Metabolomics is an emerging field that covers the identification and quantification of the suite of metabolites within an organism, tissue or cell. We apply the comprehensive metabolomics approach to study induced plant responses mediating above and belowground plant - insect interactions associated with *Brassica* spp. and in plant – insect interactions of invasive plant species.

Neuromodulation-induced neural circuit interaction in the desert locust

David Rand, Yael Zilberstein, Amir Ayali

Tel Aviv University, Tel Aviv, Israel

Introduction: Insect feeding and ecdysis-related air swallowing are complex rhythmic behaviours characterized by interactions among functionally related central pattern generator neuronal circuits. They involve rhythmic movements of mouth appendages, governed by the suboesophageal ganglion (SOG), and foregut movements, controlled by the frontal ganglion (FG). In our work we focused on the interaction between the FG and SOG circuits in the desert locust, *Schistocerca gregaria*, and specifically on the role of neuromodulation in this interaction.

Methods: *In vivo* recordings demonstrated coordination and synchronization between the motor outputs of the two neuronal centers. Simultaneous extracellular recordings were made from the FG frontal connectives and the SOG mandibular nerves in three *in vitro* configurations: (1) isolated ganglia, (2) FG-SOG preparation with intact nerve interconnections, and (3) a fully connected brain-FG-SOG preparation.

Results: Bath application of the NO donor SNP or of IBMX, followed by the muscarinic agonist pilocarpine, was found to consistently induce robust SOG rhythmic pattern, which consisted of alternating bursts of activity in the mandibular nerves (opener and closer). This finding suggests that the mandibular motor pattern in Schistocerca is activated via muscarinic acetylcholine receptors in a cGMP-dependent manner. The ongoing FG rhythm was accelerated by SOG modulation. Different extents of synchronization of the modulators-induced rhythmic patterns were observed when the FG and SOG were connected or when brain inputs were kept intact.

Conclusions: Our results imply that neuromodulation-mediated interactions between the different neural centers, in the absence of sensory inputs, is sufficient for generating the complex rhythmic motor patterns of the mandibles and gut muscles during Locust feeding or ecdysis-related air swallowing.

Status of pollination ecosystem services in South Africa

John Donaldson, Ruan Veldtman

South African National Biodiversity Institute, Cape Town, South Africa

Introduction: As part of the Global Pollinator Project funded by GEF, apples, seed onions, and sunflower seed crops were identified in South Africa to assess the importance of wild pollinators for their pollination. However, commercial agriculture dependent on insect pollination frequently makes use of managed honeybees (*Apis mellifera* L.) for crop pollination in South Africa. Consequently the importance of both wild and managed pollination services for each of the selected crops require quantification. Another factor not normally considered in crop pollination is differences in pollination at the crop edge and centre. The effective distance of pollination for wild and managed pollinators will thus also be quantified.

Methods: Contribution of wild and managed pollinators to crop pollination will be determined by pollinator exclusion experiments and simultaneous recording of insect pollinator visits. Fields sampled will vary with respect to the presence or absence of bordering natural areas and use of managed hives. For each crop, seed or fruit set will be recorded at the edge, centre, and between these two positions.

Results: Preliminary findings suggest that both wild and managed pollination is a vital part of crop pollination in South Africa. For example, in large sunflower fields surrounded by other agricultural crops managed pollination is required, while for fields bordered by natural areas resident wild honeybee populations ensure sufficient pollination.

Conclusions: Providing information on wild and managed pollination services will identify landscape management strategies that improve crop pollination and ensure conservation of both these services.

The influence of machinery innovation on *Ephestia kuehniella* population in flour mill in the Czech Republic

Vaclav Stejskal, Radek Aulicky

Crop Research Institute, Prague, Czech Republic

Introduction: In Czech Republic (CZ) *Ephestia kuehniella* is a main pest moth species infesting flour mills. In CZ, control of populations of *E. kuehniella* has been traditionally achieved by regular structural fumigation by methyl bromide (CH3Br) or hydrogen cyanide (HCN).

Methods: However, the use of both fumigants is now restricted. CH3Br, as an ozone depletor, is completely unavailable for mill fumigation in CZ. HCN is frequently not permitted by hygienic officers for mill fumigation in urban environment due to its high toxicity. In such circumstances the pest control relies solely on mechanical cleaning, spot phosphine fumigations and use of aerosol insecticides. This was also a case of the studied mill, located in the center of the town.

Results: This study documented that ususal cleaning and limited use of insecticides was not effective enough to control *E. kuehniella* in mills equipped with traditional machinery based on wood transport technology of flour. This case history provided evidence that the introduction of new automated machinery drastically decreased population of *E. kuehniella* in the year of reconstruction.

Conclusions: Although E. kuehniella population increased in the consequent years, it did not reach the population level recorded before reconstruction. This study was supported by the by MZe Project Vyzkumny zamer 0002700603.

Host regulation by a noncoding RNA of TnBV

Patrizia Falabella[1], Maria Teresa Valente[1], Lea Riviello[1], Silvia Gigliotti[2], Magda De Eguileor[3], Francesco Pennacchio[4]

[1]Università degli Studi della Basilicata, Potenza, Italy, [2]Istituto di Genetica e Biofisica - A.Buzzati Traverso; CNR, Napoli, Italy, [3]Università degli Studi dell'Insubria, Varese, Italy, [4]Università degli Studi di Napoli Federico II, Napoli, Italy

The genome of polydnaviruses shows structural features resembling those of eukaryotes, with many genes interrupted by introns and the occurrence of large noncoding regions. The immunosuppressive properties of specific viral gene products has been unequivocally demonstrated, while the possible role in the host regulation of the noncoding regions of the polydnavirus genome remains elusive.

Here we show that a small noncoding RNA of the bracovirus associated with the parasitic wasp *Toxoneuron nigriceps* (*Tn*BV) regulates the expression in the lepidopteran host, *Heliothis virescens,* of a gene which appears to be involved in the immune response. This noncoding RNA displays sequence complementarity with the regulatory 5' UTR of its target gene that it is able to silence. This host gene encodes a protein localized in membrane-delimited compartments of haemocytes, where it gives rise to amyloid fibrils, which favour melanin formation *in vitro*.

Our results demonstrate for the first time the occurrence in polydnaviruses of a noncoding RNA, which controls gene expression, likely via sequence-specific interactions with a regulatory region of a host transcript. Moreover, the discovery that the silenced gene encodes for a precursor of functional amyloids produced by haemocytes stimulates new interesting investigations on the molecular mechanisms regulating innate immunity in insects.

The observed horizontal transfer of genetic material between the host moth larvae and *Tn*BV has interesting evolutionary implications, as it corroborates the hypothesis that bracoviruses may derive from a baculovirus ancestor.

Molecular analysis of circadian system in male moth reproductive organs

Piotr Bebas[1], Joanna Kotwica[1], Jadwiga M. Giebultowicz[2]

[1]University of Warsaw, Department of Animal Physiology, Warsaw, Poland, [2]Oregon State University, Department of Zoology, Corvallis, OR, United States

Introduction: Circadian oscillator in the reproductive system of Lepidoptera is essential for male fertility. Research on the cotton leafworm, *Spodoptera littoralis*, demonstrated that circadian oscillator controls the rhythm of sperm release from the testis into the vas deferens (VD), and coordinates daily changes in the VD environment, which are necessary for sperm maturation. We report functional molecular studies aimed to understand this circadian system.

Methods: Protein expression was investigated by immunocytochemistry and gene expression by qRT-PCR. To determine functions of the molecular oscillator, we cultured testes-sperm ducts complexes *in vitro* with double-stranded *per* RNA.

Results: The clock protein PERIOD (PER) displayed clear daily rhythm in the testes and VD of *S. littoralis*. Levels of PER oscillated in cyst cells surrounding sperm bundles, in epithelial cells of the barrier separating testicular follicles from the VD, and in the epithelium of the upper VD. RNA-mediated interference (RNAi) targeting the *per* gene disrupted clock mechanism. RNAi lowered *per* transcript and PER protein levels. These changes caused transient inhibition of sperm release and a shift in the phase of the sperm release rhythm, regardless of the light/dark cycle. In addition, we demonstrated that per-based molecular oscillator regulates rhythmic expression of B and c subunits of proton pump, V-ATPase, which controls circadian changes in pH. Surprisingly, we also revealed rhythmic expression of the gene encoding yolk protein YP2, which is expected to be active only in females.

Conclusions: Our data provide new insights into the functional organization of the insect peripheral clock. MNiSZW-N300306831/2338.

Records of Scarabaeidae from Kütahya Province

Yakup Senyüz[1], Yalcin Sahin[2]

[1]Dumlupinar Üniversity, Kutahya, Turkey, [2]Eskisehir Osmangazi Üniversity, Eskisehir, Turkey

Introduction: There is not enough database about Scarabaeidae fauna of Turkey and also surroundings Kütahya Province. The samples were collected from different location in Kütahya Province and its neighborhood. The distribution of them in Turkey and also throughout the world were given by this study.

Methods: This study was done between April 2003 and October 2004 in the Kütahya Province. The samples were collected by hand and light trap from different localities and they were identified according to different identification books.

Results: The species of family Scarabaeidae evaluated and totally 20 species were found in this study.

Conclusions: This type of study was made the first time for Kütahya Province and all identified species were new record for the fauna of Kütahya Province. It is expected that detailed further studies will continue in future on this group of insects in Turkey.

To be at the crime scene with the police investigation team is vital: Two case reports

Theuns Van der Linde, Kobus Kolver, Shaun Hoffman

University of the Free State, Bloemfontein, South Africa

Introduction: In South Africa the S.A. Police Services are very reluctant to allow forensic entomologists to the crime scene. There are many reasons for this situation. In this paper two case studies will be discussed.

Methods: At the crime scene and during the autopsy the standard procedures for collecting of entomological evidence were followed.

Results: Case 1: A young mother disappeared from a New Years Party and was found 13 days later, dumped alongside a highway. At the autopsy the forensic entomologist immediately realised that something was wrong. The remains were almost skeletonized, but the only insects present were third instar *Chrysomya albiceps* larvae, no pupae or beetles. When questioning the investigating officer, he admitted that the body was wrapped in a sheet. The case was simulated, using two pigs, one wrapped and the other one naked. The two decompositions differed significantly.

Case 2: The body of a young African girl was found in the field. It was a very hot day with the surface temperature of the body at 50^0C. The body was still fresh, no skin slippage seen. The PMI was calculated to be less than 18 hours. At the autopsy the body showed severe skin slippage. The pathologist was convinced that the PMI was at least 48 hours, which was contradictory to the insects on the body.

Conclusion: It is of utmost importance to be at the crime scene with the police investigation team. Significant post-mortem changes might occur from finding the body until the autopsy is done.

Edge effects on landing patterns of aphids in commercial potato fields

Kerstin Krüger, Lezel Muller, Marié Warren

Department of Zoology and Entomology, University of Pretoria, Pretoria, South Africa

Introduction: Plant borders have been suggested as a management tool to reduce incidence of non-persistently aphid-transmitted viruses in crops, the rationale being that aphids lose transmission ability when feeding on a non-virus host plant before moving into potato fields. Although it has been shown that aphids tend to land more frequently in field borders, little information is available on the strength of edge effects in large fields. We examined aphid landing patterns within fields and tested the hypothesis that aphid landing rates in large potato fields are higher at the edges compared to the interior.

Methods: Four transects each consisting of 16 green plastic bucket traps were placed in cross-formation in three circular commercial potato fields ranging from 20-40 ha. The traps were positioned in square groups of four traps and placed at increasing distances (2, 12, 117 and 222 m) from the edge. Traps were emptied weekly for 7 weeks.

Results: Aphid landing rates tended to be higher at edges of fields for up to 7m compared to the interior. However, landing rates tended to increase again closer to the centre of a field. The strength of edge effects was not the same at all sites and sampling weeks and depended on factors such as aphid abundance, aphid species and trap position.

Conclusions: Although edge effects were apparent, patterns within and among sites were not always consistent. However, a trap crop in the centre of large fields in addition to crop borders could contribute towards reducing virus incidence.

Records of Scarabaeidae from the Sündiken Mountains

Yakup Senyüz[1], Hakan Caliskan[2], Davut Ümit Sirin[2], Cüneyt Nadir Solak[1]

[1]Dumlupinar Üniversity, Kutahya, Turkey, [2]Eskisehir Osmangazi Üniversity, Eskisehir, Turkey

Introduction: There is no enough database about Scarabaeidae fauna of Turkey and also Sündiken Mountain in Eskişehir Province. The samples were collected from different locations on the mountain. The distribution of them in Turkey and also throughout the world were given by this study.

Methods: This study was done in the Sündiken Mountain in Eskişehir Province between April and October 2005. The samples were collected by hand and light trap from different localities and they were identified according to different identification books.

Results: Scarabaeidae fauna of the mountain was investigated and totally 22 species were found in this study.

Conclusions: This type of study was made the first time for this mountain and all identified species were new record for the fauna of the Sündiken Mountain. It is expected that detailed further studies will continue in future on this group of insects in Turkey.

Does copulation corrupt resistance against real pathogens in *Tenebrio molitor*?

Terhi Valtonen, Heidi Viitaniemi, Markus J. Rantala

University of Turku, Turku, Finland

The activation and the use of the immune system are costly and should therefore be traded off against other fitness components. According to most studies immune function declines as reproduction increases and mating induces down-reculation of immune function. Previous studies with *Tenebrio molitor* have suggested that copulation corrupts immunity. However, previous immunoecological studies made in *Tenebrio molitor* have received conflicting results suggesting substantial population differences in trade-offs between immune deffence and other life history traits. We tested the effect of mating on immunity in our *Tenebrio molitor* stock population by measuring phenoloxidase activity, encapsulation response against a novel antigen and parasite reistance against real pathogens (fungus *Beauveria bassiana*). The results are discussed in the light of the life-history evolution.

Pyrethroid resistance mutations in the whitefly, *Bemisia tabaci*: an evolutionary perspective on a global scale

Christopher Jones, Kevin Gorman, Martin Williamson, Ian Denholm

Rothamsted Research, Harpenden, United Kingdom

Introduction: Delaying the selection and fixation of mutations that cause target-site resistance is one of the many challenges confronting insecticide resistance management. In this sense, the whitefly *Bemisia tabaci* is highly problematic due to its haplodiploid breeding system, migratory ability and polyphagous nature that all promote the spread of resistance genes. Moreover, *B. tabaci* exists as a complex of morphologically indistinguishable populations termed 'biotypes' that are often reproductively isolated.

Method: A high-throughput real-time PCR assay targeting a single nucleotide polymorphism (SNP) in the mitochondrial cytochrome oxidase I (mtCOI) gene was developed to distinguish between two of the most invasive and widespread biotypes (B- and Q-types). Furthermore, the occurrence of two pyrethroid resistance mutations (L925I and T929V) within the voltage-gated sodium channel gene was investigated across different biotypes along with an adjacent intron sequence to compare variation between resistant and susceptible alleles.

Results: The real-time PCR assay was highly successful at screening field collections of *B. tabaci* from around the world. The technique requires little optimisation, is designed to run on a 96-well plate and can be performed on homogenised individual insects, removing the need for DNA extraction. The pyrethroid resistance mutation, L925I, was present in resistant individuals of all biotypes examined. The reproductive incompatibility between biotypes suggests that this mutation has arisen independently several times. Interestingly, T929V was found solely in Q-type individuals.

Conclusions: Understanding how resistant mutations evolve and spread among and between biotypes will provide valuable information for resistance management tactics employed against *B. tabaci*.

Nectar amino acids and insect responses

Sue Nicolson

University of Pretoria, Pretoria, South Africa

Nectar amino acids have received less attention than the more abundant sugars. The Bakers showed in the early 1980s that amino acids occur widely in floral nectars and suggested possible adaptive significance. Nectar amino acid concentrations are surprisingly high (sometimes exceeding 100 mM) in bird-pollinated *Aloe marlothii* and some *Erythrina* species, largely due to abundant non-essential amino acids e.g. asparagine and glutamine. Other *Aloe* species have much lower concentrations. Nectar of *A. greatheadii* var *davyana*, a major South African bee plant, contains only 2.8 mM amino acids, mainly proline. Amino acids affect the taste of nectar, and chemosensory responses of flies show that the common amino acids may stimulate sugar or salt receptors, be inhibitory, or have no effect. Preference experiments with honeybees show negative responses to most single amino acids at high concentration. We have measured the proboscis extension response of honeybees to dilute sucrose solutions containing amino acids, and found significant positive responses to 2 mM proline, glycine and phenylalanine. Insect responses will depend on concentrations of both amino acids and sugars, and effects of amino acid mixtures are not easily predicted.

Scarabaeidae fauna of the Felent River Basin

Yakup Senyuz, Cüneyt Nadir Solak

Dumlupinar Üniversity, Kutahya, Turkey

Introduction: There is not enough database about Scarabaeidae fauna of Turkey and also Felent Rİver Basin in Kütahya Province. The samples were collected from different locations on the basin. The distribution of them in Turkey and also throughout the world were given by this study.

Methods: This study was done monthly on the Felent River Basin, one of tributaries of Porsuk River, between April 2005 and 2006. The samples were collected by hand and light trap from different localities and they were identified according to different identification books.

Results: Scarabaeidae fauna of the basin was investigated and totally 17 species were found in this study.

Conclusions: This type of study was made the first time for this basin and all identified species were new record for the fauna of the Felent River Basin. It is expected that detailed further studies will continue in future on this group of insects in Turkey.

An evolutionary perspective on biological invasions: insights from the harlequin ladybird, *Harmonia axyridis.*

Lori Lawson Handley[1], Cathleen Thomas[1], Remy Ware[2], Michael Majerus[2]

[1]University of Hull, Hull, United Kingdom, [2]University of Cambridge, Cambridge, United Kingdom

Biological invasions are one of the greatest threats to global biodiversity, agriculture and the economy, but we are a long way from understanding why certain species become invasive, what factors determine their success, and the impacts on the native species with which they interact. An understanding of evolutionary genetics is critical to establish the causes and consequences of invasions, since the genetic make-up of the founding population determines how it will adapt to new conditions and expand its range. Genetic data has revealed that the evolutionary history of invasive species is often complex, for example with multiple introductions or rapid population growth despite genetic bottlenecks in the founding population. Invasive species with well-documented colonisation and expansion histories provide us with excellent models to examine the evolutionary genetics of invasions. One such species is the harlequin ladybird, *Harmonia axyridis,* which is native to central and eastern Asia, and invading other regions including the USA, Europe and South Africa. Since its first recording in Kent in 2004, the UK invasion of *H. axyridis* has advanced at an incredible pace. We are currently investigating the factors contributing to the invasion success of *H. axyridis* in the UK, including the genetic make-up of the founding population, presence of suitable habitat and climatic conditions, and escape from natural enemies. This talk will focus on the theory and justification for an evolutionary perspective on biological invasions, but will also present preliminary data from our study on the evolutionary genetics of *H. axyridis*.

A global indicator for insect invasions: possibilities and challenges

Melodie McGeoch

Centre for Invasion Biology, Department of Conservation Ecology & Entomology, University of Stellenbosch, Stellenbosch, South Africa

Trends in invasive alien species is one of only two headline indicators of threat to biodiversity that forms part of the Convention on Biological Diversity's framework for monitoring progress towards the 2010 target. However, to date there is no fully developed indicator for invasive alien species that combines trends, derived from a standard set of methods, across species groups, ecosystems and regions. McGeoch et al. (2006) proposed such an indicator to meet the 2010 framework goal and targets. Based on broadly accepted principles for biodiversity indicators, single and composite indicators of the status of, and trends in, invasive alien species are used at national and global scales. The indicator includes problem-status and management-status measures, and is designed to be scalable, flexible, readily disaggregated and as far as possible draw on existing data. However, the indicator remains to be tested, in particular to assess its suitability for including poorly known taxa, such as invertebrates. Here I examine the application of the indicator to a sub-Antarctic database of alien species, including invertebrates, and in conjunction with other insect examples assess the options for a global indicator of insect invasions.

Anaerobic respiration by the mangrove ant, *Camponotus anderseni*

Mogens Gissel Nielsen

University of Aarhus, Aarhus, Denmark

Introduction: The small tree-living mangrove ant *Camponotus anderseni* McArthur & Shattuck is remarkably adapted for surviving tidal inundation. By blocking the nest entrance with a soldier's head, water intrusion into the nest cavity can be effectively prevented, but lack of gas-exchange caused extremely high concentrations of CO_2 (>30%) and very low O_2 concentrations (< 1%).

Results: The O_2 uptake in experiments with CO_2 absorption showed a linear decrease until about 4%, whereas the O_2 uptake in chambers without absorbent showed a decrease with a different pattern, consisting of three parts. The first component of this decrease is a linear decrease to about 18%, which is the normal O_2 concentration in open natural nests. The second phase is an exponential decrease continuing to about 4% O_2, showing that the CO_2 concentrations have influence on the O_2 uptake. The final component is also exponential, but with a much smaller slope.

The Respiratory Quotient (RQ) was 0.92 until CO_2 concentration increased to about 15-17%, and after that it showed a strong increase, which is due to the initiation of anaerobic respiration.

Chemical analyses of ants which have experienced anoxic conditions showed no sign of L-lactose, whereas NMR spectroscopy on very few samples shoved a complex changes in concentrations of several metabolites. RNM spectroscopy is currently carried out on a large material, and the results of these findings will be presented.

Conclusions: Anaerobic respiration has not been demonstrated for social insects before, but it is not surprising that it is found in this ant species, which lives in the extreme conditions of a hollow twig in an inundated mangrove.

The importance of stem groups and the need for an integrated approach to insect systematics

Sam Heads

Palaeobiology Research Group, University of Portsmouth, Portsmouth, United Kingdom

The importance of stem groups has been well documented by palaeontologists, who regularly find themselves faced with their novel combinations of plesiomorphic and derived character states. Within entomology, there are two camps: (1) neoentomologists, working exclusively on living taxa; and (2) palaeoentomologists, working exclusively on fossil taxa. Palaeoentomologists engaged in systematic work on fossil insects often disregard the living representatives of the groups they study. In the same token, neoentomologists regularly embark on large phylogenetic revisions of living taxa without considering the wealth of data available from fossils. It is becoming increasingly apparent that stem groups have much to offer in terms of morphological data and are invaluable in establishing character polarities for cladistic analyses. In this respect, fossil taxa are as important as living representatives in phylogenetic studies, where their novel combinations of character states can radically alter tree topology. Here I will illustrate this with examples from my own research on stem-group Orthoptera from the Early Cretaceous of Brazil, and advocate a more integrated approach to the study of fossils. Valuable data is available from both fossil and extant taxa and omitting such data is counterproductive. The future of palaeoentomology requires the study of fossil insects within a more contextualised phylogenetic framework. Similarly, the origins and phylogenetic relationships of modern taxa can never be fully realised without knowledge of their stem groups.

Impacts of the vector-delivered invasive pest, pinewood nematode: process-based modelling of the likelihood of wilt expression.

Hugh Evans, Sam Evans, Makihiko Ikegami

Forest Research, Alice Holt Lodge, Farnham, Surrey, GU10 4LH, United Kingdom

Pinewood nematode (PWN), *Bursaphelenchus xylophilus*, native in North America and normally a saprophytic organism, can induce rapid wilting and tree death given susceptible trees and suitable eco-climatic conditions. Large-scale tree mortality from PWN infestation has taken place in Japan, China, Korea and Portugal where it is an alien invasive. Mortality is driven by the nematode-plant-environment interaction after nematodes enter the host tree during maturation feeding by adult vector beetles (*Monochamus* spp). Although wilt appears to be linked primarily to summer temperature, the mechanisms behind this are unclear. The current study has described this interaction using a process-based model incorporating tree water-carbon relations and the impacts of pinewood nematode on tree physiology. It employs a fully coupled, point scale and daily time step soil-vegetation-atmosphere transfer model incorporating parameters for a forest stand of known structure, with locally determined soil and climate conditions. This 'grows' the trees and produces outputs for key physiological parameters. In the model, PWN is assumed to feed on living tissues, such as parenchyma and cambium, leading to xylem cavitation. The model simulates progression or recovery from xylem cavitation under various environmental conditions. Simulations indicate that high ambient temperatures are the main drivers of irreversible cavitation, but the outcome is tempered by soil moisture availability. In addition, the model predicts that tree mortality can occur either in the year of nematode infestation or in the following year, which has significant implications for managing the PWN problem.

Effect of floral traits and display area on insect visitation rates in lowland vegetation in the Cape Floristic Region

Sven Vrdoljak, Michael Samways

Stellenbosch University, Stellenbosch, South Africa

Introduction: Insects are important pollinators in the Cape Floristic Region, yet interactions between plants and insects, particularly at the community level, are still not fully understood. An important part of these interactions are the mechanisms by which plants attract pollinators. In this study we examine how various floral traits relate to the visitation frequency of species in a plant community during a period of peak flowering.

Methods: Visits by pollinating insects to flowers were observed in 20 standardised plots in the lowlands of the Cape Floristic Region. Each plot was observed for four ten minute intervals, repeated over four days in October 2007. Various floral traits were recorded for all flowering species in the plots and flowers in each plot were counted daily allowing total floral display areas to be calculated per plot.

Results: In total, 1771 visitations were observed in 280 observation periods. Beetles, in particular monkey beetles (Scarabaeidae: Hopliini), were the most frequent flower visitors in this study, accounting for nearly 30% of all visits. Traits such as flower form and colour were found to be significant only in certain cases, whereas visitation frequency showed a strong positive correlation to the size and density of floral displays.

Conclusions: Variation in visitation frequency to plant species is best explained by continuous variables such as the size and density of floral displays rather than other floral traits at the local scale. This concurs with other studies that indicate more non-specific relationships between insects and flowers at the community level.

Immune Responses and Their Potential Role in Insect Outbreaks

Markus Rantala

University of Turku, Turku, Finland

Introduction: Most insect populations do not reach outbreak densities, but some species are known from having populations that never reach outbreak densities as well as populations that display both irregular and regular outbreaks. The long lasting debate about the relative contributions of bottom up and top down factors in population dynamics i.e. in terminating outbreaks, have overshadowed the more important question: why the population densities start to rise in some populations. Parasites and pathogens have been found to regulate insect populations in many theoretical and empirical studies. However, insects are not helpless victims of parasites and pathogens and co-evolutionary processes have favoured the evolution of an effective immune defence system. Thus, the changes in hosts' immune defence may affect the success of parasitoids and pathogens in the host population and potentially may destabilize insect-pathogen dynamics and make control of the insect population by the disease and parasites less likely.

Results: In this talk I present evidence on the autumnal moth (*Epirrita autumnata*) and the gypsy moth (*Lymantria dispar*) that delayed inducible plant defences consequent to grazing by herbivorous insects may be linked to the performance of pathogens through increased immunocompetence of the herbivore feeding on the foliage, in which the defence induction has taken place.

Conclusions: This enhanced immunity of herbivorous insects caused by delayed induced resistance of plant may be the positive feedback effect that enables the increase in the density of moth population.

Effects of pirimicarb, buprofezin and pymetrozine on survival, development and reproduction of *Coccinella undecimpunctata* (Coleoptera: Coccinellidae).

Susana Cabral, Patrícia Garcia, António O. Soares

CIRN, Department of Biology, University of the Azores, Ponta Delgada, Azores, Portugal

Introduction: *Coccinella undecimpunctata* L. (Coleoptera: Coccinellidae) is a euryphagous predator that feeds especially on aphids and can acts as an effective biological control agent against these pests. Although *C. undecimpunctata* has a large geographic range, few studies have assessed the susceptibility of this species to insecticides. To further the development of Integrated Pest Management (IPM) against sucking pests, we evaluated the lethal and sublethal effects on C. undecimpunctata of three insecticides used for control of aphids and/or whiteflies: pirimicab (neurotoxic), buprofezin (insect growth regulator) and pymetrozine (antifeedant).

Methods: The effects of those insecticides on *C. undecimpunctata* were assessed by studying, under laboratory conditions, the survival and development of all preimaginal stages and, the survival and reproductive performance of the adults. For each insecticide treatment, were used the doses recommended by the manufacturer for the control of aphids and/or whiteflies.

Results: None of the three insecticides had significant effect on the survival of *C. undecimpunctata* eggs. When sprayed on larvae, buprofezin significantly reduced survival to adulthood to <33%, compared to > 45% for the control and other insecticide treatments. Rates of adult survival, fecundity, and fertility, and the percentage of egg hatch, were not significantly different between control and insecticide treatments. Thus larval stages were more susceptible to insecticides than were adults.

Conclusions: In general, pirimicarb and pymetrozine had no adverse effects on immature or adult stages of *C. undecimpunctata*, and hence are suitable for IPM of sucking pests.

Native and introduced dung beetles (Scarabaeidae: Aphodidae) using cattle dung in Madagascar

Heidi Viljanen[1], Pierre Rahagalala[2], Ilkka Hanski[1]

[1]University of Helsinki, Helsinki, Finland, [2]University of Antananarivo, Antananarivo, Madagascar

Introduction: Endemic Malagasy dung beetles have radiated with a diverse group of primates (lemurs), the largest native herbivores on the island. Cattle was introduced to Madagascar about 1,500 yrs ago, and thus cattle dung represents a new type of resource for indigenous dung beetles. The most specious dung beetle tribes in Madagascar, endemic Helictopleurini (65 species) and Canthonini (ca 170 species), occur primarily in forests and feed on lemur feces and carrion. In addition, there are three species of Scarabaeini, six species of Onthophagini, and 30 species of Aphodiini and Didactyliini (Aphodiidae) in Madagascar, representing both endemic and introduced species with mostly unknown ecologies.

Methods: We sampled 73 open area localities across Madagascar for dung beetles using cattle dung.

Results: Samples included 28 dung beetle species. Species composition is very homogenous in open areas across the island due to wide ranges of the species, which is in striking contrast to small ranges in forest-inhabiting species. Four endemic Helictopleurini species have been able to switch to cattle dung in open areas and thereby probably expand their ranges in comparison with relatives inhabiting forests. Aphodiini has been able to colonise eastern wet forests, where several endemic species with restricted ranges occur. In contrast, Scarabaeini and Onthophagini occur only in open areas and have not been able to enter wet forests, most likely due to competition with the older Helictopleurini and Canthonini.

Conclusions: Cattle dung is primarily used by introduced dung beetles in Madagascar, but a few endemic species have been able to switch to cattle dung and thereby greatly extend their ranges.

Science on Six Legs: The Insect Connection for Public Outreach

Frank Turpin, Steve Yaninek, Melissa Shepson

Purdue University, West Lafayette, Indiana, United States

Historically one of the goals of some entomologists and entomology departments around the world has been has been to connect with the general public. Today we categorize such programs as outreach and these programs provide an opportunity to engage and teach students and the general public about science using insects as the medium. Current Purdue University programs dedicated to outreach include: “Insectaganza” a program centered on insects which provides 5th grade students with a college-type experience, “Bug Bowl” a festival-type event for the general population which features insects, cockroach racing at the Indiana State Fair, a butterfly count involving people from the local community, and special presentations at schools or for groups that visit campus. These programs engage the audience and connect the public to the science of entomology in a fun way to promote science literacy. The events also provide a training opportunity for Purdue students to develop presentation skills and create programs that are useful for outreach. Our outreach efforts have increased the visibility of the Department of Entomology at Purdue University and enhanced public appreciation for insects and science.

Cognitive processes involved in decision making by honey bees: applications for agriculture

Sharoni Shafir

Hebrew University of Jerusalem, Rehovot, Israel

Introduction: About one-third of our diet is attributed to pollination services provided by insects, predominantly by honey bees. The saying "you can lead a horse to water, but you can't make him drink" applies to the use of honey bees for crop pollination. Bee hives can be placed in the orchard, but ultimately the bees are free to choose which flowers to visit and whether to collect nectar or pollen. Furthermore, bees can be used to efficiently deliver biological agents to control fruit disease. Thus, it is valuable for improving crop quantity and quality to understand, and possibly influence, the bees' decision making processes.

Methods: I will illustrate some techniques used to study bee cognition in studies ranging from basic to applied research. These include the proboscis-extension response paradigm with harnessed bees in the lab, choice of free-flying bees between artificial flowers in enclosures, and assessment of foraging behavior in the field. In addition, hive management techniques and selective breeding can influence the bees' foraging behavior.

Results: Findings from basic research show that bees do not assess absolute values of rewards, but rather that their evaluations are comparative and depend on the other available options. We also have a better understanding of how bees evaluate

variability in rewards. More applied research has concentrated on avocado and various Rosaceae crops (apples, pears, plums). We found that the high mineral content of avocado nectar reduces its attractivity to bees, which is also manifested in their recruitment dances. In Rosaceae crops, naïve bees are better pollinators than experienced bees, which learn to rob the flowers or to forage elsewhere. These findings could guide the management of orchards that will be more attractive to bees. For example, sequential introductions of bee hives into Rosaceae orchards has greatly increased fruit set and yield.

Conclusions: Honey bee perception and decision-making and subsequent behavior determine the quality of services that bees provide to agriculture. The knowledge base from basic research in bee cognition, in addition to applied research, can yield solutions to agricultural problems. Selective breeding can further contribute to developing bee lines with desirable behavioral traits.

Sciapodinae from Baltic amber (Diptera: Dolichopodidae): systematic position and possible palaeoclimatic implications

Igor Grichanov

All-Russian Institute of Plant Protection, St. Petersburg, Pushkin, Russian Federation

The subfamily Sciapodinae was first recorded from Baltic amber (BA) by Meunier (1907), but some other species were misplaced by him at generic level. Bickel (1994) supposed that species described by Meunier in the genus *Nematoproctus* belong to the sciapodine genus *Mesorhaga*. Negrobov and Selivanova (2003) described four BA species of *Amesorhaga*. H. Ulrich (pers.com.) has noted after examination of the type material that *Wheelerenomyia* is a sciapodine genus, as also *Neurigona* sensu Meunier (Grichanov, 2008). The comparison of descriptions and figures provided by Meunier, Negrobov & Selivanova leaves no doubt that all 15 species from BA with strongly sinuate vein M should be transferred into the fossil genus *Wheelerenomyia*. This genus is also known from Ukrainian amber, being recorded previously as *Neurigona* (Grichanov, 2000).

There is practically no true Sciapodini+Chrysosomatini in BA, as fossil specimens have distinct preapicals on mid and hind femora and unbranched M. *Wheelerenomyia* is close to Mesorhagini, differing in many plesiomorphic characters. Tertiary Baltic-Dnieper Subprovince embraces large area of modern Europe. Bickel noted that its fauna has no any Gondwanan palaeotropical elements, and the western Palaearctic appears to have been isolated to recent time. Therefore, it is not surprising that extant Mesorhagini are absent in Europe and adjacent regions. The question is still open: could *Wheelerenomyia* give origin to other sciapodine clades? Anyway, their comparative abundance in amber correlates with mainly tree trunk and tree canopy habitats of almost all Sciapodinae. The subfamily is now basically pantropical that supports opinions about subtropical climate of the Baltic region during the Eocene.

Mass occurrences of *Thaumatomyia notata* (Diptera: Chloropidae) on buildings in Europe

Marion Kotrba[1], Emilia Narchuk[2]

[1]Zoologische Staatssammlung München, München, Germany, [2]Zoological Institute, Russian Academia of Sciences, St. Petersburg, Russian Federation

Introduction: Mass occurrences of *Thaumatomyia notata* on buildings in fall have been known and described in the literature for centuries. They constitute a considerable nuisance for the inhabitants and can even diminish the monetary value of a particular building. The reasons for their appearance at the same location year after year are still not understood and effective control strategies have yet to be developed.

Results: Based on literature records and numerous own observations, the phenomenon of the mass occurrences with tens of millions of flies hibernating in the top region of certain buildings is described. The present state of knowledge on the biology of the species and its hygienic and economic implications for man are summarized. More than 350 historic and new data are evaluated regarding the distribution of the mass occurrences in time and space and their possible correlation with climatic factors. The distribution spans almost all of Europe between 42-61° N. An all time high in southern Bavaria was reached in 2003 after a particularly long and hot summer, with more than 100 cases reported from the region between Munich and the Alps alone.

Conclusions: Mass occurrences of *T. notata* on buildings are not a rare and, therefore, negligible problem. It is expected that with the current global warming the problem will persist or even increase. The need for effective control strategies calls for a sound investigation of the biology of this species and especially the orientation mechanisms on which the formation of the aggregations is based.

Arrival and rapid spread of *Harmonia axyridis* (Coleoptera: Coccinellidae) in South Africa

Riaan Stals

South African National Collection of Insects, Queenswood, Pretoria, South Africa

The Asian lady beetle *Harmonia axyridis* (Pallas) (Coleoptera: Coccinellidae) has emerged as a significant invasive organism in recent years, being eurytopic, broadly polyphagous, very dispersive and phenotypically highly plastic. It can cause complex ecological effects involving changes in invaded communities, besides impacting on agriculture and human health, and potentially being a household nuisance.

Harmonia axyridis established widely in Western Europe since the 1980s. By 1988 it had established in the USA, and subsequently spread rapidly throughout most of the continental USA and southern Canada. In South America, the invader was first recorded in 2002. It reached the UK in 2004 and Scandinavia in 2007. In all of its adopted ranges it spreads rapidly, widely establishing feral populations.

Harmonia axyridis has now also appeared in South Africa, the first known established population discovered in Spring 2004 at Riviersonderend, Western Cape Province. The species' identity was only confirmed in 2006. Subsequently, a South African specimen collected in December 2002 came to light in an European museum.

No structured sampling has been done, yet the rapid spread of *H. axyridis* in South Africa has been noted. It was found in the Eastern Cape Province in Summer 2005/2006, some 600 km from the Riviersonderend locality. Reports of its presence in the eastern Free State Province started in May 2007. In November 2007 it was found in numbers in the KwaZulu-Natal Midlands, and in the Gauteng Province the first specimens were discovered in January 2008. These localities are all widely separated.

There is no reason to seriously doubt that *H. axyridis* will spread rapidly throughout much of South Africa and beyond and bring to bear its negative invasive characteristics here. The early detection of this apparently inadvertent introduction to South Africa presents a rare opportunity to study an anticipated biological invasion virtually from its incipience.

Effects of different routes of exposure to pesticides on the predatory mite *Phytoseiulus persimilis* Athias-Henriot (Acari Phytoseiidae) and its prey

Carlo Duso, Alberto Pozzebon, Paola Tirello, Paulina Bermudez Ortiz

University of Padua, Padova, Italy

Phytoseiulus persimilis Athias-Henriot (Acari Phytoseiidae) is a major predator of spider mites, in particular of *Tetranychus urticae* (Acari Tetranychidae). Predator-prey interactions may be affected by pesticides used to control other pests, and thus knowledge of pesticide side-effects is essential to manage spider mite populations following IPM tactics. Here, we present the results of laboratory studies involving both predator and prey that considered differential routes of exposure. Insecticides with different modes of action and in-plant translocation (e.g. spinosad, thiamethoxam) were used. We evaluated the pesticide effects on *T. urticae* females exposed to pesticide leaf residues, topical applications and systemic applications. Regarding *P. persimilis*, we also considered the effects induced by the contaminated prey. The evaluation of the pesticides impact in relation to differential routes of exposure considered mite survival, fecundity and egg-hatching. The implications of these studies for IPM are discussed.

Ecology of harvesting in stingless bees

Marilda Laurino

University of São Paulo, São Paulo, SP, Brazil

Introduction: Stingless bees are social bees living in tropical and subtropical areas of the world, and today they encompass over 600 species. Considering pollen analysis and collection in flowers, they are polytrophic, which is associated to its perennial nest and social life.

Methods: Most of the bees studied are located in a small experimental station placed in the Amazon forest, specifically Xapuri - Acre. The flight activities, the harvested material, as well as the nests, were observed during dry and rainy seasons. Nectar collected by workers returning to the nest and males in congregations were compared.

Results: The bees harvested all day long, nonetheless the peak of activities occurred in the first hours of the day. Regarding the botanic origin of the pollen, most of them presented Myrtaceae pollen as a dominant component (> 75.8%). Rubbery-gum resin, which was present in small quantities in dry season, has an orange color and oval seeds tagged along with it. Mud appeared only in the rainy season. Meliponini males when leaving their nests may form congregations where they dehydrated nectar with 11-27% of sugar whereas returning workers with 18-36%.

Conclusions: The bees harvest different proportion of resource according to each season, but they still continue to maintain fidelity to temperature and humidity for these activity. Seeds tagged along with the resin make bees another dispersal instrument of some Amazon flowers. Volume and percentage of nectar sugar from males were always lower than those sampled from returning foragers.

Competitive Exclusion Principle and Understanding Parasitoid Success

Robert Luck

University of California, Riverside, Riverside California, United States

Aphytis melinus, an ectoparasitoid of California red scale, *Aonidiella aurantii*, was introduced into southern California citrus groves in 1957. Once established, it rapidly displaced its congener, *Aphytis lingnanensis*. By 1967, it had excluded *A. lingnanensis* from most of the interior groves where it once had been the dominate parasitoid. Although *A. melinus* had also been released in the intermediate inland groves, it took another six or seven years for it to displace *A. lingnanensis* from them. By 1972, *A. lingnanensis* had been relegated to the cooler coastal groves. We also found that both *Aphytis* species allocated male offspring to smaller scales and female offspring to larger scales. Of more interest was the comparison of the scale size from which the female *Aphytis* emerged: *A. lingnanensis* females emerged from larger scales than did *A. melinus* females. Moreover, *A. melinus* offspring emerging from these larger scales where sometimes gregarious, yielding one male and one female or one male and two females. Thus, although these parasitoids utilized the same red scale stages, *A. melinus* produced daughters on a smaller scale and more daughters on larger scales than did *A. lingnanensis.* It was this difference in female progeny production that led to the displacement of *A. lingnanensis* from most of southern California. We then used this information to develop an augmentative release program to suppress California red scale in San Joaquin Valley citrus where third instar scales are small and their age structure is more synchronized than it is in southern California citrus groves.

Community modules and trait-mediated effects: Some theoretical perspectives

Robert Holt

University of Florida, Gainesville, Florida, United States

There is now a large amount of theory on “community modules” – small numbers of species interacting in defined configurations, such as apparent competition, food chains and intraguild predation. Until recently this body of theory assumed organisms had fixed traits, but there is increasing interest in examining the community-level consequences of labile traits. In this paper, I will revisit some classic results for such modules (e.g., involving the potential for trophic cascades, the conditions for prey coexistence, and system stability along productivity gradients), and ask how these conclusions are altered if one incorporates trait-mediated effects. I will touch on commonalities and differences between plastic trait responses, and evolutionary trait responses. Part of my talk will be a review, and part will be new material.

Development of control tactics against the invasive cactus moth, *Cactoblastis cactorum*, in North America

Stephen Hight[1], James Carpenter[2], Stephanie Bloem[3], Kenneth Bloem[3], Joel Floyd[4]

[1]USDA-ARS, Center for Medical, Agricultural, & Veterinary Entomology, Tallahassee, FL 32308, United States, [2]USDA-ARS, Crop Protection Management and Research Unit, Tifton, GA 31794, United States, [3]USDA-APHIS, Center for Plant Health Science Technology, Raleigh, NC 27606, United States, [4]USDA-APHIS, Plant Safeguarding & Pest Identifications, Riverdale, MD 20737, United States

Introduction: The most successful classical biocontrol of weeds program has been the control of invasive prickly-pears (*Opuntia* spp.) by the Argentine cactus moth *Cactoblastis cactorum*. However, the moth has invaded North America and its ability to control its host plant raises concerns for the safety and survival of the many important *Opuntia* spp. in North America.

Methods: A variety of tools and tactics were developed to study and control *C. cactorum*. A survey tool was developed to identify the presence of the moth. Insecticide trials were conducted. In support of a Sterile Insect Technique (SIT), studies were conducted on mass rearing, radiation biology, overflooding ratios, transport - cold storage - release techniques, and sanitation efforts.

Results: Mating of *C. cactorum* takes place within the hour before sunrise. Female sex pheromone components were characterized, and a sticky-bottom wing trap baited with a synthetic female pheromone lure was developed as the survey tool. This trap identified three generations/year in the USA across a large latitudinal gradient. Three insecticides effectively killed eggs and neonate larvae. A radiation dose of 200 Gy is sufficient to fully sterilize females.

Conclusions: Wing traps are a useful survey tool to identify when and where wild insects are present and where to deploy the SIT. Sanitation and SIT are complimentary control tactics. Sanitation is effective in high populations and SIT is effective in low populations. Insecticides may be useful to control *C. cactorum* if restrictions are placed on the movement of Opuntia nursery stock.

Coevolution and the adaptive value of autumn tree colours: colour preference and growth rates of a southern beech aphid

Claudio Ramirez, Blas Lavandero, Marco Archetti

[1]*Universidad de Talca, Talca, Chile,* [2]*University of Oxford, Oxford, United Kingdom*

Introduction: The evolutionary explanation for the change in leaf colour during autumn is still debated. Autumn colours could be a signal of defensive commitment towards insects (coevolution) or an adaptation against physical damage due to light at low temperatures (photoprotection). These two hypotheses have different predictions. Insects should not prefer red leaves in autumn and grow better in spring on trees with green autumn leaves (coevolution) and should prefer and grow better on trees with red leaves because they provide better nutrition (photoprotection).

Methods: In central Chile we studied field abundance of *Neuquenaphis staryi* on trees of *Nothofagus alessandrii* differing in colours in autumn. We also performed a laboratory choice test of colour preference and measured in the field the performance in spring of aphids born on trees that had different leaf colours in the previous autumn.

Results: We found higher abundance of aphids on green rather than red or yellow trees, preference for green leaves in autumn but no differential performance of aphids in spring. No correlation was found between the growth rates of aphids in spring and the autumn colours of the trees.

Conclusions: Preference for green in autumn is consistent with the coevolution theory, but lack difference in growth rate of aphids in spring is not. Autumn colours would confer an advantage to the tree by reducing the impact of parasites but the advantage for aphids seems to be restricted to autumn and not related to growth rates in spring.

Intraspecific variability in the number of larval instars in insects

Toomas Esperk[1], Toomas Tammaru[1], Sören Nylin[2]

[1]University of Tartu, Tartu, Estonia, [2]Stockholm University, Stockholm, Sweden

The number of larval instars varies widely across insect species. However, intraspecific variability in the number of instars is not an exceptional phenomenon either. Nevertheless, the knowledge about the subject has remained fragmentary. In our recent review (J. Econ. Entomol. 100: 627-645), we show that intraspecific variability in the number of larval instars is widespread across insect taxa, occurring in most major orders, in both hemimetabolous and holometabolous insects. Temperature, photoperiod, food quality and quantity, humidity, rearing density, physical condition, inheritance and sex are the most common factors influencing the number of instars. We discuss adaptive scenarios, which may provide ultimate explanations for the plasticity in instar number. The data available largely support the compensation scenario, according to which instar number increases in adverse conditions when larvae fail to reach a species-specific threshold size for metamorphosis. In more specific cases, the adaptive value of the variability in instar number may be in reaching or maintaining the developmental stage adapted to hibernation, producing additional generations in multivoltine species, or increasing the probability of surviving in long-lasting adverse conditions. Finally, we present a life-history perspective of the reaction norms for age and size at maturity for individuals developing through different number of instars.

Activity evaluation of cocoa pod borer sex pheromone in different geographic locations and in cacao fields in Malaysia and Indonesia

Aijun Zhang, Lip Foo Kuang, Navies Maisin, Bhanu Karumuru, David Hall, Ike Virdiana, Smilja Lambert, Hussin Bin Purung, Shifa Wang, Prakash Hebbar

USDA, ARS, PSI, Beltsville/MD, United States

Introduction: The cocoa pod borer, *Conopomorpha cramerella* (Snellen) (Lepidoptera: Gracillariidae), has been reported as the most serious pest of cacao, *Theobroma cacao* L., in Southeast Asia. The sex pheromone of *C. cramerella* were identified in 1986 and field tested in Sabah, Malaysia. However, the use of pheromones against *C. cramerella* was halted in the early 1990s attributed to the possibility of existence of more than one strain of *C. cramerella* in Asia that behaved differently to the pheromone blend.

Methods: Activity of synthetic sex pheromone was re-evaluated using the Delta trap in the cacao fields and release rate of pheromone formulation was tested in the laboratory condition.

Results: It was found that lures containing 100-µg of synthetic sex pheromone blend, (*E,Z,Z*)- and (*E,E,Z*)-4,6,10-hexadecatrienyl acetates and the corresponding alcohols in a ratio of 40:60:4:6 in a polyethylene vial, attracted male *C. cramerella* moths in Sabah and peninsular Malaysia and in Sumatra and Sulawesi, Indonesia, suggesting that the same pheromone strain existed in a wide stretch of the Indo-Malayan archipelago. A release rate study of pheromone formulation demonstrated that a satisfactory “half-life time” of a 100-µg loading is about 6-wk.

Conclusions: Our research results had shown that the presence of a single pheromone strain of *C. cramerella* in a wide geographic region extending throughout the Indo-Malayan archipelago. Development of cost-effective pest management strategies should also include pheromone-based monitoring, mass trapping, and possibly mating disruption at a later date, in addition to regular and complete harvesting, rational use of effective pesticides, biological control, and plastic sleeving.

Activity evaluation of cocoa pod borer sex pheromone in different geographic locations and in cacao fields in Malaysia and Indonesia

Aijun Zhang, Lip Foo Kuang, Navies Maisin, Bhanu Karumuru, David Hall, Ike Virdiana, Smilja Lambert, Hussin Bin Purung, Shifa Wang, Prakash Hebbar

USDA, ARS, PSI, Beltsville/MD, United States

Introduction: The cocoa pod borer, *Conopomorpha cramerella* (Snellen) (Lepidoptera: Gracillariidae), has been reported as the most serious pest of cacao, *Theobroma cacao* L., in Southeast Asia. The sex pheromone of *C. cramerella* were identified in 1986 and field tested in Sabah, Malaysia. However, the use of pheromones against *C. cramerella* was halted in the early 1990s attributed to the possibility of existence of more than one strain of *C. cramerella* in Asia that behaved differently to the pheromone blend.

Methods: Activity of synthetic sex pheromone was re-evaluated using the Delta trap in the cacao fields and release rate of pheromone formulation was tested in the laboratory condition.

Results: It was found that lures containing 100-µg of synthetic sex pheromone blend, (*E,Z,Z*)- and (*E,E,Z*)-4,6,10-hexadecatrienyl acetates and the corresponding alcohols in a ratio of 40:60:4:6 in a polyethylene vial, attracted male *C. cramerella* moths in Sabah and peninsular Malaysia and in Sumatra and Sulawesi, Indonesia, suggesting that the same pheromone strain existed in a wide stretch of the Indo-Malayan archipelago. A release rate study of pheromone formulation demonstrated that a satisfactory “half-life time” of a 100-µg loading is about 6-wk.

Conclusions: Our research results had shown that the presence of a single pheromone strain of *C. cramerella* in a wide geographic region extending throughout the Indo-Malayan archipelago. Development of cost-effective pest management strategies should also include pheromone-based monitoring, mass trapping, and possibly mating disruption at a later date, in addition to regular and complete harvesting, rational use of effective pesticides, biological control, and plastic sleeving.

The spread of viral and parasitic diseases due to climate change

Andrew Githeko

Kenya Medical Research Institute, Kisumu, Kenya

Today's life styles are energy dependent and energy intensive. For example in 2005 the daily global consumption for petroleum was 85 million barrels/day. Human activities produce gases such as carbon dioxide, methane, nitrous oxides and fluro-carbons, known as green house gases and which are deposited in the atmosphere. Evidence of climate change includes an increase in the mean temperature and larger magnitude in departures from the mean temperature.

Insects and micro-organisms cannot regulate their internal temperature and their reproduction and feeding rates is dependent on external temperature. Insects such as mosquitoes, ticks, mites and snails carry human diseases and their populations' sizes are dependent on environmental factors including temperatures. Some of these insects cannot survive in low or very high temperatures and because of this some disease have been absent in regions that experience long periods of low temperatures. However as the earth's climate continues to change the insects are adapting to the new world.

In recent years changes have been observed in the distribution of insect-borne diseases such as malaria, dengue, Lyme disease and West Nile Fever. Evidence of changing disease patterns from Africa, Europe, North and South Americas and Asia indicate that this is a global phenomenon where the common factor is climate change. In Eastern Africa the frequency of malaria epidemics in the highlands and the spread of the disease to new areas have been observed.

Effect of a retardant dose of glyphosate on biocontrol agents of water hyacinth, *Eichhornia crassipes* (Mart.) Solms-Laubach

Ashwini Jadhav[1], Martin Hill[2], Naweji Katembo[1], Marcus Byrne[1]

[1]University of the Witwatersrand, Johannesburg, South Africa, [2]Rhodes University, Grahamstown, South Africa

Introduction: Water hyacinth, *Eichhornia crassipes* (Mart.) Solms-Laubach (Pontederiaceae) has a negative impact on aquatic ecosystems in South Africa despite biocontrol which remains hampered by high nutrient levels and low temperatures. Often, the biocontrol agents are unable to overcome rapid weed growth, necessitating the need for intervention by herbicidal control. However, lethal doses of herbicides have adverse environmental consequences and may kill the biocontrol agents,

Methods: This study tested the effects of a retardant dose of glyphosate on the water hyacinth weevils, *Neochetina eichhorniae* Warner and *N. bruchi* Hustache, and the water hyacinth mirid, *Eccritotarsus catarinensis* (Carvalho). Beetles and mirids were exposed to the herbicide indirectly by spraying plants with glyphosate. Insect numbers were counted and feeding scars were recorded in the laboratory trials and field trials. Survival, feeding and reproduction were recorded.

Results: A retardant dose of 0.8% glyphosate did not influence numbers of adult insects or the immature stages, thereby maintaining population numbers on the weed. However, the retardant dose stunted the growth of the weed in terms of ramet production, but did not kill the plants, thereby preserving the habitat for the biocontrol agents since the mat did not sink. The herbicide may improve the quality of the plant for insect herbivores.

Conclusion: This method offers a low impact, integrated weed management tool for weed affected water systems.

Effect of a retardant dose of glyphosate on biocontrol agents of water hyacinth, Eichhornia crassipes (Mart.) Solms-Laubach

Ashwini Jadhav[1], Martin Hill[2], Naweji Katembo[1], Marcus Byrne[1]

[1]University of the Witwatersrand, Johannesburg, South Africa, [2]Rhodes University, Grahamstown, South Africa

Introduction: Water hyacinth, *Eichhornia crassipes* (Mart.) Solms-Laubach (Pontederiaceae) has a negative impact on aquatic ecosystems in South Africa despite biocontrol which remains hampered by high nutrient levels and low temperatures. Often, the biocontrol agents are unable to overcome rapid weed growth, necessitating the need for intervention by herbicidal control. However, lethal doses of herbicides have adverse environmental consequences and may kill the biocontrol agents,

Methods: This study tested the effects of a retardant dose of glyphosate on the water hyacinth weevils, *Neochetina eichhorniae* Warner and *N. bruchi* Hustache, and the water hyacinth mirid, *Eccritotarsus catarinensis* (Carvalho). Beetles and mirids were exposed to the herbicide indirectly by spraying plants with glyphosate. Insect numbers were counted and feeding scars were recorded in the laboratory trials and field trials. Survival, feeding and reproduction were recorded.

Results: A retardant dose of 0.8% glyphosate did not influence numbers of adult insects or the immature stages, thereby maintaining population numbers on the weed. However, the retardant dose stunted the growth of the weed in terms of ramet production, but did not kill the plants, thereby preserving the habitat for the biocontrol agents since the mat did not sink. The herbicide may improve the quality of the plant for insect herbivores.

Conclusion: This method offers a low impact, integrated weed management tool for weed affected water systems.

Insects in Asian culture

Kenichi Nonaka

Rikkyo University, Tokyo, Japan

Insects are an important natural resource, both for self-sufficiency and as commercial products in South-east Asia including Korea and Japan. People living there have established various relationships with large amounts of many species of insects such as food, medicine, ornaments, decoration and other miscellaneous uses and adaptations including insect repellents. Insects are also portrayed in songs, tales and beliefs. They also reflect regional preferences and socio-cultural significance, which can be described in terms of regional differences. Activities involved in collecting insects, and also their habitats, are related to subsistence farming, which mainly consists of rice cultivation in the rural areas, where land-use involves a combination of paddy fields and surrounding forests. This study explores and discusses some of the diverse relationships between humans and insects in Asia, where there are various nations and a range of different levels of subsistence as well as diverse environmental conditions, and goes on to discuss the characteristics of insect-use in relation to rice-cultivation and related other subsistence activities and commercialization arising from economic development. Case studies are discussed based on the author's fieldworks focusing the collecting and cooking, marketing and nature-society relationship.

Seasonal distribution and comparison of methods for sampling psocids in stored wheat

James E. Throne, George P. Opit, and Paul W. Flinn

USDA-ARS Grain Marketing and Production Research Center, 1515 College Avenue, Manhattan KS 66502, United States.

Introduction: Psocids are an emerging problem in stored grain and in grain processing facilities in the U.S., yet we know little about which species infest these products or the ecology of these species as related to pest management.

Methods: We compared several methods for sampling psocids in wheat stored in steel bins – cardboard refuges on the surface of the grain and near the bin hatch, grain trier samples, and automated sampling using the StorMax Insector system.

Results: The predominant psocid species found was *Liposcelis entomophila* in 2005 and *L. decolor* in 2006. Numbers of psocids were low immediately after bins were filled in July 2005, peaked in October, dropped to almost zero in December as temperatures decreased during winter, and then remained at low levels until the study was ended in April. In 2006, the number of psocids increased gradually from August to mid- October, and then generally declined until the study was ended in early November. Numbers of psocids in cardboard refuges and the Insectors were indicative of numbers of psocids in grain samples in both years.

Conclusions: The results indicate that cardboard refuges or Insectors may provide an efficient method for sampling psocids in bins of wheat, and that psocid populations can increase quickly to high levels during storage even though they are low early in the storage period.

New genes for new phylogenies: possible candidate genes from termite EST libraries

Srini Kambhampati And Matthew Steller

Department of Entomology, Kansas State University, Manhattan, KS 66506 USA

Introduction: Recent studies on the phylogenetic position of termites in relation to cockroaches have generated controversy. These studies suggest that cockroaches are paraphyletic and/or termites are nested within the cockroaches. Confidence in a phylogeny is generated when several independent genes result in a tree topology that is similar to one another. With the development of genomic resources for termites, there is an opportunity to identify and utilize many different genes for estimating phylogenies for termites, cockroaches, and mantises.

Methods: We have constructed 5 cDNA libraries from *Reticulitermes flavipes*: workers, soldiers, alates, early larvae, and late larvae. We sequenced ~15,000 clones, undertook bioinformatic and gene ontology analyses, and compiled a ~5000 gene EST library. We attempted to identify genes for the resolution of deep (oridinal), medium (family), and terminal (genera) divergences based on percent sequence identity. We constructed preliminary trees from sequences available from public data bases to obtain an indication of the phylogenetic information contained in these genes.

Results: Several genes were identified that are potentially useful for inferring a phylogeny for termites, cockroaches, and mantises. In any phylogeny involving multiple Orders, several independent genes must be used to obtain resolution of different divergences. We hope that our identification of these potential candidate genes will help in generating a robust phylogeny for termites, cockroaches, and mantises.

Conclusions: The genomic resources being developed for termites are likely to be a rich source of genes for inferring robust phylogenies for termites, cockroaches, and mantises.

Across spatial scales dynamics of *Anopheles gambiae* populations and malaria transmission

Gianni Gilioli[1] , Johann Baumgartner[2], Gabriele Cola[3], Andrew P. Gutierrez[4], Hans R. Herren[5], Bernt Lindtjorn[6], Luigi Mariani[3], Sara Pasquqali[7], Wakgari Deressa[8]

Universita Mediterranea di Reggio Calabria, Diparimento di Gestione dei Sistemi Agrari e Forestali, Reggio, Calabria, Italy[1], Università degli Studi di Milano, Istituto di Entomologia agrarian, Milano, Italy[2], Università degli Studi di Milano, Dipartimento di Produzione Vegetale, Milano, Italy[3], University of California Berkeley, Department of Environmental Science, Policy and Management, Berkeley, California, USA[4], Millenium Institute, Arlington, VA, USA[5], Centre of International Health, Bergen, Norway[6], CNR-IMATI, Milan, Italy[7], Department of Community Health, Addis Ababa, Ethiopia[8]

Introduction: In many African regions, *Anophles gambiae* is the main vector of falciparum malaria. The dynamics of vector populations and malaria transmission is modelled at mesoscale (1x1 km resolution) and microscale (0.1x0.1 km resolution).

Methods: The epidemiological system consists of four interacting components: hydrology (water bodies), environment (land use and meteorological driving variables), vector population, and human population. Modeling strategy consisted of: (i) developing and testing a spatially-explicit hydrological model of water bodies in relation to environmental variables; (ii) adding a spatially-explicit model representing the dynamics of stage-structured mosquito populations and malaria transmission. Simulations have been performed at the two spatial scales. Input data for the models are from Kenya and Ethiopia, and parameters are obtained from literature and remote sensing.

Results: At the mesoscale level, the hydrological model, tested with remotely sensed data, yielded a satisfactorily description of the spatial distribution of the potential breeding sites. The addition of vector populations and malaria transmission produced a realistic spatial pattern of malaria prevalence. At the microscale, the models are used in developing adaptive management of vectors and malaria control at the community level.

Conclusions: Mesoscale results suggest strategic planning options at the national level, and the microscale analysis suggests adaptive strategies for ecosocial system management in East Africa. Modeling the epidemiological system at two spatial scales increases the opportunities for parameter estimation in the face of limited data, provides an additional mechanism for model validation and improves model flexibility and use.

Effect of mating on queen quality and consequences for queen-worker interactions in honey bees (*Apis mellifera*).

Freddie-Jeanne Richard, David Tarpy and Christina Grozinger

Department of Entomology and Genetics, W.M. Keck Center for Behavioral Biology, North Carolina State University, Raleigh, NC

Mating profoundly alters honey bee queen behavior and physiology. After mating, queens cease taking flights and remain in the hive to initiate egg laying. There are also dramatic differences in the pheromone profiles of mated versus virgin queens, which lead to different queen-worker interactions. Furthermore, honey bee queens are highly polyandrous. While the effect of mating number on colony fitness have been considered in detail, it is unclear if there are direct effects of mating number on queen physiology or queen-worker interactions. We have used behavioral analyses, analytical chemistry, and functional genomics to determine the effects of mating number on honey bee queen pheromone profiles, physiology, and worker interactions. Furthermore, we have examined the roles of insemination volume and substance (e.g., semen versus saline) on producing these dramatic changes. Singly versus multiply inseminated queens have significantly different pheromone profiles in both the mandibular and Dufour's glands, queen-worker interactions, and gene-expression levels in the brain and fat bodies. Insemination volume appears to be a major factor in producing these changes. These studies elucidate the effects of mating number at the level of queen physiology, gene expression, and behavioral interactions with the workers, lay the groundwork for characterizing the molecular and physiological mechanisms underlying reproduction in honey bee queens.

Protecting a holiday village from termites in a natural park: a challenging experience in Andalusia (Spain)

Elena Pedroni[1], M. Angeles Lopez Martinez[2], Rafael Ocete Rubio[2], Francisco Correa Rodriguez[3], Lara Maistrello[1]

[1]Department of Agricultural & Food Sciences, University of Modena and Reggio Emilia, Reggio Emilia, Italy, [2]Laboratory of Applied Zoology, Department of Physiology and Zoology, Faculty of Biology, University of Seville, Seville, Spain, [3]Integral de Plagas, S.L. Sanidad Ambiental, Santa Ana, 2, 41900, Camas, Seville, Spain

Introduction: Subterranean termites are a serious threat in urban environments and termite management can be difficult in areas with special constraints. This work was carried out in Priego de Cordoba, a place of great historic and naturalistic relevance in South-Eastern Spain, belonging to the Parque Natural de las Sierras Subbeticas, and the intervention was performed in a holiday village (14000 m^2) where an underground spring had been found.

Methods: A preliminary inspection showed the presence of *Reticulitermes grassei* in many buildings of the village so the termite bait system SENTRI^{tm} Tech Dow AgroSciences was chosen as the most appropriate. In March 2007, 135 underground monitoring stations were initially installed in the constructions basement vaults, along the buildings perimeter and in the garden areas, covering all the areas where termite damage could have been most probable. Periodical inspections were performed and when active infestations were found, the monitoring wooden sticks were replaced with Hexaflumuron treated baits.

Results: Monitoring data revealed that termite infestation was rather uniformly distributed all over the village and had a high potential of serious damage. The highest number of active stations (46%) and the highest number of termites was detected in May. After the baiting program, the number of active stations, number of termites and bait consumption gradually decreased and by October only 4% of the stations was still active.

Conclusions: The chosen control method guaranteed protection without negative environmental consequences and additional costs. Early and timely termite management interventions can prevent serious damages and economical losses.

Utilising sex pheromones of raspberry cane midge, Resseliella theobaldi, and apple leaf midge, Dasineura mali, for pest monitoring and control

Jerry Cross[1], David Hall[2], Michelle Fountain[1], Adrian Harris[1], Dudley Farman[2]

East Malling Research, East Malling, Kent, United Kingdom[1], Natural Resources Institute, Chatham Maritime, Kent, United Kingdom[2]

Pheromone identifications: The sex pheromones of the raspberry cane midge and apple leaf midge, have been identified and synthesised and are highly attractive to males. They are acetoxyketones, a new chemical class of midge pheromone.

Pheromone monitoring traps: Standard delta sex pheromone traps with rubber septa lures releasing the sex pheromone racemate have been developed for each species. The height of trap deployment has a large effect on the numbers of midge males caught and standard height of 0.5 m is recommended. Traps for both species have been deployed in fruit plantations in several different countries. 3-5 generations have been recorded, depending on latitude with large variations in numbers captured per season. Linear relationships between the numbers of midges captured for a particular generation and the numbers of galls or larvae that develop subsequently in the crop for that generation have been demonstrated for both species. The traps have proved useful for pest monitoring.

Control attempts: Large scale field experiments investigated the use of the pheromones for control in commercial plantations by mating disruption, attract-and-kill and mass trapping have been conducted in the UK over 2 seasons. A very high degreee of, though not complete, suppression of catches of male midges in traps deployed in the centres of treated plots has been demonstrated. For apple leaf midge, no sustained reduction in galling damage occurred. Good results were obtained in one trial with *R. theoboldi* in an unprotected raspberry crop but not in several other experiments in protected crops. The reasons for the failures will be discussed.

How costly is it to be an intraguild predator?

António O. Soares, Marlene Terra, Rafael Arruda, Patrícia V. Garcia

University of Azores, Ponta Delgada, Azores, Portugal

Introduction: Cages studies were used to evaluate the costs and the benefits for *Harmonia axyridis* (IGpredator) to prey on different preimaginal stages of *Trichogramma cordubensis* (IGprey).

Methods: Eggs, larvae and pupa of *T. cordubensis* were provided *ad libitum* to the fourth larval stage and adults of *H. axyridis*. Voracity, body-weight gain and reproductive performances of *H. axyridis* were evaluated and compared with predators fed on eggs of *Ephestia kuehniella* (EGprey).

Results: The amount of biomass consumed by the adults or larvae of *H. axyridis* on EGprey, eggs and larvae of IGprey was similar, but it significantly decreased when the predator fed on IGprey pupae. The proportion of eggs consumed by the adults or larvae of *H. axyridis* was the same independently of the age of the IGprey. Body-weight of the adults of *H. axyridis* decreased with the age of the IGprey, being more severe in females. After three days feeding on IGprey the number of clutches and eggs laid by *H. axyridis* decreased significantly, being much lower when feeding on IGprey pupae. Development rate and body-weight gain of *H. axyridis* larvae generally decreased after feeding on eggs, larvae and pupa of IGprey.

Conclusions: The results show that long term exploitation of an intraguild prey of low quality is very costly for the biology of the IGpredator. Considering the outcome of the interaction, the results suggest that the IGprey is killed and consumed and, also that the intraguild predation generates sublethal effects on the IG predator.

Development of zero pesticide residue Integrated Pest and Disease Management programmes for UK fruit crops

Jerry Cross, Angela Berrie

East Malling Research, East Malling, Kent, UK

Soft and top fruit crops grown in the UK are subject to attack by a wide range of damaging pests and diseases. Unless these are controlled effectively the crops can not be grown economically. Pest and disease control largely relies on pesticides, though there are a number of biocontrol successes that are widely adopted. Pesticide residues surveillance shows that a high proportion of produce contains residues above reporting limits, though Maximum Residue Levels are rarely exceeded. Several important multiple retailers in the UK are asking their suppliers to strive towards elimination of pesticide residues from fresh produce including fruits to maintain and improve consumer trust. This is providing a strong driver for development and implementation of Integrated Pest Management programmes. General approaches to reducing the occurrence of residues are discussed, including increasing harvest intervals and alternative non-chemical control approaches. Work to develop zero residue programmes was spearheaded by us on apple. A 'zero residue' Integrated Pest and Disease Management (IPDM) programme for apple has been developed at East Malling Research. In the programme conventional pesticides are not used during fruit development. The zero residues IPDM programme has been highly successful even on the most pest and disease prone varieties. Work is in progress to develop zero residue IPDM programmes for raspberry and strawberry. This is particularly challenging because of the short period of flowering and fruit development. Pest control approaches being investigated will be overviewed.

Divergence between populations of the dampwood termite *Schedorhinotermes lamanianus* driven by ancient climate fluctuations

Andreas Marten[1], Manfred Kaib[2], Roland Brandl[1]

[1]Department of Animal Ecology, University of Marburg, Marburg, Germany, [2]Department of Animal Physiology, University of Bayreuth, Bayreuth, Germany

Till the Miocene the tropical forests of Africa formed one single forest block. This block became fragmented by climatic changes as well as the formation of the Great Rift Valley 10 Mya leading to the establishment of an arid corridor that runs from the Horn of Africa to the Cape region. This corridor had a strong impact on the biogeographic history of forest-dwelling species.

We chose the dampwood termite *Schedorhinotermes lamanianus* to estimate the divergence between populations of lowland forest species west and east of the arid corridor. We sequenced a 658bp fragment of the mitochondrial COI gene for individuals of colonies scattered across the range of this termite species.

We found two clusters of sequences: a cluster of sequences from individuals sampled west and a cluster from individuals sampled east of the arid corridor. Mean sequence divergence between these two clusters was 3% with negligible divergence within clusters. These findings corroborate former results using morphometry, AFLP analysis and the occurrence of termitophile tineid moths (*Paraclystis*) in eastern and western populations. The clear separation of a western and an eastern clade in *S. lamanianus* highlights the strong effect of the arid corridor on the biogeographic history of African forest biota. However, assuming a substitution rate of 1-2% per My, the estimated divergence time between the two clades is younger than the fragmentation of the ancient forest block during the Miocene. This result suggests some exchange between western and eastern forests during wetter periods until the early Pleistocene.

Invasive hymenopterans of the Neotropical Region

Paul Hanson[1] and Michael Schauff[2]

[1]*Escuela de Biología, Universidad de Costa Rica, San Pedro, San José, Costa Rica*
[2]*Systematic Entomology Laboratory, c/o National Museum of Natural History, NHB 168, Washington, D.C., U.S.A.*

Introduction: The continental Neotropics harbor numerous invasive hymenopteran species. The list of invasive species is still incomplete but the preliminary results suggest some patterns.

Methods: A recent compilation of the taxonomic and biological literature on the Hymenoptera of the Neotropical Region was used to prepare a preliminary list of invasive species in the region (excluding islands).

Results: Some species have been deliberately introduced while others have arrived unintentionally. The introduction of the African honeybee (*Apis mellifera scutellata*) in 1956 is the best documented hymenopteran invasion in the region although the ecological impact of this species is still debated. In the Galapagos islands and Chile introduced eusocial hymenopterans (e.g. vespids) have had a notable impact on the native biota. Although exotic ants are omnipresent in disturbed habitats, they appear to be relatively insignificant in primary forests in most of the continental Neotropics. Among parasitoids, it is often difficult to distinguish between undocumented introductions for biological control and accidental introductions, but preliminary evidence suggests that there are numerous instances of the latter, especially among parasitoids associated with Sternorrhyncha, stored grain pests, etc. Thelytokous species or races appear to be especially successful invaders. Finally, some introduced species of sawflies, but very few phytophagous Apocrita, have become pests in the region.

Conclusions: It is often difficult to determine the original distribution of widely dispersed species and more taxonomic research is needed to resolve this question. The preliminary evidence suggests that the ecological impact of invasive species has been less severe in the continental Neotropics than in nearby islands.

Current status of termite management in Brazil

Ana Maria Costa-Leonardo[1]

[1]*Department of Biology, São Paulo State University – UNESP, Av. 24A No.1515, 13506-900, Rio Claro, SP, Brazil.*

Brazil is a large tropical country with abundant and varied termite fauna. The most destructive termite genera of structural wood in urban areas are *Cryptotermes*, *Coptotermes* and *Heterotermes*. Considerable damage is also caused by species of *Nasutitermes* in some regions, including Amazonia, and among them, *N. corniger* is the most frequent urban pest. The main agricultural pests of São Paulo State are represented by *Heterotermes*, *Procornitermes* and *Neocapritermes*, which infest sugarcane fields. The introduced species *Coptotermes gestroi* is the most economically serious pest with heavy infestations in the city of São Paulo, where it finds shelter for nesting and sources of humidity in high-rise buildings. This termite causes major damage to buildings, telephone cables, electrical wires and living trees in urban environments. The advance of edifications on natural environments has led to the appearance of native species causing damage to structural timber, case of *Nasutitermes aquilinus, Nasutitermes ehrhardti* and *Microcerotermes* spp., and on the lawns, case of species of *Syntermes.* Preventive measures are not being used in new buildings, and the common practice is to bury wood and cellulosic wastes close to the edifications or fill up the structural voids with this material. The principal management practice is the protection of structures through application of chemical barriers in the soil or local insecticides on the wood. The most common insecticides used in termite management are pyrethroids, nicotinoids and fenilpirazol, however, the use of hexaflumuron bait has increased in the city of São Paulo, for both preventive and curative treatment.

Insecticide resistance and genetic structure of *Cydia pomonella* (L.) (Lepidoptera: Tortricidae) from apple orchards in central Chile

Eduardo Fuentes-Contreras[1], Maritza Reyes[2], Blas Lavandero[3], Wilson Barros[1], Claudio C. Ramírez[3]

[1]Departamento de Producción Agrícola, Facultad de Ciencias Agrarias, Universidad de Talca, Talca, Chile, [2]Instituto de Producción y Sanidad Vegetal, Facultad de Ciencias Agrarias, Universidad Austral de Chile, Valdivia, Chile, [3]Instituto de Biología Vegetal y Biotecnología, Universidad de Talca, Talca, Chile

Introduction: Codling moth, *Cydia pomonella* (L.), is the main pest of pome fruits worldwide. Regular applications of insecticides have been the main management practice against codling moth in Chile. Therefore, we addressed the insecticide resistance and genetic structure of codling moth populations from central Chile.

Methods: We evaluated the mortality of larvae to diagnostic doses of organophosphate, pyrethroid, neonicotinoid and diacylhidrazine insecticides. We also evaluated the activity of detoxifying enzymes, i.e. glutathione s-transferases (GST), cytochrome P-450 monooxygenases (P450) and esterases (EST). An analysis of neutral genetic variability using microsatellites was performed for the same codling moth populations, in order to estimate gene flow and population differentiation.

Results: Post-diapause larval mortality was reduced for organophosphates in several of the analysed orchards. Significantly higher GST activity was associated with insecticide resistance. No relation was found between P450 or EST activity and insecticide resistance. Neonate larval mortality was not significantly reduced in any of the analysed orchards or insecticides. Therefore, insecticide resistance has not yet reached the threshold of field control failure. In spite of the geographical distances between some orchards (approx. 200 km), there was low genetic differentiation and high gene flow between codling moth populations, with only slight isolation by distance.

Conclusions: Low levels of insecticide resistance were found for codling moth in apple orchards from central Chile, mainly based on enhanced GST activity in post-diapause larvae. The maintenance of rather susceptible populations in managed orchards seems to be related with high levels of gene flow between orchards.

Pollinator networks, alien species and the conservation of rare plants: *Trinia glauca* as a case study

Luisa G. Carvalheiro[1*], Eduardo R. M. Barbosa [1] and Jane Memmott[1]

[1]*School of Biological Sciences, Woodland Road, Bristol, BS8 1UG*

Introduction: Despite the essential role of pollination in the maintenance of many rare plant species, conservation management plans rarely consider the service of pollination. *Trinia glauca* (Apiaceae) is a rare English plant species present in natural areas where the removal of alien plants is a part of the conservation management plans.

Methods: We use a community level approach to identify the main flower visitors of *T. glauca* as well as the direct and indirect links between *T. glauca* and other species of the study site plant community. Effectiveness of pollination of the main visitors was tested in a field experiment and the likely consequences of the removal of alien plants on *T. glauca* pollination were simulated.

Results: This study showed that ants were the main pollinators of *T. glauca* and that over the field season 33% of the ants' visits to flowers were to alien plants, with *Cotoneaster horizontalis* making a particularly high contribution (58%) during the *T. glauca* flowering period. Although positive or neutral effects are possible, a negative effect is also possible, whereby the removal of alien plants leads to a crash in ant populations, potentially reducing pollinator visits to *T. glauca* by up to 85.2%.

Conclusion: Management measures involving removal of alien plants should consider possible negative impacts on rare plants through changes in pollinator populations. In this case, a staged removal is likely to prove the best conservation approach, allowing the pollinators' response to be assessed before any serious negative effects occur.

Molecular systematics of braconid wasps (Hymenoptera: Ichneumonoidea)

Ashley Dowling[1], Michael Sharkey[2], Barbara Sharanowski[1]

[1]University of Arkansas, Fayetteville, AR, United States, [2]University of Kentucky, Lexington, KY, United States

Introduction: Braconidae is a megadiverse group of Hymenoptera that exhibits a variety of parasitic lifestyles and host associations. This work is part of the HymAToL project and represents the most taxonomically diverse dataset analyzed to date.

Methods: Genetic information from 28S (domains 1-10) and the variable expansion regions of 18S was obtained for a diverse set of braconid taxa including 137 members from 41 currently recognized subfamilies. Data was aligned using MAFFT and analyzed under parsimony, likelihood, and Bayesian optimality criteria.

Results: Nuclear ribosomal data does an adequate job resolving the majority of the braconid phylogeny. Preliminary results suggest that some traditionally recognized groups are supported by molecular evidence, but new relationships are resolved as well.

Conclusions: Results strongly support some major groupings, but indicate that information from additional gene regions may be necessary to obtain a robust assessment of braconid phylogeny.

Evolution and radiation of stick insects (Phasmatodea) in the Pacific Ocean Region

Thomas Buckley[1], Sven Bradler[2]

[1]Landcare Research, Auckland, New Zealand, [2]Johann-Friedrich-Blumenbach-Institut für Zoologie und Anthropologie, Georg-August-Universität, Göttingen, Germany

Introduction: Stick insects (Phasmatodea) are widespread and diverse throughout the Australasian and the Southwest Pacific. We have used phylogenetic analysis to reveal monophyletic groups and to study the biogeographic history of these clades.

Methods: We have analyzed DNA sequence data from two mitochondrial (cytochrome oxidase subunits I and II) and two nuclear genes (histone subunit 3 and 28S ribosomal RNA) from wide range of stick insects from throughout the Pacific area, with a focus on New Zealand, New Caledonia and Australia. Phylogenetic analyses were performed using maximum likelihood and Bayesian methods.

Results: Our results show the presence of a large monophyletic group of stick insects, corresponding to the Lanceocercata clade (Bradler 2001), distributed from the Mascarene Islands, to New Zealand, including many genera from some Pacific Islands, Australia, New Zealand and New Caledonia. This clade is also supported of a number of morphological synapomorphies. Surprisingly, the Lanceocercata contains taxa previously unsuspected of belonging to this clade. Our analyses also show a close relationship between the stick insect faunas of New Zealand and New Caledonia.

Conclusions:.Our analyses show striking examples of convergent evolution in body form in the Australasian region, where taxa have converged on stick insects from other continental regions. The phylogenetic relationship between the stick insects of New Zealand and New Caledonia exemplifies the importance of the New Caledonian biota in understanding New Zealand biogeography. Several regions of our phylogenetic tree show evidence of bursts of evolution, making the exact branching patterns difficult to resolve.

Constitutive and Inducible Plant Resistance for Rice Pest Management

Michael Stout

Louisiana State University Agricultural Center, Baton Rouge, United States

Introduction: Plant resistance is an important component of the management programs for many key rice insect pests. For some of these pests, resistance is controlled by major genes that confer high levels of resistance. For other key pests, however, high levels of resistance have not been found in screening programs. The rice water weevil (*Lissorhoptrus oryzophilus*), the most important early season pest of rice in the U.S., is an example of the latter type.

Methods: A variety of field and greenhouse experiments were conducted, with the goal of incorporating plant resistance into the management program for the rice water weevil.

Results: A long-standing screening program in Louisiana failed to find accessions or varieties with high levels of resistance to this root-feeding insect. More recent experiments have demonstrated that variation in resistance to the weevil exists among current commercial varieties, and moderate levels of resistance have been found in a few unimproved lines. Experiments were conducted to test the hypothesis that varietal improvement in the southern U.S. has been accompanied by an increase in resistance to the weevil. In addition, a line of research has been initiated to investigate inducible resistance to insects in rice. This research may reveal methods for manipulating plant resistance to the rice water weevil in the field, and will help elucidate the biochemical and morphological bases of resistance to the rice water weevil.

Conclusions: The potential for integrating inducible and constitutive resistance into the management program for the rice water weevil will be discussed.

Coping with asymmetry: Perturbed hovering flight in sphingid moth

Tyson Hedrick

University of North Carolina, Chapel Hill, NC, United States

Insects exhibit a remarkable ability to continue flying despite damage to their wings. These capabilities, both the biomechanical consequences of damage as well as the animal's compensatory response, were investigated in the hovering flight of *Manduca sexta*, L.

As a proxy for natural wing damage, the most distal 18% of the area of a single wing was removed following a baseline flight recording. This asymmetric damage represents a 40% reduction in lift and 50% reduction in torque. As expected, this caused rapid failure in a simulation of moth flight. Actual moths were able to resume flight shortly after wing reduction and exhibited normal flower feeding behaviour. Their response to wing asymmetry was quantified and took the form of 1) a <10% increase in wingbeat frequency, 2) an increase in wing sweep amplitude on the reduced wing, and 3) a decrease in wing sweep amplitude on the intact wing. This response was found to stabilize the simulated moth, although many other kinematic changes would have served the simulated moth equally well.

Furthermore, the addition of a muscle with non-linear force and contractile velocity response to the simulated moth was shown to stabilize it in the face of wing asymmetry and led to wing kinematics similar to those used by actual moths. The benefits of adding the simulated muscle were not dependent on the details of the muscle; all tested muscle parameter improved performance. These results suggest that muscle physiology may play a previously unappreciated role in locomotor stability for animals moving in a fluid environment.

Fine tuning of foraging behaviour to increase control impact of natural enemy

Louise E.M. Vet

[1]Netherlands Institute of Ecology (NIOO-KNAW), Maarssen, Netherlands, [2]Wageningen University, Wageningen, Netherlands

A key component of the success of natural enemies in biological control lies in their ability to efficiently and consistently locate their hosts or prey. Unpredictable foraging behaviour can thus severely hamper the reliability of natural enemies as control agents. There is a clear need to understand the mechanisms that underlie variation in foraging efficiency and to find ways to control them. Empirical and theoretical fundamental research on parasitoids and predators has elucidated important causes of behavioural variation. This relates to both variations in cues and in responses. Considering the cues, a limited availability of key signals can play a crucial role. Over the years, crop plants have been selected for other traits than attracting natural enemies. We now see innovative, also ecogenomic developments to restore this omission. Next there are factors internal to the insects. First there is genotypic variation in responses to important foraging cues, an area of research that has received only limited attention. Second, the insect's physiological state (e.g. its hunger state) can influence its ability and propensity to respond to host or prey cues. A third and well studied cause of behavioural variability is the insect's experience during pre-adult and adult life. Especially for insect parasitoids in multitrophic systems it is almost common knowledge that associative learning can play a steering role in the foraging process. Both genotypic variation and phenotypic plasticity in foraging create the potential to modify behaviour to improve foraging efficiency. It is therefore surprising that it has received such limited attention from practitioners of biological control. I will plea for a strong joint effort to change this situation.

Evolutionary history of Actinote (Heliconiinae, Acraeini) in Southeastern Brazil

Karina Silva-Brandão[1], Ronaldo Francini[2], Niklas Wahlberg[3], Ana Maria Azeredo-Espin[1], André Freitas[1]

[1]Universidade Estadual de Campinas, Campinas, SP, Brazil, [2]Universidade Católica de Santos, Santos, SP, Brazil, [3]University of Turku, Turku, Finland

Introduction: *Actinote* occurs through Central and northern South America to southern Brazil, where 21 species are known – the second largest generic-level radiation of Nymphalidae. A phylogenetic hypothesis for the genus based on molecular data is proposed, and the reasons that led to the present distribution of its species on SE Brazil were investigated.

Methods: The genes COI-COII, EF1alpha and wingless were used to propose a phylogenetic hypothesis to *Actinote*. Three ecological characters were investigated: evolution of host plant use (number of species and genera of Asteraceae), geographical range and altitudinal speciation pattern.

Results: Parsimony searches resulted in one most parsimonious tree. By this hypothesis, *Actinote* is a monophyletic group, and the ancestral state of the genus is the use of a single species of Asteraceae in the genus *Mikania*. During its evolutionary history, there was a tendency to increase both the number of species and of genera of plants used. The geographical distribution of the species of *Actinote* also increased throughout their phylogenetic history, with the spread of species occurring mainly from higher to lower altitudes.

Conclusions: For *Actinote*, and maybe for the entire tribe Acraeini, the tendency in using more species and genera of plants might be related to the amplification of their geographical range. It is believed that the origin of the Neotropical Acraeini has been the Andean region, and we can infer that during the evolution of the group some species had spread to low altitudes together with the expansion of their geographical range.

Evolutionary history of Actinote (Heliconiinae, Acraeini) in Southeastern Brazil

Karina Silva-Brandão[1], Ronaldo Francini[2], Niklas Wahlberg[3], Ana Maria Azeredo-Espin[1], André Freitas[1]

[1]Universidade Estadual de Campinas, Campinas, SP, Brazil, [2]2Universidade Católica de Santos, Santos, SP, Brazil, [3]University of Turku, Turku, Finland

Introduction: *Actinote* occurs through Central and northern South America to southern Brazil, where 21 species are known – the second largest generic-level radiation of Nymphalidae. A phylogenetic hypothesis for the genus based on molecular data is proposed, and the reasons that led to the present distribution of its species on SE Brazil were investigated.

Methods: The genes COI-COII, EF1alpha and wingless were used to propose a phylogenetic hypothesis to *Actinote*. Three ecological characters were investigated: evolution of host plant use (number of species and genera of Asteraceae), geographical range and altitudinal speciation pattern.

Results: Parsimony searches resulted in one most parsimonious tree. By this hypothesis, *Actinote* is a monophyletic group, and the ancestral state of the genus is the use of a single species of Asteraceae in the genus *Mikania*. During its evolutionary history, there was a tendency to increase both the number of species and of genera of plants used. The geographical distribution of the species of *Actinote* also increased throughout their phylogenetic history, with the spread of species occurring mainly from higher to lower altitudes.

Conclusions: For *Actinote*, and maybe for the entire tribe Acraeini, the tendency in using more species and genera of plants might be related to the amplification of their geographical range. It is believed that the origin of the Neotropical Acraeini has been the Andean region, and we can infer that during the evolution of the group some species had spread to low altitudes together with the expansion of their geographical range.

Improvement of *Paecilomyces fumosoroseus* as a biological control agent against Formosan subterranean termites by application of keratin foam

Maureen S. Wright[1], Christopher A. Dunlap[2], Mark A. Jackson[2], Edward D. Freytag[3]

[1]USDA-ARS-SRRC, New Orleans, LA, United States, [2]USDA-ARS-NCAUR, Peoria, IL, United States, [3]NOMTCB, New Orleans, LA, United States

Introduction: Subterranean termites cause several billion dollars in damage in the US annually. Formosan subterranean termites (FST) cause an increasing proportion of this total. In the laboratory *Paecilomyces* sp. have been shown to cause mortality of FST.

Methods: Video observation of the interior of trees confirmed FST infestation. Trees were treated with a liquid formulation of *P. fumosoroseus* (Pfr) blastospores by injection through drill holes. At 12 days post-treatment there was no FST activity in two trees and reduced FST activity in one tree. At 27 and 60 days FST activity was reduced from the pre-treatment level but present in all trees. The reappearance of FST indicated the need for a formulation that allowed expansion of the fungal spores throughout the FST carton nest inside the tree. Biologically-compatible foams were investigated. A formulation of keratin foam and Pfr blastospores was injected into different infested trees. Additional trees were injected with keratin only or left untreated as controls.

Results: On day 9 after the keratin/Pfr treatment the number of observed FST in the trees was significantly reduced. Observations on days 38, 52 and 100 revealed no FST activity in 3 of the treated trees. The remaining treated tree, the largest, in which the carton nest was not filled with foam, had reduced termite activity. FST activity in the foam control and null control trees remained high throughout the observation period.

Conclusion: These studies indicate that the keratin formulation enhanced the effectiveness of Pfr as a treatment against FST in trees.

The influence of fundatrix density and plant module size on gall induction success in adelgids: a test of the dose-dependent gall induction stimulus hypothesis

Dan Quiring, Leah Flaherty

University of New Brunswick, Fredericton, New Brunswick, Canada

Introduction: The dose-dependent gall induction hypothesis states that insects induce galls by injecting a chemical gall induction stimulus into host plants. Gall induction is only successful when the dose injected is large enough to "overcome" normal plant development.

Methods: This hypothesis was evaluated in field studies with two galling adelgids, *Adelges cooleyii* on interior spruce, and *Adelges abietis* on white spruce. The gall induction success of fundatrices on different-sized buds was evaluated for buds with a range of fundatrix densities. Variations in fundatrix densities were assumed to result in similar variations in the dose of gall induction stimulus injected into buds.

Results: As predicted by the dose dependent gall induction hypothesis, gall induction success increased when two or more fundatrices colonized the same bud, especially on larger modules.

Conclusion: These results strongly support the dose-dependent gall induction hypothesis and re-emphasize that the selection of host plant modules is often the result of the trade-off between ease of gall induction on small modules and the increased availability of resources in large modules.

The Hymenoptera Name Server

Norman Johnson

The Ohio State University, Columbus, Ohio, United States

The Hymenoptera Name Server is an on-line database web portal designed with the goal of serving as resolver for the names used for taxa within the order, providing the context in which to understand the meaning of the formal strings used to represent real taxa. The database contains information on over 210,000 names representing nearly 150,000 taxonomic concepts. A taxonomic concept is a class representing the published description or delimitation of a new taxon. Concepts are arranged in a hierarchical structure with parent-child relationships representing either membership in a taxon or a synonymy between concepts. The operating standards used to choose among alternative relationships and to flag names considered to be valid are discussed.

The data associated with names include its position within the taxonomic hierarchy, the status of the name, the citation of its original description, links to an on-line versions of the original description (pdf of the original document and an XML version from plazi.org), and a listing of the synonyms and alternative forms in which the names for that concept have appeared within the literature.

The Hymenoptera Name Server also provides Life Sciences Identifiers for these entities, that is, globally unique identifiers for the names, concepts, publications, and citations. The LSID resolver provides the data in RDF (resource description format) implementing the Taxonomic Concept Schema and is suitable for semantic web applications. The information is also shared with the Integrated Taxonomic Information Service and, thereby, to the Catalogue of Life and the Electronic Catalogue of the Names of Known Organisms. All services are available at the URL purl.oclc.org/NET/hymenoptera/hns.

Metabolite profiling for genotypic discrimination of aspen clones and determination of herbivore resistance

Benedicte R. Albrectsen

Umeå University, Umeå, Sweden

Clone specific measurements of defence compounds and nutrients are often related to damage patterns to the same clones in the field. But how reliable is metabolite profiling as a selection tool for genotype discrimination in a natural population of European Aspen (*Populus tremula* L.)? This is a presentation of a G by E study of twelve wild aspen clones grown in three environments. Clone phenotyping was performed in three ways: metabolomics profiling (GC/MS), phenolic glycoside profiling (HPLC) and profiling of natural herbivore damage under field conditions (general damage score, and presence of specific herbivores). The degree of clone specificity was tested for, and responses were divided into three types: 1. clone consistency, 2. environmental consistency and 3. unpredictable. Damage by two herbivores *Phyllocnistis labyrinthella* (Bjerkander, 1790, Lepidoptera: Gracillariidae) and *Phratora vitellinae* (L. 1758, Coleoptera: Chrysomelidae) was related to clone consistent compounds (from the phenolic pathway, some disaccharides and amino acids) that indicated a canalised and thus potential target candidate for resistance properties; those compounds that mainly varied with environment were considered plastic (for example flavonoids, catechin) or independent of clone or environment (mostly primary metabolites). The results are related to known preferences for phenolic compounds from the literature and genotyping in a trans-omic perspective is discussed.

Characterization of a protein kinase C from Choristoneura fumiferana which may related to Steroid hormone-dependent gene expression

Guo-Xing Quan, Daniel Doucet, Tim ladd, Peter Krell, Basil Arif

[1]Great Lakes Forestry Centre, Sault Ste. marie,ON, Canada, [2]University of Guelph, Guelph, ON, Canada

Steroid hormone 20-hydroxyecdysone (20E) is essential for the development, metamorphosis and reproduction in insects. The hormone signal is transduced by the heterodimer ecdysone receptor (EcR) and USP and binds to specific response elements in the genome and consequently regulates target genes transcription. The phosphorylation of the receptors is a pre-requisite for function. The intracellular signal transduction pathway involved in receptor phosphorylation has not yet been fully elucidated. Previous work in *Drosophila* and *C. fumiferana* indicated that a protein kinase C (PKC) might be involved in the 20E-dependent gene expression. The aim of this study was to identify the PKC involved in this pathway. A *C. fumiferana* PKC (CfPKC) was cloned by RT-PCR and 5' and 3'RACE. The full-length cDNA was 2.3 Kbp with an open reading frame potentially encoding a protein of 669 amino acids. Northern and Western blotting analyses showed that CfPKC was ubiquitously expressed in various tissues at all development stages. Western blot analysis of over expressed CfPKC fused to a GFP tag revealed that it is distributed throughout the cytoplasm, and that activation with phorbol 12-myristate 13-acetate (PMA) resulted in rapid localization of the protein to the cell membrane. Knockdown of CfPKC by double-stand RNA interference (RNAi) in CF-203 cells reduced the 20E-triggered expression of the E75 and CHR3 molting genes. PKC inhibitors also reduced the 20E-induced gene expression, thus supporting the role of CfPKC in 20E signal transduction.

Interspecific competition between parasitoid wasps: sneak vs. guard, who wins?

Tara J. Murray[1], Tara J. Murray[2], Sarah Mansfield[3]

[1]Scion (New Zealand Forest Research Institute Ltd), Rotorua, New Zealand, [2]Lincoln University, BioProtection & Ecology Division, Lincoln, New Zealand, [3]Faculty of Agriculture, Food & Natural Resources, University of Sydney, Sydney, Australia

Paropsis charybdis (Coleoptera: Chrysomelidae) is a pest of Eucalyptus in New Zealand and is attacked by two egg parasitoids (Hymenoptera: Pteromalidae). The first, *Enoggera nassaui*, was introduced as a biological control agent against this pest in 1987, while the second, *Neopolycystus insectifurax*, was self introduced and discovered in 2001. Both species are known to be polyphagous and both achieve almost 100% parasitism of *P. charybdis* in the laboratory. Field observations between 2000 and 2005 indicated that *N. insectifurax* does not parasitise *P. charybdis* as successfully as *E. nassaui.* Laboratory observations showed that the parasitoids have different oviposition behaviours and both will compete with their conspecifics for access to hosts. In this study *The Observer*, a computer software package designed for the collection, management and analysis of observational data, was use to help compare the behavioural characteristics of each of these two species when presented with host eggs in the presence of the other species. Initial results indicate that although *E. nassaui* usually locates and begins ovipositing into host eggs first, it is usually chased away once *N. insectifurax* locates the eggs. *N. insectifurax* then guards the eggs, continuing to chase off *E. nassaui* if it approaches again. Despite this *E. nassaui* frequently manages to oviposit in some host eggs due to its ability to sneak in and assess and oviposit in eggs more quickly than its slow aggressive competitor. The dynamics and results of these interactions are discussed.

Evolution in the New Zealand Subantarctic: Systematics and genetics of *Pseudhelops* Beetles (Tenebrionoidea)

Richard Leschen[1], Eve Butler[2], Thomas Buckley[1], Peter Ritchie[2]

[1]New Zealand Arthropod Collection, Auckland, New Zealand, [2]Victoria University, Wellington, New Zealand

The 8 species of the saprophagous genus *Pseudhelops* is restricted to New Zealand's 5 Subantarctic Island groups, as well as Chatham and Stewart Islands. Here we investigate the phylogenetic relationships among the species and genetics of *P. tuberculatus*. Morphological and mitochondrial DNA data were analyzed using parsimony, Bayesian, ML (trees rooted with mainland *Cerodolus*). Populations of *P. tuberculatus* (Auckland Islands) are geographically structured along a North-South gradient suggests a southern refugia. On Auckland Island's southernmost island (Adams Island) one individual showed a marked genetic divergence from remaining members and study of museum material indicates that this individual corresponds to *P. wenhami*, a species previously synonymised with *P. tuberculatus*. A species-level analysis resulted in the following relationships: (*P. quadricollis* [Snares] + *P. chathamensis* [Chatham]) (*P. capitalis* [Stewart] ((*P. clandestinus* [Antipodes] + *P. liberalis* [Bounty]) (*P. posticalis* [Campbell]*, P. antipodensis* [Antipodes] (*P. tuberculatus* [Auckland] + *P. wenhami* [Auckland]))). These data suggest a widespread *Pseudhelops* + *Cerodolus* ancestor inhabiting the Campbell Plateau and mainland New Zealand, with subsequent divergence in the subantarctic and off-shore islands. The Antipodes Islands may have been colonized twice: once by a *P. clandestinus* + *P. liberalis* ancestor with apomorphic striate elytra, and second by an ancestor of *P. posticalis* and relatives on Auckland and Campbell Islands that lack distinct elytral striations. Meanwhile, the sympatric *P. wenhami* and *P. tuberculatus* diverged from a common Auckland Islands ancestor, and their speciation may have been habitat-mediated by associations with tussocks (*P. wenhami*) and forests (*P. tuberculatus*).

Pheromone mating disruption of codling moth, *Cydia pomonella*, in walnuts and pears using intermediate release rate dispensers

Stephen Welter, Frances Cave

University of California, Berkeley, CA, United States

Introduction: Logistic problems of large tree canopy size and increasing costs of labor associated with hand-applied pheromone dispensers has limited the adoption of pheromone mating disruption in walnuts. New “meso” dispensers were developed with release rates that ranged between 10-30 mg ai codlemone per dispenser per day and evaluated using few point sources per ha.

Methods: Release rates of different combinations of membrane type and size were determined under laboratory and field conditions. Replicated plots were established in pear and walnut orchards using 30-60 dispensers per ha. Using replicated 2 ha plots within a single orchard, the effect of the number of point sources on codling moth suppression was compared for a range of dispenser densities from 30-500 dispensers per ha in a mature walnut orchard.

Results: Effect suppression of codling moth damage was observed using 60 meso-emitters per ha in insecticide treated and organic walnut orchards ($P<0.05$), whereas extreme pressures found in the test pear orchards failed to suppress outbreak situations. Within the point-source trial, all combination programs of pheromone mating disruption plus insecticide treatments outperformed the insecticide treatment alone ($P<0.05$) relative to infestation at harvest. No improvement in control of codling moth was associated with increasing the number of point sources.

Conclusions: Using higher release rates per dispenser, the number of point sources was effectively reduced by >90% without any measurable loss of program performance.

No tri-trophic impacts of transgenic insect-resistant avidin tobacco on predatory carabid beetles fed pure or mixed diets

Elisabeth Burgess[1], Bruce Philip[1], John Christeller[2], Emma Barraclough[1], Richelle Marshall[2]

[1]HortResearch, Auckland, New Zealand, [2]HortResearch, Palmerston North, New Zealand

Adult predatory beetles, *Ctenognathus novaezelandiae,* were fed pure and mixed diets of field-collected prey and/or *Spodoptera litura* laboratory-reared on transgenic avidin tobacco and/or isogenic non-transgenic control tobacco. Female beetles consuming only tobacco-fed prey retained their weight over 140 days regardless of the proportion of avidin vs control tobacco in the diets of their prey, while male beetles fed only tobacco-fed prey lost weight. Females provided with any proportion of field food in addition to avidin tobacco significantly increased in weight over 140 days while males generally retained their starting weight. There were no significant differences among treatments in female survival (mean duration: 209 to 261 days). Males given any amount of field food survived a similar length of time to females (222 to 272 days). However those consuming only tobacco-fed prey, whatever the proportion of avidin and control fed prey, had greatly reduced survival (111 to 126 days). The mean fecundity of all females consuming only tobacco-fed prey was low (0.02 to 0.09 eggs per beetle per fortnight over a year), while those consuming some field food produced 0.5 to 1.4 eggs per fortnight. Egg fertility did not differ among treatments. In a second experiment beetles were fed 33% field food and 67% either avidin or control tobacco-fed prey. There were no treatment effects on beetle mass after 94 or 163 days, although female beetles were larger than males at both time points. Treatment had no impact on food consumption, fertility, fecundity or within-gender survival.

Sex peptide receptor, a G-protein coupled receptor that mediates the post-mating switch in *Drosophila* reproductive behaviours

Young-Joon Kim, Nilay Yapici, Carlos Ribeiro, Barry Dickson

Institute of Molecular Pathology, Vienna, Austria

At various stages in their lifespan, animals undergo marked switches in their innate behavioural patterns. Such behavioural switches provide attractive opportunities to explore the genetic and neural control of the innate behaviours. Mating in many species triggers a dramatic switch in female reproductive behaviour. For example, virgin females are receptive to courting males and retain their eggs, whereas those that have recently mated are unreceptive and lay eggs. In most insects, these changes in female behaviour are induced by factors present in the male's seminal fluid. How these factors exert such profound effects in females is unknown. Here, we identify a receptor for the *Drosophila melanogaster* sex peptide (SP), the primary trigger of post-mating responses in this species. Females that lack the sex peptide receptor (SPR), either entirely or only in the nervous system, fail to respond to SP and continue to show virgin behaviours even after mating. Furthermore, SPR gene encodes a GPCR high sensitive and selective for SP. SPR is expressed in the female's reproductive tract and central nervous system. The behavioural functions of SPR map to the subset of neurons that also express the fruitless gene, a key determinant of sex-specific reproductive behaviour. SPR is highly conserved structurally and functionally across insects, opening up the prospect of new strategies to control the reproductive and host-seeking behaviours of agricultural pests and human disease vectors. Our identification of SPR is the critical step in explaining this behavioural switch at the molecular, cellular and circuit levels.

Eradication and containment of *Cactoblastis cactorum* in Mexico and the United States

James Carpenter[1], Stephen Hight[2], Arturo Bello[3], Rafael Zetina[4]

[1]USDA-ARS, Crop Protection Research Unit, Tifton, GA 31794, United States, [2]USDA-ARS, Center for Medical, Agricultural, & Veterinary Entomology, Tallahassee, FL 32308, United States, [3]SEGARPA, Dirección General de Sanidad Vegetal, México DF, Mexico, [4]Comité Estatal de Sanidad Vegetal de Quintana Roo, Cancún, QR, Mexico

Introduction: To address the advancement of *Cactoblastis cactorum* along the southeastern gulf coast of USA and new incursions in Mexico, control tactics including sanitation and the Sterile Insect Technique (SIT) were validated and implemented.

Methods: Three sites were selected for the SIT validation study: control (no manipulation of infested plants); sanitation only (removal of eggsticks, infested pads/larvae, and pupae); and sanitation plus SIT (removal plus strategic release of sterile moths). Population change and treatment efficacy were monitored with pheromone traps and sentinel plants. Parentage of eggsticks was determined to evaluate sterile/wild moth interaction. Sanitation and host plant removal were part of a multifaceted control program on Isla Mujeres, Mexico, and sanitation and SIT were used on Isla Contoy, Mexico.

Results: In the SIT validation study sanitation alone reduced moth populations but sanitation coupled with SIT lowered the population to immeasurable levels. Effective overflooding ratios (~10:1) (sterile:wild males caught in traps) and collection of eggsticks from wild female and sterile male matings indicated that sterile males were competitive with wild males. Control tactics and other program initiatives used in Mexico greatly reduced or eliminated pest populations on Isla Mujeres and Isla Contoy.

Conclusions: The success of the SIT validation study justified the transfer of this technology to other outbreaks at the western leading edge of *C. cactorum* in Alabama, and to assist Mexico in the removal of *C. cactorum* recently established on two islands off the Yucatan Peninsula.

Advances in semiochemical based management of coleoptera

Cam Oehlschlager

ChemTica Int., San Jose, Costa Rica

Rhynchophorus palm weevils are world-wide pests of oil & coconut palm. In Central & South America *R. palmarum* cause direct larval damage & vectoring of red ring nematode. Our group and collaborators have developed a management system of pheromone trapping & removal of red ring nematode infested palms that is the only economically viable technique used in the Americas used to combat the palm weevil problem. In the Middle East and Southern Europe *R. ferrugineus* is a has become serious pest of date palm. Pheromone / food based trapping is again the method of choice for management. Mass trapping is also used on a wide scale to manage *Cosmopolites sordidus*, the banana corm weevil, as well as *Oryctes rhinoceros*, a pest of newly planted oil palm in South East Asia. Recently, mating disruption has emerged as a strategy applicable to Coleoptera. Pre-commercial application in the United States targets *Exomala orientalis*, Oriental beetle. Repellents are firmly established as management tools for several species of tree infesting Coleoptera in ecologically sensitive areas.

Spatial and temporal dynamics of predators of brassica pests

Heimoana, V.[1], Gurr, G. M.[1], Raman, A.[1], and Pilkington, L.J.[2]

[1]School of Rural Management, Charles Sturt University, P.O.Box 883, Orange, NSW, 2800, [2]NSW, Department of Primary Industries, Gosford Horticultural Institute, Locked Bag 26, Gosford, NSW, 2250

The ladybird beetle, *Hippodamia variegata* (Goeze) (Coleoptera: Coccinellidae), a recent arrival in Australia, and a native brown lacewing, *Micromus tasmaniae* (Walker) (Neuroptera: Hemerobiidae), are being investigated as potential biological control agents for arthropod pests in brassica crops. Monthly surveys of various habitats on vegetable farms in the Central West of New South Wales, Australia have shown that both species are an important numerical component of the natural enemy fauna. Numbers increased during spring but were not uniformly high over summer months possibly reflecting broad-spectrum pesticide use and lack of available prey. Predator densities in non-crop habitats are relatively high in the period leading up to brassica crop planting and may be an important source of natural enemies. Findings from mark/recapture studies of the predators will be presented with results from the use of DNA identification of their gut contents. Results will be integrated to formulate habitat manipulation strategies suitable for maximising the impact of natural enemies in brassica field crops.

Spatial and temporal dynamics of predators of brassica pests

Heimoana, V.[1], Gurr, G. M.[1], Raman, A.[1], and Pilkington, L.J.[2]

1. *School of Rural Management, Charles Sturt University, P.O.Box 883, Orange, NSW, 2800*
2. *NSW, Department of Primary Industries, Gosford Horticultural Institute, Locked Bag 26, Gosford, NSW, 2250*

The ladybird beetle, *Hippodamia variegata* (Goeze) (Coleoptera: Coccinellidae), a recent arrival in Australia, and a native brown lacewing, *Micromus tasmaniae* (Walker) (Neuroptera: Hemerobiidae), are being investigated as potential biological control agents for arthropod pests in brassica crops. Monthly surveys of various habitats on vegetable farms in the Central West of New South Wales, Australia have shown that both species are an important numerical component of the natural enemy fauna. Numbers increased during spring but were not uniformly high over summer months possibly reflecting broad-spectrum pesticide use and lack of available prey. Predator densities in non-crop habitats are relatively high in the period leading up to brassica crop planting and may be an important source of natural enemies. Findings from mark/recapture studies of the predators will be presented with results from the use of DNA identification of their gut contents. Results will be integrated to formulate habitat manipulation strategies suitable for maximising the impact of natural enemies in brassica field crops.

Higher level phylogeny of the true Swallowtail Butterflies (Lepidoptera: Papilionidae: Papilioninae) with special reference to the enigmatic and endangered genera Teinopalpus and Meandrusa, and the subgenera within the genus Papilio

Thomas Simonsen*, Evgueni Zakharov**, Felix Sperling*

University of Alberta, Edmonton, Alberta, Canada, University of Guelph, Guelph, Ontario, Canada***

The true Swallowtail butterfly family Papilioninae is comprised of approximately 550 species in 24 genera and three tribes. The two genera *Teinopalpus* and *Meandrusa* are not at the moment definitively associated with any tribe. Though the Swallowtails are among the best known invertebrates, the genus-level phylogeny of Papilioninae is poorly understood. Here we present a "total evidence" phylogenetic analysis of the subfamily based on morphological characters (mainly from literature) and molecular characters from seven genes. The phylogeny is then used to analyze zoogeographical and biological aspects of the Papilioninae.

Morph-specific circadian rhythm for the juvenile hormone titer in wing polymorphic crickets*:* Functional and evolutionary implications for the endocrine basis of morph specialization

Anthony J. Zera

School of Biological Sciences, University of Nebraska, Lincoln, NE 68588-0118

Since the 1960's, juvenile hormone has been proposed to be a major regulator of wing polymorphism, with differences in the JH titer above or below some threshold controlling alternate morph development, reproduction, and dispersal. Although this widely-held hypothesis has nearly attained the status of dogma, experimental support has been surprisingly weak, coming almost exclusively from indirect, hormone manipulation studies, which are often difficult to interpret regarding endocrine mechanisms. Recent direct measurement of the hemolymph JH titer in wing-dimorphic crickets (*Gryllus*) has produced an exciting and unanticipated finding: the blood JH titer exhibits a large-amplitude circadian rhythm (50-fold change in titer within 4-6 hours) in the long-winged (LW) morph, and a nearly temporally-invariant titer in the short-winged (SW, flightless, reproductive) morph. The JH titer in the LW morph cycles above and below the titer in the SW morph. These morph-specific titer differences occur in laboratory as well as in field populations, and represent the first detailed endocrine investigation of insects in natural populations. The morph-associated circadian/temporally-invariant profiles are primarily caused by morph differences in temporal rates of JH biosynthesis. By contrast, the ecdysteroid titer is consistently higher in short-winged vs. long-winged female morphs, in the laboratory and in the field; male morphs do not differ in the ecdysteroid titer. The extent to which the JH circadian profile occurs within or outside of the Orthoptera is unknown. The functional significance and evolutionary implications of these morph-specific differences in the JH titer will be discussed.

Development of an artificial diet rearing system for woolly apple aphid (*Eriosoma lanigerum* H.)

Dario Stefanelli, Kevin S. Powell

Department of Primary Industries, BioScience Research Division, Rutherglen, Victoria, Australia

Introduction: Woolly apple aphid (WAA), *Eriosoma lanigerum* (Hausmann), is one of the economically important pests of apple, *Malus domestica* (Borkh.). Artificial diets are an important tool to study insect development, feeding behaviour, symbiont activity and to screen for novel antimetabolites which may aid in their control. Prior to this study, artificial diets were available for a range of aphids but not WAA. The aim of this study was to develop an *in vitro* rearing system using artificial diets for WAA.

Methods: Two WAA stock populations were reared under greenhouse conditions on susceptible apple seedlings. Two feeding chamber designs ("conventional" and "inverted"), three sucrose concentrations (5%, 10% and 20%), and one diet formulation (Febvay et al, 1988) were tested. In all experiments a no diet control was used. Fifty first instar nymphs were utilised for each treatment and control. The geographical provenience of the aphid populations were tested separately as factors.

Results: The "inverted" chamber design was best suited for WAA feeding and utilised for all subsequent testing. Five and 10% sucrose concentration were statistically different from the control but suboptimal in terms of insect development and survival. Twenty percent sucrose and the Febvay diet more than doubled the survival time, up to 19 days, and evidence of ecdysis was observed. There was a significant difference in the survival curve and duration between the two aphid populations, which is indicative of genetically distinct characteristics.

Conclusions: An *in vitro* feeding system was developed for WAA which could be used to screen antimetabolites.

Occurrence and Control of Psocids in China

Jinjun Wang, Wei Dou

Key Laboratory of Entomology and Pest Control Engineering, College of Plant Protection, Southwest University, Chongqing 400716, P. R. China

Introduction: As small, polyphagous insects generally ignored in most grain storage systems, psocids have recently become a serious problem in food industries and stored products in China. The review is to elucidate the distribution of psocid species in China and may assist in formulating strategies in the control of these rapidly proliferating pests.

Occurrence: *Liposcelis* psocids have gained much prominence as pests in the Chinese grain ecosystem. The specific biological traits (small body size and short generation period) contribute to rapid and substantial psocid population growth. A survey of numerous farms and central storages suggested that four *Liposcelis* spp., *L. bostrychophila* Badonnel, *L. entomophila* (Enderlein), *L. decolor* (Pearman) and *L. paeta* Pearman, are the most commonly detected of these in stored grain.

Control: Routine fumigation of warehouses and storage facilities with methyl bromide or using insecticides has failed to control psocids, which can readily reinfest grain in storage after fumigation or insecticides treatments. As an alternative treatment to the use of methyl bromide for post-harvest insect control, controlled atmospheres (CA) has showed promise for control of stored product pests. Similarly, extensive use of CA in insect control could lead to selection of insect populations resistant to hypercarbia and hypoxia.

Conclusions: Despite numerous reports of resistance to many insecticides, chemical control will continue to play an important role in psocids control programs. Studies on population ecology and resistance development to control treatments are fundamental to the development Integrated Pest Management (IPM) strategies for psocids.

Occurrence and Control of Psocids in China

Jinjun Wang and Wei Dou

Key Laboratory of Entomology and Pest Control Engineering, College of Plant Protection, Southwest University, Chongqing 400716, P. R. China

Introduction: As small, polyphagous insects generally ignored in most grain storage systems, psocids have recently become a serious problem in food industries and stored products in China. The review is to elucidate the distribution of psocid species in China and may assist in formulating strategies in the control of these rapidly proliferating pests.

Occurrence: *Liposcelis* psocids have gained much prominence as pests in the Chinese grain ecosystem. The specific biological traits (small body size and short generation period) contribute to rapid and substantial psocid population growth. A survey of numerous farms and central storages suggested that four *Liposcelis* spp., *L. bostrychophila* Badonnel, *L. entomophila* (Enderlein), *L. decolor* (Pearman) and *L. paeta* Pearman, are the most commonly detected of these in stored grain.

Control: Routine fumigation of warehouses and storage facilities with methyl bromide or using insecticides has failed to control psocids, which can readily reinfest grain in storage after fumigation or insecticides treatments. As an alternative treatment to the use of methyl bromide for post-harvest insect control, controlled atmospheres (CA) has showed promise for control of stored product pests. Similarly, extensive use of CA in insect control could lead to selection of insect populations resistant to hypercarbia and hypoxia.

Conclusions: Despite numerous reports of resistance to many insecticides, chemical control will continue to play an important role in psocids control programs. Studies on population ecology and resistance development to control treatments are fundamental to the development Integrated Pest Management (IPM) strategies for psocids.

Social evolution of the Allodapine bees

Luke Chenoweth, Michael Schwarz

Flinders University, Adelaide, South Australia, Australia

Background: The major lineages of eusocial insects, the ants, termites, stingless bees, honeybees and vespid wasps, all have ancient origins (≥ 65 mya) with no reversions to solitary behaviour. This has prompted the notion of a 'point of no return' whereby the gradual evolutionary elaboration and integration of behavioural, genetic and morphological traits leads to a situation where reversion to solitary living is no longer an evolutionary option.

Methods: We use information on nest composition and dissection data to explore the ubiquity of social behavior in another group of social insects, the allodapine bees, by examining the social behavior of a key species. *Halterapis nigrinervis* is unique in that it is believed to be the only example of a solitary nesting allodapine. We then use molecular phylogenetic techniques to re-estimate the origin of social behavior within the tribe.

Results: We show the allodapine bees have a single origin of sociality > 40 mya. We also show that *H. nigrinervis* is truly social, and our findings therefore indicate there have been no losses of sociality among extant allodapine clades. All females in virtually all allodapine species are capable of nesting and reproducing independently, so the species within this tribe clearly do not fit the 'point of no return' concept.

Conclusions: We argue that allodapine sociality has been maintained by ecological constraints and the benefits of alloparental care, and that similar vulnerabilities may also help explain the lack of reversions to solitary living in other taxa with ancient social origins.

Using artificial neural networks to predict and quantify risk of invasion by insect pests

Dean Paini[1], Sue Worner[2], Matt Thomas[1], David Cook[1]

[1]Cooperative Research Centre for Plant Biosecurity, Canberra, ACT, Australia, [2]Lincoln University, Christchurch, New Zealand, [3]Penn State University, University Park, Pennsylvania, United States

Introduction: Predicting which species are most likely to invade a particular region presents significant challenges to researchers and government agencies. In order to rank the potential list of invasive species, experts and stakeholders are often consulted for their opinion. This method, while valuable, can bring a level of subjectivity to the process. Artificial neural networks, specifically self organising maps (SOM's), present the possibility of objectively identifying and quantifying the risk of invasion by insect pests.

Methods: Using presence/absence data of insect pests from the CABI Crop Pest Compendium we generated SOM's and subsequently a quantitative risk list of invasive insect pests to Australia.

Results: As SOM's are initiated from a randomly assigned starting point, there is the risk of generating significantly different lists each time a new SOM is generated. We examined these variations and the parameters involved in generating a SOM and found that lists were generally very stable, regardless of the various parameters used. We then tested how the presence of errors in the original presence/absence data and their subsequent corrections could affect these lists. We found that the lists were sensitive to these errors and that the size of the SOM's generated and the number of iterative steps influenced the robustness of these lists.

Conclusions: SOM's offer a novel method to identifying and ranking the risk of pest species invading a particular region.

Spider venoms as source of bioinsecticides: a comparison of the insecticidal toxicity of various tarantula venoms

Margaret C. Gentz, Glenn F. King

Institute for Molecular Bioscience, University of Queensland, St. Lucia, Queensland, Australia

Introduction: Spiders are master insect killers that have been optimizing their venoms for over 300 million years. The venoms of modern spiders are a complex chemical cocktail containing hundreds, if not thousands, of discrete components. By comparing the potency of venoms from different species of Australian and American tarantulas we aim to select specific species for isolation of specific compounds that might have application as bioinsecticides.

Methods: Immature domestic crickets (*Acheta domesticus*) and adult houseflies (*Musca domestica*) were injected with dilutions of crude tarantula venom in insect saline. Tarantulas consisted of an unidentified *Phlogiellus* species from north of Cairns, Queensland (Aranea: Theraphosidae), Australia; pooled venom from a cohort of funnel-web spiders *Hadronyche infensa* (Aranea: Hexathelidae) all collected from Fraser Island, Queensland, Australia; pooled venom from Mexican tarantulas *Brachypelma hamorii* and *B. ruhnaui* (Aranea: Theraphosidae).

Results: The Mexican tarantula *B. hamorii* was the most potent, followed by the Australian funnel-web spider, *B. ruhnaui*, and finally *Phlogiellius*. LD_{50} values were in the picogram of crude venom/gram of cricket weight range, which approximates values found previously for peptide toxins from Australian funnel-web spiders.

Discussion: Tarantulas from Australia and Mexico exhibit similar, but subtly different, toxicity in both crickets and flies. However, all crude venoms caused lethality to flies and crickets at roughly $1/100^{th}$ of the concentration delivered during an envenomation.

An integrated approach to management of sweetpotato whitefly and cucurbit yellow stunting disorder

Eric Natwick, William Wintermantel, Robert Gilbertson, Yen-Wen Kuo, Gregory Walker, Jolene Dessert

[1]University of California ANR, Holtville, CA, United States, [2]USDA-ARS, Salinas, CA, United States, [3]University of California Davis, Davis, CA, United States, [4]University of California Davis, Davis, CA, United States, [5]University of California Riverside, Riverside, CA, United States, [6]Imperial County Agricultural Commissioner's Office, El Centro, CA, United States

In 2006 *Cucurbit yellow stunting disorder virus* (CYSDV) was detected in Southern California cucurbit crops. This was verified with RT-PCR and sequence analysis. RT-PCR also verified that *Bemisia tabaci* (Genn.) biotype B was transmitting the virus. Due to the economic impact of CYSDV on melon production it was critical to limit the spread of CYSDV and develop management strategies. Cucurbit germplasm was screened for resistance to both CYSDV and *B. tabaci* in a series for field trials. Trials also were conducted to determine if rowcovers and insecticides could exclude *B. tabaci* and prevent or delay CYSDV infection in melon. The geographic range of CYSDV in the Imperial Valley was determined in the spring and fall of 2007 via surveys of all melon fields. Because the only known (non-experimental) hosts of CYSDV were species in the *Cucurbitaceae* family, cucurbit-free periods were recommended during the summer to prevent severe damage to fall cucurbit crops and to prevent further spread of CYSDV. Common non-Cucurbitaceae weeds and crops in the region were also screened as potential hosts of CYSDV. The spring survey established that the virus had overwintered or been reintroduced (though inefficiently) in spite of an extended freeze the previous winter. Although 2007 fall melon crops were extensively infected with CYSDV, growers produced marketable fruit. Lettuce had been listed as an experimental host of CYSDV; but the virus was detected in Romaine lettuce from the Imperial Valley, indicating that lettuce can be a host of the virus. CYSDV was transmitted from infected lettuce back to melon by *B. tabaci*. Romaine lettuce is potentially an important bridge host for CYSDV between spring and fall melon crops, due to the large acreage of lettuce in the region during the winter months.

Characterising feeding behaviour and nutritional requirements of leafhopper *Orosius orientalis* using *in vitro* and *in planta* systems

Piotr Trebicki[1], Rob M. Harding[1], Brendan C. Rodoni[2], Kevin S. Powell[3]

[1]Queensland University of Technology,, Centre for Tropical Crops and Biocommodities, Brisbane, Queensland, Australia, [2]Department of Primary Industries, Bioscience Research Division, Knoxfield, Victoria, Australia, [3]Department of Primary Industries, Bioscience Research Division, Rutherglen, Victoria, Australia

Introduction: *Orosius orientalis* (Matsumura) (Hemiptera, Cicadellidae) is a leafhopper vector of many plant pathogens. Little is known about *O. orientalis* in relation to its host plant interactions requirements and epidemiology of pathogen transmission/acquisition. To develop alternative management options, we have been investigating *in vitro* and *in planta* systems to study the feeding behaviour and nutritional requirements of this insect.

Methods: Stock colonies of *O. orientalis* (Matsumura) were maintained on celery (*Apium graveolens* L.) and bean (*Phaseolus vulgaris* L.) under glasshouse conditions. Two artificial diet formulations were tested ands enhanced survival was obtained on the PT-07 diet. The antimetabolic activity of three compounds, *Galanthus nivalis* agglutinin (GNA), wheat germ agglutinin (WGA), cowpea trypsin inhibitor (CpTI) towards first instar nymphs was assessed at 0.1% (w/v) concentration in this diet formulation. An electrophysiological technique was used to assess feeding activity on both artificial diet and host plants.

Results: An i*n vitro* diet bioassay system for *O. orientalis* was developed and it could survive for up to 46 days on PT07 diet. GNA and WGA had significant antimetabolic activity and reduced the insects survival duration to 22 and 16 days respectively. CpTI had no significant antimetabolic activity. Preliminary characterisation of feeding waveforms were assessed on first instar nymphs both *in planta* and *in vitro*.

Conclusion: This is the first study to optimise an artificial diet feeding bioassay system for *O. orientalis*, identify potential feeding inhibitors and examine the feeding behaviour by using the EPG system on both host plant and artificial diets.

Can we exploit nature's influence on arthropods and mechanisms of the 'push-pull' technology in resistance management to Bt-maize?

Charles Midega[1], Zeyaur Khan[1], Johnnie van den Berg[2], Ansie Dippenaar[3], John Pickett[4]

[1]International Centre of Insect Physiology and Ecology, Nairobi, Kenya, [2]Northwest University, Potchefstroom Campus, Potchefstroom, South Africa, [3]ARC- Plant Protection Institute, Pretoria, South Africa, [4]Rothamsted Research, Herpenden, United Kingdom

Introduction: A 'push-pull' Technology (PPT) and Bt-maize have been developed to manage cereal stemborers. PPT involves intercropping maize with a moth repellent plant, Desmodium, while an attractant plant, Napier grass, is planted as a trap crop around this intercrop. Studies were conducted to assess (1) numerical response of ground dwelling arthropods to both strategies, using spiders as an indicator group; and (2) potential role of the PPS in stemborer resistance management in Bt-maize through influence on the pests' oviposition and mortality from predation.

Methods: Plots were established in western Kenya and in South Africa. Spiders were sampled using pitfall traps and soil samples. Oviposition preference was evaluated, and predation rates of naturally and artificially infested stemborer eggs and larvae were assessed in natural enemy exclusion studies.

Results: A total of 2175 spiders, 70 species in 18 families, were recovered in Kenya and 658 spiders, 49 species in 12 families, in South Africa. Spider abundance was significantly higher in PP than in control plots. Bt-maize had no direct impact on spider abundance and diversity. Significantly more eggs were oviposited in control than in PP plots. Predation rates of eggs and early-instar larvae were similarly significantly higher in PP than in control plots.

Conclusion: PPS can play a significant role in Bt-resistance management through reduction of pest population getting exposed to Bt-toxin.

Influence of sexual cannibalism on paternity in the Australian praying mantid *Pseudomantis albofimbriata*

Katherine Barry

Macquarie University, Sydney, NSW, Australia

Although the potential benefits of male consumption are well documented for females of many sexually cannibalistic species, the fitness consequences for males are often less obvious, and largely depend on the timing of cannibalism in relation to insemination. If cannibalism occurs during/after mating, a male's loss of future reproductive output may be at least partially outweighed by associated benefits. For example, the male soma may contribute to the fecundity of his mate thereby enabling her to produce more eggs, and/or cannibalised males may fertilise a higher proportion of eggs when mating with a polyandric female. The current study examines the influence of sexual cannibalism on paternity in the Australian praying mantid *Pseudomantis albofimbriata,* a species in which males can initiate copulation and transfer sperm while being consumed. A series of single mating experiments showed that cannibalistic females significantly improved their body condition as a result of male consumption and subsequently produced heavier egg cases than their non-cannibalistic counterparts. Furthermore, female body mass was a significant predictor of egg case mass (positively related to egg number), suggesting females utilize nutrients from the male soma to increase the absolute number of eggs available for fertilization. Since *P.albofimbriata* males are able to mate with several females, we also carried out double mating experiments to compare the paternity allocation of cannibalized and non-cannibalized males under a polyandrous scenario (sterile male technique). We discuss the results of these experiments in the context of male mating strategies, mate choice and sperm competition in praying mantids.

The biology of an emerging mite pest of grains, *Balaustium medicagoense*, in southeastern Australia

Aston Arthur, Andrew Weeks, Ary Hoffmann

Centre for Environmental Stress and Adaptation Research, Department of Genetics, The University of Melbourne, Parkville, Vic, Australia

Balaustium medicagoense have recently been identified as a potential emerging pest mite within the Australian agricultural industry. The damage caused by *B. medicagoense* in Australia has increased in the last decade, with reports indicating that these mites have caused extensive damage to a variety of grain crops and pastures, yet little is known about their biology. Here we address this by gaining insight into the plant host range, pesticide tolerance and population genetics of *B. medicagoense* in Australia. A shade-house experiment showed that *B. medicagoense* causes significant damage and can persist for a generation on five different agriculturally important plant hosts. Pesticide bioassays show that *B. medicagoense* has a much greater level of tolerance than another earth mite species (*Halotydeus destructor*) to several chemicals registered for their control. To determine levels of genetic variation within and between populations, we used the amplified fragment length polymorphism method. The AFLPs showed that *B. medicagoense* reproduces asexually, has limited genetic variation and is made up of a limited number of clones with populations dominated by several common clones. The results suggest that *B. medicagoense* could be a pest of significance to the grains industry within Australia that will be problematic to control.

A simulation model of the greyback canegrub and its pathogens, with special emphasis on *Metarhizium anisopliae*

Frank Drummond[1], Peter Samson[2], Keith Chandler[2], Mohamed Sallam[2]

[1]University of Maine, Orono, Maine, United States, [2]BSES limited, Queensland, Australia

Introduction: A simulation model was developed to explore the dynamics of key factors that influence the long-term population dynamics of the greyback canegrub, *Dermolepida albohirtum* (Waterhouse) (Coleoptera: Scarabaeidae). The model is a stage-specific representation of the canegrub life history.

Methods: A statistical disease sub-model was incorporated in a greyback cane grub computer simulation model. The model is a delay-differentyial equation model that simulates each life stage of the beetle. This model incorporated total disease due to the fungus *Metarhizium anisopliae*, the protozoan *Adelina* sp., and the bacterium *Paenibacillus popillae*. A mechanistic submodel of *M. anisopliae* was developed with relationships developed in laboratory bioassays and field experiments.

Results: Four years of field data from 2003-2006 suggests that *Metarhizium* infections may affect greyback canegrub populations in the following year. However, it appears that disease incidence of 25% or greater is necessary for declines in population levels the following year. Simulation runs suggest that disease mortality (from all sources) can significantly regulate canegrub populations, but only in a stochastic version of the model when intra-specific canegrub larval competition was also incorporated into the model. The design of a probabilistic sub-model of *Metarhizium anisopliae* based upon encounters with infective cadavers will be discussed.

Automated image-analysis arthropod identification

Andrew Moldenke, David Lytle, Tom Dietterich, Eric Mortensen, Robert Paasch

OSU, Corvallis, OR PNW, United States

Introduction: The analysis of ecological samples (aquatic dipnet, Berlese, sweepnet) is often seriously limited by the complexity of the sample (number of individuals/species) and by adequately trained taxonomic personnel. Automated computer-assisted recognition and sorting could significantly decrease time/cost and permit limiting taxonomic expertise to be far more efficiently utilized.

Methods: We are integrating 1) recent advances in computer vision algorithms; 2) novel robotic devices for specimen manipulation; and 3) extensive digital image databasing. We utilize non-specified imaging region detectors so that the protocol can theoretically process images of any type of arthropod. Our initial test samples were non-diverse (1-10 spp) immature aquatic Plecoptera characterized by logarithmic size differences and considerable within-population pattern variability. Currently we are adapting the process for soil mesoarthropods.

Results: We have developed 2 robotic devices for handling, imaging and archiving the specimens. Larger specimens (Plecoptera) are: 1) placed one-at-a-time into a circulating fluid system; 2) sucked through the tubing to a transparent display under the microscope; 3) stopped by an electronic eye and positioned automatically by peripheral fluid jets; 4) photographed with 2 contrasting background colors (so that the stonefly image can be 'segmented' unambiguously from the background); and 5) subsequent to identification, directed to a designated vial. Smaller specimens (mesofauna) are: 1) placed in a Petri plate on a motorized microscope stage; 2) individually recognized from a collage image of the total Petri plate; 5) identified and then removed by a robot arm equipped with a pipette; and 6) placed in an appropriate well plate.

Being prepared: ecological informatics and computational intelligence methods applied to invasive insect risk assessment

Susan P. Worner[1], Michael J. Watts[2], Muriel Gevrey[3], Joel P.W. Pitt[1]

[1]National Centre for Advanced Bio-Protection Technologies, Lincoln University, Canterbury, New Zealand, [2]School of Biological Sciences, University of Sydney, NSW 200, Australia, [3]Laboratoire "Evolution et Diversité Biologique" (EDB) UMR 5174 - Université Paul Sabatier / CNRS, Toulouse Cedex 9, France

As increasing numbers of species are moved around the world and as ranges alter in response to climate change, risk assessment of potential alien invasive species becomes increasingly important. Risk assessment and analysis are required to make decisions concerning which species are likely to cause economic or environmental damage and to allocate resources to prevent or control an incursion. Risk assessments are usually qualitative and reactive and often focused on individual species. Yet, when large numbers of insect species have potential for harmful impact in regions where they are not normally found, conventional risk assessment does little to help prioritise the risk. New approaches based on neural networks, machine learning and spatially explicit models are described that allow pre-emergent species to be identified, potential establishment to be predicted with high accuracy, and spread over a detailed heterogeneous landscape to be simulated. Prioritisation of potential invasive insect species with respect to risk adds a new tool to the risk analysis framework. Additionally, prediction of potential establishment and simulation of spread over topographic, climatic and land-cover features, results in realistic dispersal patterns and identification of potential 'hotspots'. Given appropriate data, a spatially explicit model such as that described here not only allows sampling programs for detection to be tested, eradication strategies to be evaluated, but also bioeconomic models of impact to be refined before an incursion occurs. These quantitative approaches allow uncertainty to be evaluated and utilised for a more informed approach to the threat of non-native insect incursion.

Behaviour of caterpillars on plants at a fine scale: hairs, waxes and chemicals

Bronwen W Cribb[1], Lynda E Perkins[2], Jim Hanan[3], Ezekiel Glaze[2], Myron P Zalucki[2]

[1]Centre for Microscopy & Microanalysis, University of Queensland, Brisbane, Queensland, Australia, [2]School of Intergrative Biology, University of Queensland, Brisbane, Queensland, Australia, [3]ARC Centre of Excellence in Integrative Legume Research, University of Queensland, Brisbane, Queensland, Australia

Introduction: In order to model movement of an herbivorous insect on a plant so that the resultant model becomes predictive, we have divided interactions of the insect with the plant into two scales: the macro and the micro. At the micro scale, insects are exposed to the plant surface structure, local physical properties, and chemistry.

Methods: We have used the polyphagous caterpillar, *Helicoverpa armigera*, along with a range of plants, including the garden pea, cotton, tobacco and cabbage to investigate interactions at the fine scale. Scanning electron microscopy has been used to image plant surfaces (e.g. waxes and trichomes) and document physical interactions between the insect and plant, such as silk attachment points and feeding sites. A range of local and general physical properties have been measured, and insect behaviour has been recorded by direct observation as well as by video.

Results: Only a limited suite of local stimuli appear to be important in effective modeling of the movement behaviour of *H. armigera*. Movement rates and directions are greatly affected by diffuse stimuli perceived in the local environment. Interestingly, the first instar *H. armigera* shows the capacity to modify its local environment for effective feeding behaviour. The relative importance of local versus general sensory input will be discussed

Conclusions: In modeling movement of *H. armigera* effectively, only a limited array of micro-scale data need be included.

Timing and patterns of diversification in beetles (Coleoptera)

Duane McKenna

[1]Harvard University, Cambridge, MA, United States, [2]Museum of Comparative Zoology, Cambridge, MA, United States

Introduction: Modern beetles exhibit extraordinary ecological and taxonomic diversity. However, the absence of a robust phylogeny for beetles has hampered efforts to clarify higher-level relationships, and timing and patterns of beetle diversification.

Methods: Using molecular phylogenetic, fossil, and other data, I will present a brief overview of beetle macroevolution using examples from my research at various taxonomic levels, including (1) the four suborders of living beetles (Adephaga, Archostemata, Myxophaga, Polyphaga), (2) weevils (superfamily Curculionoidea), and (3) herbivorous Neotropical leaf beetles (family Chrysomelidae, genus *Cephaloleia*).

Results: I will present evidence for the rapid radiation of beetle suborders in the late Permian, the codiversification of weevils and angiosperms, and the roles of climate change, geological events, and codiversification in the evolutionary radiation of 'hispine' beetles in the genus *Cephaloleia*.

Conclusions: Taken together, this research show that biological, geological, and climatological events have played important, often synergistic roles in the diversification of beetles.

The 1999–2001 Australian plague locust outbreak in eastern Australia from the perspective of insect monitoring radar

Haikou Wang[1], V Alistair Drake[2], Edward D Deveson[1]

[1]Australian Plague Locust Commission, Australian Government Department of Agriculture, Fisheries and Forestry, GPO Box 858, Canberra, ACT 2601, Australia, [2]School of Physical, Environmental and Mathematical Sciences, UNSW@ADFA, Australian Defence Force Academy, Canberra, ACT 2600, Australia

Introduction: The outbreaks of Australian plague locusts, *Chortoicetes terminifera* (Walker), in the agricultural/horticultural region of south-eastern Australia had long been believed to originate in the arid interior from sudden population developments there after good spring and summer rain, despite northward migrations having been observed with scanning entomological radars over 20 years ago. More recent observations with automated insect monitoring radars (IMRs) with vertical-pointing beams have provided new evidence on how outbreaks of this locust develop.

Methods: Two IMRs have been set up 300 km apart in inland eastern Australia, at Bourke, NSW and Thargomindah, Qld. They run automatically for 11 hours every night starting around sunset. The digitised radar signals are analysed the following morning and estimates of each target's height, speed, displacement direction, body alignment, size, shape, wingbeat frequency, and wingbeat modulation form extracted. Their characteristic echo signature allows overflying plague locusts to be identified with high confidence. Their migration trajectories are calculated from IMR detected flight parameters and related to population distributions and development states obtained from field surveys.

Results: About 140 nights were identified with detectable plague locusts over Bourke during the three seasons 1998–2001 and 31 nights over Thargomindah during 1999–2000. Most plague locusts flew for 6–8 hours after sunset and travelled 200–330 km over the semi-arid region around Bourke, but flew all night covering about 400 km over the arid subtropical region of Thargomindah. These observations revealed that the plague locusts undertake a northward return migration in spring and early summer that helps maintain population persistence. Successful migrations to favourable interior habitats lead to rapid population growth and a risk of an autumn invasion of the south-eastern agricultural belt.

Conclusions: The near real-time data from the IMRs can provide the early warning of significant infestation needed for effective preventive control. Consecutive successful migrations of plague locusts in the variable and heterogenous habitats of eastern Australia contribute significantly to the development of locust outbreaks and their movement into cropping regions.

Dynamic population density of the coconut hispine beetle, *Brontispa longissima* Gestro (Coleoptera: Chrysomelidae)

Sopon Uraichuen[2], Kittiya Suksen[1], Wiwat Suasa-ard[1]

[1]National Biological Control Research Center, Bangkok, Thailand, [2]Kasetsart University, Bangkok, Thailand

Introduction: The coconut hispine beetle, *Brontispa longissima* Gestro was accidentally introduced into continental Southeast Asian countries, presumably in the early 2000's, with ornamental palms. Since then it become one of the most serious insect pest of coconut in Thailand.

Methods: Dynamic population density study of *B. longissima* was taken place by using 3 coconut fields at Kamphaeng Saen, Nakhon Pathom province in the Central Region of Thailand. Data collection was done twice a month. The sampling program was set by using 5 leaves as a sample unit and 16 samples per location. The number of eggs, larvae, pupae and adults of the beetle were recorded from August 2006 to December 2007. All data were subsequently analyzed and considered with density independent (DI) factors.

Results: Analysis results of the combinative DI factors affected to dynamic population of *B. longissima* indicated that rain volume, temperature and relative humidity caused change of the beetle population. The result revealed that the more rain volume and the less relative humidity, the greater number of egg pest. Meanwhile, temperature was a negative additional effect to the survival beetle larvae. Regard to adult population, the DI factors did not directly make a change in its population. Nevertheless, they could substantially give the lower egg laying rate of the female adult as well as the lesser hatch percentage.

Conclusions: The DI factors, rain volume, temperature and relative humidity which seasonal alter through the year round were the combinative effect to the dynamic change of *B. longissima* population.

Status of occurrence and monitoring of ambrosia beetles with alcohol bait traps in Korean apple orchards

Kyung-Hee Choi, Soon-Won Lee, Dong-Hyuk Lee, Dong-Ah Kim

Apple Experiment Station, Gyeongsangbukdo, Republic of Korea

Recently, ambrosia beetles has become very important pest of 2~5years old apple trees with M9 dwarf rootstocks in South Korea. It has killed the branches and stems of the young trees, especially, freeze-damaged trees in winter or drought stressed tree in spring. As the high density apple planting system with M9 dwarf rootstocks reduces the effort of management and enhances the yields, the area of that has been sharply increased since the latter 1990's. But M9 rootstock is weak in frozen damages in winter and then ambrosia beetles has become key pest in Korean apple orchards using M9 rootstock.

According to the survey of damaged apple trees by ambrosia beetles in 1998, *Xylosandrus germanus* Blandford was 62.5%, *Xyleborus apicalis* Blandford was 31.9%, and *Xyleborus minutus* Blandford was 5.5%, while in 2007, *Xylosandrus germanus* Blandford was 75%, *Xyleborus minutus* Blandford was 18%, *Xyleborus apicalis* Blandford was 4%, and *Xylosandrus crasiussculus* Motschulsky was 3%. Although the ambrosia beetles were well trapped in the ethyl alcohol of both 70% and 95%, 70% was considered to be more economical on account of alcohol's volatility. And they got trapped most effectively when traps were equipped at a one-meter height. They began to active and search for a suitable host(apple trees) when the highest temperature of a day exceed 20□ in spring.

From the middle of the 2000's, high density apple planting system has been greatly expanded, and ambrosia beetles which come flying in mountainous area now tend to be the primary hosts as they form density for winter survival themselves in apple orchards.

Morphometrics as applied to medical entomology

Jean-Pierre Dujardin

[1]IRD, Montpellier, France, [2]CVVD, Bangkok, Thailand

Introduction: In medical entomology, one of the main priorities is the set up of low cost but efficient tools for species recognition, especially cryptic species. Morphometrics provides this tool with additional virtues: the one of characterizing local populations, the one of identifying sources of re-infestation after insecticide treatments, and among others not cited here the one of detecting and interpreting population structuring.

Methods: species recognition makes use of PCA and CVA on shape variables, and would benefit from the existence of pictures data bases, re-infestation studies uses the resemblance between offspring and parents, and population structure studies benefits from associated genetic studies when allowing comparisons between Qst and Fst. To improve a strictly morphometric interpretation of population structure, we suggest an original method based on shape similarity between individuals.

Results: A few examples are given about species and re-infestation studies. More detailed presentation is made of the population structure study method, with a few examples combining morphometric and genetic approaches.

Conclusions: The main application of morphometrics to medical entomology, species identification, still needs the set up of relevant images data bases. The perspective of interpreting population structure is suggested.

Parasitoids for biocontrol of coffee berry borer: Past, present and future

Juliana Jaramillo[1], Juliana Jaramillo[2], Fernando E Vega[3]

[1]International Center of Insect Physiology and Ecology, icipe, Nairobi, Kenya, [2]Institute of Plant Diseases and Plant Protection, University of Hannover, Hannover, Germany, [3]Sustainable Perennial Crops Laboratory, United States Department of Agriculture, Agricultural Research Service, Maryland, United States

Introduction: The coffee berry borer (CBB) (*Hypothemenus hampei* (Ferrari); Col.: Curculionidae) is the most important pest of coffee throughout the world. Endemic to Africa, CBB has been accidentally introduced to most coffee producing countries, where it has become a highly damaging pest. In many countries, management of CBB relies on the use of synthetic insecticides, but due to their adverse effects on human health and the environment, other alternatives such as biocontrol are increasingly important. So far, three CBB parasitoids of African origin have been introduce to the Americas, *Prorops nasuta* Waterston, *Cephalonomia stephanoderis* Betrem (Hym.: Bethylidae) and *Phymastichus coffea* LaSalle (Hym.: Eulophidae). However, their impact has been rather limited.

Methods: Detailed surveys for CBB parasitoids were initiated in October 2006 in two coffee growing areas of Kenya (Kisii and Embu). In total, five organic coffee plantations have been sampled every 2-3 weeks. On each sampling date, CBB-infested coffee berries collected from the tree or from the ground were taken to the laboratory and placed in containers. Daily emergence of parasitoids was assessed.

Results: All emerging parasitoids are being identified at the Systematic Entomology Laboratory (USDA, ARS) and their possible role as natural enemies of CBB is being investigated. The most abundant species are *P. nasuta* and *Ceraphron* sp., (Hym.: Ceraphronidae). Our preliminary findings indicate that *Ceraphron* sp. is a hyperparasitoid of *P. nasuta*. Both insects exhibit a distinct phenology linked to the population dynamics of CBB. Emergence data from berries collected from the ground (i.e., in the leaf litter strata), largely exceeds those from the trees, indicating that these berries form an important reservoir for natural enemies.

Conclusions: In Kenya, CBB populations are being controlled mainly by a complex of parasitoids that work synergistically in different periods of the year. Of these parasitoids, the most important species seems to be the bethylid *P. nasuta*. The importance of natural enemies harboured in coffee berries in the leaf litter strata for integrated pest management is discussed.

Brachyceran assemblages (Diptera) as indicators of terrestrial palaeoenvironments in the Late Mesozoic

Mike Mostovski

Natal Museum and School of Biological & Conservation Sciences, UKZN, Pietermaritzburg, South Africa and Paleontological Institute, Moscow, Russia, Pietermaritzburg, Moscow, South Africa

The diversification of brachyceran Diptera started during the Middle or Late Jurassic and continued successfully over Cretaceous and entire Cainozoic. Although there is a number of extinct families, the majority of them is extant. This gives an opportunity to use presumed ecological characteristics of their representatives for reconstructing palaeoenvironments at sites of their burial. Data from the following oryctocoenoses have been examined: Karatau (Kazakhstan; Callovian–Kimmeridgian), 'Tsagaan-Tsav' (several localities in Mongolia; basalmost Cretaceous), Purbeck and Wealden (England; Berriasian–Barremian), Baissa (Transbaikalia; Valanginian–Hauterivian), Bon-Tsagaan (Barremian–Aptian), Obeshchayushchiy (Russian northern Far East; Senomanian), Orapa (Botswana; Senomanian–Turonian). Collecting bed-by-bed at Baissa gives a chance to analyse the environmental history of the deposition basin. The proportion of Empididae *s.l.* seems to be particularly important for establishing humid or mesic *vs.* dry environments. Strong fliers like members of Eremochaetidae, Therevidae, Asilidae, Nemestrinidae, Bombyliidae, and Mydidae indicate the presence of open landscapes. Presumed pollinators like Nemestrinidae and Mydidae suggest the presence of "flowering" plants in the surrounding vegetation.

Revision of some parasitic wasps (Hymenoptera) from Florissant, USA, with certain palaeoenvironmental inferences

Victor Kolyada[1], Mike Mostovski[2]

[1]Zoological Museum of Moscow University and Paleontological Institute, Moscow, Russian Federation, [2]Natal Museum and School of Biological & Conservation Sciences, UKZN, Pietermaritzburg, South Africa

Proctotrupidae is a relatively small and world-wide distributed family of parasitic wasps that prefer temperate and humid habitats. At the beginning of the last century, Brues (1910) and Cockerell (1915) described three species of parasitic wasps from the Florissant locality (Colorado, USA; Upper Eocene/Lower Oliogocene, Florissant Formation) in the families Proctotrupidae, Diapriidae and Scelionidae. Re-examination of types confirms that all this material belongs to Proctotrupidae and represent genera *Oxyserphus*, *Pschornia*, *Mischoserphus*, and *Nothoserphus*. Species of *Oxyserphus* live in temperate and subtropical forests and parasitise on larvae of Curculionidae and Anthribidae (Coleoptera); only recently this genus has been found in the palaeontological record (Lower Oligocene Bembridge Marls and Late Eocene Baltic amber). Species of *Pschornia* are found in temperate and mountain forests and parasitise on larvae of Cleridae (Coleoptera); this is the first record of this genus as fossil. Species of *Mischoserphus* occur in temperate and subtropical forests, preferring mesic habitats, and parasitise on larvae of fungus gnats (Diptera: Mycetophiloidea); only recently this genus has been found in the palaeontological record (Bembridge Marls and Baltic amber). Species of *Nothoserphus* inhabit temperate and subtropical forests and parasitise on larvae of Coccinellidae (Coleoptera); this is the first record of this genus as fossil.

Revision of some parasitic wasps (Hymenoptera) from Florissant, USA, with certain palaeoenvironmental inferences

Victor Kolyada[1], Mike Mostovski[2]

[1]Zoological Museum of Moscow University and Paleontological Institute, Moscow, Russian Federation, [2]Natal Museum and School of Biological & Conservation Sciences, UKZN, Pietermaritzburg, South Africa

Proctotrupidae is a relatively small and world-wide distributed family of parasitic wasps that prefer temperate and humid habitats. At the beginning of the last century, Brues (1910) and Cockerell (1915) described three species of parasitic wasps from the Florissant locality (Colorado, USA; Upper Eocene/Lower Oliogocene, Florissant Formation) in the families Proctotrupidae, Diapriidae and Scelionidae. Re-examination of types confirms that all this material belongs to Proctotrupidae and represent genera *Oxyserphus*, *Pschornia*, *Mischoserphus*, and *Nothoserphus*. Species of *Oxyserphus* live in temperate and subtropical forests and parasitise on larvae of Curculionidae and Anthribidae (Coleoptera); only recently this genus has been found in the palaeontological record (Lower Oligocene Bembridge Marls and Late Eocene Baltic amber). Species of *Pschornia* are found in temperate and mountain forests and parasitise on larvae of Cleridae (Coleoptera); this is the first record of this genus as fossil. Species of *Mischoserphus* occur in temperate and subtropical forests, preferring mesic habitats, and parasitise on larvae of fungus gnats (Diptera: Mycetophiloidea); only recently this genus has been found in the palaeontological record (Bembridge Marls and Baltic amber). Species of *Nothoserphus* inhabit temperate and subtropical forests and parasitise on larvae of Coccinellidae (Coleoptera); this is the first record of this genus as fossil.

The impact of herbivorous insects on the photosynthetic characteristics of three cecidomyiid galls and their hosts

Meng-Yuan Huang[1], Yung-Ta Chang[1], Man-Miao Yang[2], Chi-Ming Yang[3]

[1]Department of Life Science, National Taiwan Normal University, Taipei, Taiwan, [2]Department of Entomology, National Chung-Hsing University, Taichung, Taiwan, [3]Research Center for Biodiversity, Academia Sinica, Taipei, Taiwan

Introduction: Multiple changes in response to gall inducers have been found in host plant tissues. While much attention has been focused on the morphology and anatomy of insects or their induced galls, relatively little work has been done on the photosynthesis. Our previous data showed that some photosynthetic apparatus, such as pigment-protein complexes of PSI and PSII, of gall are life time deficient. Based on assumptions of source-sink hypothesis, we predicted that leaf-derived cecidomyiid galls play the role as novel sink in *Machilus thunbergii* and *Litsea acuminata* leaves.

Methods: Gas exchange, chlorophyll fluorescence, scanning electron microscopy were used to investigate the photosynthetic characteristics of leaf-derived cecidomyiid galls and their host leaves.

Results: No gas exchange was found in all galls investigated, whereas the gall-resided and gall-free leaves demonstrated normal gas exchange at equal level. No stoma structure was found on the inside and outside surface of gall. Inside surface of galls was full of fungal hyphae. While chlorophyll fluorescence of gall was at the level of 0.6-0.7, that of gall-resided and gall-free leaves 0.8.

Conclusions: Combination of previous and present result suggested that herbivorous insects may dramatically alter photosynthetic efficiency of leaf-derived gall via changing partial apparatus of PSI and PSII on the thylakoid membrane, but do not alter that of their host leaves. The results further suggest that the leaf-derived cecidomyiid galls are sinks in *Machilus thunbergii* and *Litsea acuminata* leaves.

Comparing mushroom body with surrounding neuropil of insect brains

Friedrich-Wilhelm Schurmann

University of Gottingen, Johann-Friedrich-Blumenbach-Institut fur Zoologie und Anthropologie, Gottingen, Germany

Introduction: Insect brains show two forms of neuropil structure, mainly refered to as so called glomerular, “ordered“ neuropil or “diffuse“ neuropil. A comparison of the two forms of neuropil is presented for the mushroom body and surrounding neuropil.

Methods: Morpological features of brain neuropils of fruit flies, bees and crickets have been analyzed by immuncytochemical, light and and electron microscopic approaches.

Results: Selected similaraties and differences in neuropil design with special reference to mushroom body calycal synaptic microcircuits are considered. Classical and modern light microscopical studies show the obvious geometrical order of repeated arrays of classes of local interneurons in mushroom bodies pointing to redundant nerve cells. In contrast, local and relay neurons in the “diffuse“ neuropil appear as unique neurons identified by structure and forming networks with a “hidden“ order.Transmitters and neuromodulators so far detected are encountered in both forms of neuropil, but their distribution and accumulation underline the ordered neuropil character of mushroom bodies versus surrounding “diffuse“ neuropil stucture. Synapse and vesicle markers appear randomly distributed in the diffuse neuropil, whereas in mushroom bodies synaptic sites are concentrated in subcompartments. A unifying character of both forms of neuropil is their equipment with complex synaptic circuits.

Outlook: The meaning of structural neuropil differences and problems to generalize are considered.

The evolution of psyllids and galls: a review

Daniel Burckhardt

Naturhistorisches Museum, Basel, Switzerland

Introduction: Psyllids (Hemiptera, Psylloidea) often induce galls on the leaves, flowers, woody stems or roots of their host plants. Generally their host plant ranges are very narrow at the species and at higher taxonomic levels. The morphology of psyllid galls is quite diverse ranging from open pits to closed spherical structures. Gall induction is mostly associated with larval stages but eggs and feeding adults can provoke deformations on the host as well.

Result: Gall inducing species are well represented among the Psylloidea but their distribution is taxonomically and geographically uneven. Species of the large genera *Acizzia* (Acizziinae) and *Cacopsylla* (Psyllinae) do not or rarely induce galls, whereas most *Calophya* (Calophyidae) and many *Pseudophacopteron* (Phacopteronidae) species induce conspicuous galls. The gallicolous species are particularly numerous in the tropics. In Java (Indonesia) about 5 % of all galls are induced by Psylloidea. The variation of gall types and distributional patterns is illustrated with examples such as the South American psyllids of the genera *Calophya* and *Tainarys* associated with *Schinus* (Anacardiaceae). Evolutionary aspects are discussed.

Conclusions: Psyllids are specialized with regard to their host species as well as the site on the host where they feed and develop. This specialization probably helps to use food resources more efficiently, and may be an evolutionary strategy to escape predators and parasitoids. A phylogenetic interpretation suggests that the presence and type of galls can be predicted by the psyllid phylogeny in some instances and by the host plant phylogeny in others.

Apterous males in Mutillidae (Hymenoptera: Aculeata): Pattern and process

Denis Brothers

University of KwaZulu-Natal, Scottsville, South Africa

Introduction: In Mutillidae (velvet ants), females are invariably apterous but males are generally fully winged. The differences are thought to relate to the need for females to find suitable hosts, often involving digging, where wings could be impediments or subject to damage, while the males could still disperse widely, thus promoting outcrossing. Some species show phoretic copulation, where males carry females during mating, emphasising the importance of males for dispersal. In several genera, however, males show wing reduction, from brachyptery to complete aptery. The mesosoma (thorax) in females always shows fusion of some or all sutures and most have no ocelli. Winged males have the sutures fully developed and well developed ocelli, but wing reduction or loss is associated with varying degrees of mesosomal modification and even loss of ocelli.

Methods: The form of the mesosoma and ocelli was surveyed in both sexes across the genera of Mutillidae on a worldwide basis.

Results: Males of Pseudophotopsidinae, Myrmosinae (including Kudakrumiini) and Rhopalomutillinae are all fully winged. Brachypterous or apterous males are found in Ticoplinae: Smicromyrmillini (few species, Afrotropical and Oriental); Sphaeropthalminae: Dasylabrini (several species, Afrotropical) and Sphaeropthalmini (few species, New World); Myrmillinae (several species, Palaearctic and Afrotropical) and Mutillinae: Smicromyrmina (few species, Afrotropical). This tendency is apparently most common in southern Africa. The patterns of mesosomal modification in males do not mirror those in females. The paucity of knowledge about the biology of Mutillidae, and the relevant species in particular, prevents any conclusions about the reasons for the distributional or developmental patterns of apterous and brachypterous males.

How does herbivore-induced plant regrowth govern geographic and genetic variation in a feeding preference of a leaf beetle?

Shunsuke Utsumi, Yoshino Ando, Takayuki Ohgushi

Center for Ecological Research, Kyoto University, Otsu, Shiga, Japan

Introduction: We hypothesized that a feeding preference of the specialist leaf beetle *Plagiodera versicolora* adults to new leaves of willows would be favored by natural selection for adaptation to the temporal patterns in food resource recruitment, depending on the extent of induced regrowth response of willows.

Methods: To examine geographic variation in new leaf production of willows and the beetle preference, we conducted field survey and laboratory choice test. Also, to detect a genetic basis for the preference, an half-sib analysis was conducted. Finally, evolutionary change in the preference was examined by directional selection experiment using different leaf age types.

Results: Some allopatric populations displayed strong preference to new leaves of *Salix eriocarpa*, but others showed no preference. There was a positive correlation between new leaf production in early summer and feeding preference to new leaves. Willow regrowth is likely to be responsible for geographic variation in new leaf production in early summer. A genetic basis for the feeding preference was detected; additive genetic variance and heritability were significantly different from zero. Our directional selection experiment resulted in divergence of the feeding preference. A population confined to new leaves produced by regrowth displayed an increased preference to new leaves, and a population confined to mature leaves displayed a decreased preference to new leaves.

Conclusion: Induced willow regrowth would maintain geographic variation in the feeding preference of the leaf beet adult and govern a locally adaptive preference.

Introduction to the biodiversity and heteronomy in Strepsiptera

Jeyaraney Kathirithamby

University of Oxford, Oxford, United Kingdom

Introduction: Since the use of molecular techniques for the study of Strepsiptera we have uncovered several interesting aspects in this group which remained a puzzle before. Aspects such as cryptic speciation are critical for the study of the biodiversity of this bizarre entomophagous parasitoids.

Heteronomy: Heteronomy is less common and often overlooked type of polymorphism and is found only in two lineages of insects: in the hymenopteran subfamily Coccophaginae (Aphelinidae), and in the strepsipteran family Myrmecolacidae. Walter (1983) introduced the term heterotropic heteronomy for the complex and extreme form of behaviour. In the aphelinid the mother (a hymenopteran) selects a totally different host for her male and female eggs. As a consequence the males develop in a different host to the female. The host relationships of the females are conserved and they develop as endoparasites of Sternorrhyncha (whiteflies) (Hemiptera) and males develop as primary endoparasites in eggs of Lepidoptera. The separation of male and female host differs from that in strepsipteran Myrmecolacidae, because in the aphelinid it is the mother which seeks the host to lay the egg of an appropriate sex.

In the strepsipteran family Myrmecolacidae, the males develop as primary parasites in ants (Formicidae: Hymenoptera), and the females as primary parasites in grasshoppers, mantids and crickets (Orthoptera: Tettigoniidae, Grillidae; Mantidae). Yet it is the first instars that encounter/seek the appropriate host. This is a unique form of heterotrophic heteronomous life history, a polymorphism not found in any other insect parasitoid.

Is *Bacillus thuringiensis* better than pesticides in vegetable brassica production systems?

R. Srinivasan[1], B.S. Rekha[2], T.M. Bharpoda[3], Hirak Chatterjee[4], A.R.V. Kumar[2], R.C. Jhala [3], Mei-Ying Lin[1]

[1]AVRDC-The World Vegetable Center, Shanhua, Tainan, Taiwan, [2]University of Agricultural Sciences, Bangalore, Karnataka, India, [3]Anand Agricultural University, Anand, Gujarat, India, [4]Palli Siksha Bhavana, Visva Bharati, Birbhum, West Bengal, India

Introduction: Efforts are underway to develop and introduce *Bacillus thuringiensis* (Bt)-based insect resistant transgenic brassicas, either with a single gene or with two genes. Hence, it becomes imperative to assess the likely impact of Bt on target and non-target organisms.

Methods: Simulated field experiments were undertaken in India and Taiwan to assess the impact of Bt on phytophagous insects, natural enemies and soil arthropods in vegetable brassicas.

Results: The simulated field experiments with *Xentari*, a Bt formulation based on *B. t.* subsp. *aizawai* containing both Cry1A and Cry1C toxins recorded lower infestations of diamondback moth, cabbage head caterpillar and cabbage web worm. However, insects such as aphids, whiteflies and flea beetles were not controlled by Bt. Bt did not have any significant adverse effects on the population of parasitoids like *Cotesia plutellae*, predators such as spiders, and soil arthropods including coleopterans, dermapterans, hymenopterans, lepidopterans and arachnida. However, the populations of ladybird beetles and field crickets were reduced in Bt-treated plots compared to the untreated plots, although the Bt-treated plots recorded higher numbers of these insects when compared to plots receiving synthetic chemical pesticides.

Conclusions: Bt containing two or more Cry toxins kept the population of major lepidopterans on vegetable brassicas under check. However, it was not effective against sucking insects and flea beetles. Comparatively Bt was safer to natural enemies and soil arthropods.

Family-group names in Coleoptera

Patrice Bouchard[1], Yves Bousquet[1], Miguel A. Alonso-Zarazaga[2], John F. Lawrence[3], Chris H. C. Lyal[4], Alfred F. Newton[5], Michael Schmitt[6]

[1]Canadian National Collection of Insects, Arachnids and Nematodes, Agriculture and Agri-Food Canada, Ottawa, Canada, [2]Departamento de Biodiversidad y Biología Evolutiva, Museo Nacional de Ciencias Naturales, Madrid, Spain, [3]Australian National Insect Collection, CSIRO Entomology, Canberra, Australia, [4]Department of Entomology, The Natural History Museum, London, United Kingdom, [5]Zoology Department, Field Museum of Natural History, Chicago, United States, [6]Zoologisches Forschungsmuseum Alexander Koenig, Bonn, Germany

Correct usage of family-group names in zoology has received increased interest in the last 25 years. The motivation behind this recent attention is to standardize and stabilize their usage through time. Sabrosky (1999) reviewed all known Diptera family-group names (based on approximately 2000 type genera) in what could be considered the most comprehensive treatment of such names to date.

In Coleoptera, Lawrence and Newton (1995) presented a landmark review of the higher classification of world beetles as well as a nomenclatural treatment of some family-group names (family and subfamily names only). They estimated that there may be in excess of 10 000 family-group names (including tribes and subtribes) based on distinct type genera in Coleoptera literature. While reviews of Coleoptera family-group names for some of the major clades have been published recently (e.g. Geodephaga, Staphyliniformia, Cucujoidea, Scarabaeoidea, Curculionoidea), an effort to thoroughly review literature associated with names of all groups has not been attempted yet.

The specific goal of our project is to provide a complete catalogue of available family-group names (families, subfamilies, tribes, subtribes) proposed in the order Coleoptera since 1758. This treatment will include recent discoveries on historical entomological literature and will be based on a consistent application the ICZN rules within the entire order. The resulting catalogue will include names of both extant and extinct taxa, will be based on the most recent classification scheme of the order and will be made available freely through an open-access journal.

Conservation of the endemic and endangered Karkloof blue butterfly *Orachrysops ariadne*

Adrian Arnstrong, Sharon Louw

Ezemvelo KZN Wildlife, Pietermaritzburg, KwaZulu-Natal, South Africa

Introduction: This study aims to improve the conservation status of the Karkloof blue butterfly *Orachrysops ariadne*, including through joint community management.

Methods: An egg-monitoring system was developed by comparing a known-area count and an index count. The areas of the host-plant (*Indigofera woodii* var *laxa*) at the known colony sites were delimited. Host-plant seeds were collected from one site and germinated *ex situ*. A host-ant (*Camponotus natalensis*) distribution survey was carried out at that site. Prediction of suitable habitat in which to search for other colonies was carried out by distribution modelling.

Results: The index count was more efficient. A precipitous decline in egg numbers over three consecutive years was recorded at one site, caused by mammalian browsing and uncontrolled fire. After the establishment of a firebreak, an increase in the number of host-plants and hatched eggs was recorded. Host-plant distribution areas at three of the four sites varied from 1.35 ha to almost 10 ha. At one site, the distribution of the host-plant and the host-ant were largely congruent. The number of unrecorded colonies is likely to be few.

Conclusions: Total egg counts will be continued annually at one site and the index method used triennially at each of the other sites. Regular monitoring of eggs allows timeous conservation action to be initiated, and joint community management is important for success. Host-plants germinated *ex situ* and planted where host-ants occur may increase the potential number of oviposition sites. Fencing should help further reverse the decline in egg numbers.

Triphasic screening of cultivated grapevines *Vitis* species for resistance to grapevine phylloxera *Daktulosphaira vitifoliae*

Kevin Powell[1], Ginger Korosi[1], Carolyn Trethowan[1], Ary Hoffmann[2]

[1]Department of Primary Industries, Biosciences Research Division, Rutherglen Centre, Rutherglen, Victoria, Australia, [2]CRC for Viticulture and Centre for Environmental Stress and Adaptation Research, Bio21 Molecular Science and Biotechnology Institute, Building 102, Level 2, 30 Flemington Road, The University of Melbo, Melbourne, Victoria, Australia

Introduction: Screening for resistance or tolerance to grapevine phylloxera *Daktulosphaira vitifoliae* Fitch has generally focused on selecting populations of insects and not the use of genetically distinct clonal lineages. It has also focused on the use of one or more protocols including laboratory, glasshouse and field screening.

Methods: A systematic triphasic approach to screening for phylloxera 'resistance' has been developed using up to six genetically distinct clonal lineages of *D. vitifoliae*. Laboratory studies utilised an excised root bioassay protocol, glasshouse studies utilised a quarantine mesh system, to avoid cross contamination of phylloxera genetic strains and field studies were conducted using trapping techniques to monitor population abundance in commercial vineyards with natural infestations of grapevine phylloxera.

Results: Six genetic strains of phylloxera were tested for resistance under glasshouse and laboratory to a range of commercially available rootstocks and showed different virulence levels on both rootstocks and susceptible *Vitis vinifera* L. Abundance of phylloxera on rootstocks under field conditions was influenced by rootstock and site conditions.

Conclusions: A triphasic screening system has been developed for rootstock 'resistance' to grapevine phylloxera. This will lead to improved rootstock resistance ratings based on genotypic interactions.

Single locus molecular markers can give a misleading trace of the origin and spread of species.

Felix Sperling

University of Alberta, Edmonton, Alberta, Canada

Although mitochondrial DNA and various other molecular markers can be useful for identifying specimens to species when there is good information available on background variation, there have been very few studies that test the efficacy of these markers rigorously. Such markers have been employed to resolve one or more of several distinct problems: 1) identification of a known species, 2) discovery of new species, 3) delimitation of species, and 4) reconstructing phylogenetic relationships. These questions demand different properties from molecular markers. For example, mitochondrial DNA may identify a specimen to species in only part of its geographic range, but this problem is often not be detected because surveys of variation are not geographically comprehensive. Single locus markers may give intriguing hints of cryptic species, but without being integrated into parallel sampling across other character types they can be profoundly misleading about the genomic integrity of species boundaries as well as the origin and spread of species. Since there is much at stake when molecular markers are used to justify holding up shipments or implementing control measures, it is important to have a statistically defensible framework for evaluating the probability of correct identification or source for a sample.

Polytomies and rapid radiations - phylogenetics of the Coenonymphina-Hypocystina group of butterflies (Nymphalidae: Satyrinae)

Ullasa Kodandaramaiah[1], Niklas Wahlberg[2]

[1]Dept of Zoology, Stockholm University, Stockholm, Sweden, [2]Laboratory of Genetics, Department of Biology, University of Turku, Turku, Finland

Rapid radiations have been identified in several groups of organisms and numerous studies have highlighted the problems involved in the reconstruction of their phylogenies. In particular, the combination of short internal and long external branches can lead to near-polytomous nodes, thus misleading tree reconstruction using both Maximum Parsimony (MP) and model-based methods such as Maximum Likelihood (ML) and Bayesian Inference (BI). Based on simulation and empirical studies, several features of rapid radiations with respect to tree reconstruction are identified. In the current study, these features are used to identify nodes that are likely to be near-polytomous, within a group of butterflies - the subtribes Coenonymphina and Hypocystina (Nymphalidae: Satyrinae). We suggest that this approach can be used under certain circumstances to distinguish nodes at which rapid bursts of speciation have occurred from normal nodes. We also argue that in many cases, it is not practically feasible or even impossible to resolve near-polytomous nodes and in such cases the search for a fully bifurcating tree leads to erroneous results. Thus polytomies should be incorporated as a valid hypothesis in phylogenetic reconstruction.

Enhancing sustainability in vegetable farming: Clarification of *Macrolophus* species that colonize tomato and the potential of alternative host plants in conservation biological control

Dionyssios Perdikis[1], Nikolaos Garantonakis[1], Athanassios Giatropoulos[1], Theodoros Gouvitsas[2], Anna Kourti[2], Dionyssios Lykouressis[1], Antonios Peraskevopoulos[3], Efthalia Gkinala[1], Argyro Fantinou[4]

[1]Laboratory of Agricultural Zoology and Entomology, Agricultural University of Athens, Athens, Greece, [2]Department of Agricultural Biotechnology Agricultural University of Athens, Athens, Greece, [3]Directorate of Rural Development, Trifylia, Kyparissia, Greece, [4]Laboratory of Ecology and Environmental Sciences Agricultural University of Athens, Athens, Greece

Introduction: In recent years there is a fast growing interest to increase sustainability in vegetable production by applying less intensive methods for pest control. Under this concept, key functional component of tomato agroecosystems in the Mediterranean region are the widespread, polyphagous predators *Macrolophus melanotoma* (= *M. caliginosus*) and *M. pygmaeus* (Hemiptera: Miridae) originated from two very common non-crop plants *Dittrichia viscosa* L. (Asteraceae) and *Solanum nigrum* (Solanaceae), respectively.

Methods: Open field sampling, greenhouse and laboratory experimentation along with molecular studies were performed to answer: i) which of the two predators colonize tomato and ii) which of non-crop plants could be anticipated to be natural reservoir or banker plant for implementation in conservation biological control schemes in the open field or in the greenhouses.

Results: Field experiments did not detect edge effects on tomato crop colonization. *M. pygmaeus* from *S. nigrum* was proved to be the *Macrolophus* species that can colonize tomato. In contrast, *M. melanotoma* showed, in all scale experiments, a strong preference for its origin host plant, *D. viscosa*.

Conclusions: Our results addressed a main set of uncertainties regarding the conservation of *Macrolophus* predators in vegetable habitats. It was proved that *S. nigrum* could be a main element of cropping systems that aim to take benefit from the conservation of *M. pygmaeus.*

Potential indirect impact of the invasive leaf-miner, *Cameraria ohridella*, on native leaf-miners

Christelle Péré[1], Sylvie Augustin[3], Rumen Tomov[4], Ted Turlings[2], Marc Kenis[1]

[1]CABI Europe-Switzerland, Rue des Grillons 1, 2800 Delémont, Switzerland, [2]University of Neuchâtel, rue Emile Argand 11, CP 158, 2009 Neuchâtel, Switzerland, [3]INRA, 2163 av. de la Pomme de Pin, BP 20619, Ardon, 45166 Olivet Cedex, France, [4]University of Forestry, Bul. Kliment Ohridski 10, 1756 Sofia, Bulgaria

Introduction: The horse-chestnut leaf-miner, *Cameraria ohridella*, is a moth of unknown origin that was first observed in Macedonia in 1984 and has now invaded most of Europe. It is attacked by several native leaf-miners' parasitoids. Despite the low parasitism rates observed in *C. ohridella*, populations are so high that an unusual amount of polyphagous parasitoids are produced in the vicinity of infested horse-chestnut trees two or three times per year. In spring, the bulk of the parasitoids emerge at least six weeks before the first suitable *C. ohridella* larvae or pupae are available. These parasitoids could massively attack the first indigenous leaf-miners developing in spring. We tested the hypothesis that the presence of *C. ohridella* has a negative effect on populations of native leaf-miners through shared natural enemies (apparent competition).

Methods: Species richness and abundance of indigenous leaf-miners were assessed in presence and absence of *C. ohridella*, in Switzerland, France and Bulgaria.

Results: In spring, the species richness of indigenous leaf-miners was significantly lower in the presence of *C. ohridella* than in its absence. Some native leaf-miners, such as the beech and oak leaf-mining weevils, *Orchestes fagi* and *O. quercus*, sharing their parasitoid complex with *C. ohridella,* were significantly less abundant at sites with horse-chestnuts attacked by *C. ohridella* compared to control sites.

Conclusion: Parasitoids, and possibly predators, are the only link between *C. ohridella* and native leaf-miners feeding on other host-plants and are thus probably responsible for the decrease.

The control of *Callosobruchus maculatus* L. (Bruchidae: Coleoptera) in different cereals with Spinosad dust

Adel Khashaveh[1], Nouraddin Shayesteh[2], Farzaneh Attighi[1]

[1]Urmai University, Urmia/west Azarbaijan, [2]Islamic Azad University, Branch of Mahabad, Mahabad/west Azarbaijan, Islamic Republic of Iran

Introduction: Spinosad is a new bacterial-based insecticide. Most available experimental data are for liquid formulations, while very little is know about applying spinosad as a dust.

Methods: The effectiveness of spinosad dust formulation (0.125% a.i.) against *Callosobruchus maculatus* (L) was assessed on four commodities, Cowpea, Chickpea, Lentil and yellow split pea. The experiment was carried out with 4 replication and thirty 0-24 h old adults were used for each replication. Commodities treated with three dose rate; 0.1, 0.2 and 0.3 g/kg at 27℃ and 60± 5% r.h. The mortality of *C. maculatus* adults was measured after 24 h, 48 h, 5 d and 10 d. After the 10-day mortality count, all surviving insects were removed and the samples retained under the same conditions for a further 35 days to assess progeny production.

Results: The increase of dose and exposure interval increased mortality and significant difference was recorded among the four cereal types. After 10 days of exposure, mortality received to 100 % in all commodity at high rate (0.3 g/kg) except of yellow split pea that it was significantly lower than other commodities (79/46% after 10 d exposure). The application of spinosad significantly reduced progeny production in the four commodities tested in comparison with the untreated ones. High reduction in progeny production was recorded when spinosad applied at the rate of 0.3 g/kg on Lentil and Cowpea (94/33 and 94/21, respectively).

Conclusions: This research counseled that spinosad dust formulation could control different life stages of *C. maculatus* in different cereals.

Population dynamics and diversity of leafhopper Cicadellidae vectors of Tobacco Yellow Dwarf Virus (TYDV)

Piotr Trebicki[1], Rob M. Harding[1], Brendan C. Rodoni[2], Gary Baxter[4], Kevin S. Powell[3]

[1]Centre for Tropical Crops and Biocommodities, Queensland University of Technology, Brisbane, Queensland,, Australia, [2]Department of Primary Industries, Bioscience Research Division, Knoxfield, Victoria, Australia, [3]Department of Primary Industries, Bioscience Research Division, Rutherglen, Victoria, Australia, [4]Department of Primary Industries, Ovens, Victoria, Australia

Introduction: To assess geographical distribution, population dynamics and diversity of leafhoppers a variety of different trapping methods are available. Many leafhopper species are important agricultural pests and damage occurs directly through feeding and indirectly through transmission of pathogens. Determining the population dynamics and distribution of potential leafhopper vectors can lead to improve suitable management practices through optimisation of control options. This study compared trapping techniques and assessed the relative abundance of potential leafhopper vectors with the ability to transmit and acquire TYDV.

Methods: During two growing seasons the population dynamics and relative seasonal abundance of Cicadellidae were monitored at four commercial field sites in NE Victoria, Australia. Three different trapping methods; sticky trap, yellow pan water trap and sweep net were assessed on a weekly basis around the borders of cultivated tobacco farms. The presence of TYDV in leafhoppers and host plants was assessed using standard PCR protocols.

Results: During two seasons, the yellow pan trap proved the most effective trapping technique for monitoring diversity and population dynamics of leafhoppers. A greater diversity of leafhoppers were recorded using this technique and a ten-fold increase in some species compared to the sweep net and sticky trap methods. TYDV was detected in *Zygina spp*. and in *O. orientalis* during the summer period.

Conclusion: Trapping techniques were optimised to monitor the seasonal distribution of potential leafhopper vectors and host plants for TYDV. The knowledge gained can improve management practices for this insect-virus complex.

Diabrotica virgifera virgifera LeConte (Coleoptera: Chrysomelidae) appearing in Germany 2007: surprise, disaster, challenges, and consequences for IPM

Hans E. Hummel

Justus-Liebig-University Giessen, Organic Agriculture, Giessen, Germany

In July of 2007 the first leaf beetles of Western corn rootworm (WCR) were detected in maize fields of Southern Germany. Two sites in the States of Baden-Württemberg and Bavaria reported spot infestations with close to six hundred WCR indicating undetected earlier (2005 or 2006) immigration events. Public reactions ranged from surprise to warnings of pending disaster for maize agriculture in north central Europe, while for experts simultaneous detection at 5 sites within two States hardly came as a surprise. The author had predicted this scenario of introduction on numerous occasions. The public, however, decided to adopt a "wait and see" attitude relying both on ecologically questionable, non sustainable insecticide treatments and on EU emergency directives.- While the new findings of WCR in Germany are a blow to quarantine measures, they hardly qualify as an immediate disaster since *Zea mays* can tolerate a modest infestation rate without significant yield loss. Rather, recent WCR infestations may be viewed as a challenge for integrated pest management whose components may consist of 1. mandatory crop rotation as practiced in Switzerland for several years, 2. quarantine, 3. biological and biotechnical control measures, 4. classical selection of resistant maize varieties and 5. a narrow network of monitoring stations. - Further introductions from the US into Europe, including Eastern Europe, by hitchhiking beetles aboard airplanes, ships and trucks cannot be ruled out, nor can transport of WCR to Africa and East Asia be excluded. An even greater challenge may arise from the recent discovery by Hummel et al. (2007a and b) and Hummel (2007) of WCR acquiring additional secondary host plants such as members of the Cucurbitaceae, soybean, sunflower, *Amaranthus, Ambrosia* and *Chenopodium* spp. Given the enormous biotic and genetic potential of WCR, under certain constant selection pressure these plants may, with time, develop into primary hosts and thus diminish their present value for crop rotation. - Sustainable WCR management in Europe is a severe challenge for all entomologists, including the younger members of the profession. Predictions of constant conflicts of *Homo sapiens* with pest insects made by Steven Forbes, State Entomologist of Illinois, close to one hundred years ago, lost nothing of their actuality, and fully apply to WCR in Germany and Europe.

Mosquito species diversity and abundance in relation to land use in a riceland agroecosystem in Mwea, Kenya

Josephat Shililu[1], Ephantus Muturi[2], John Githure[1], Robert Novak[2]

[1]I.C.I.P.E, Nairobi, Kenya, [2]UAB, Birmingham, AL, United States

Introduction: The full scale of mosquito diversity has been scarcely studied in rice agroecosystems despite the strong link between irrigation agriculture and disease transmission. Studies have tended to focus on specific malaria vectors ignoring other mosquito species thriving in rice agroecosystems.

Methods: Adult mosquitoes were sampled bimonthly indoors by PSC and outdoors by CDC light traps for 12 months in 3 villages representing different rice cropping regimen. The mosquitoes collected were identified morphologically to species using taxonomic keys.

Results: Irrigation had a marked effect on the mosquito diversity and abundance with 17 species (n= 66,828) collected in the planned rice growing village, 22 species (n= 21,074) in the unplanned rice growing site and 20 species (n= 10,808) in the non- rice growing village. The density of *Anopheles arabiensis* and other anophelines was higher in the rice field environments than in the non-irrigated sites. The predominant species collected indoors were *An. arabiensis* (80.1%), *Culex quinquefasciatus* (18.2%), and *An. funestus* (1.5%) whereas outdoors common species included *C. quinquefasciatus* (54.7%), *An. arabiensis* (25.9%), *An. pharoensis* (10.3%), *An. coustani* (2.6%), *C. annulioris* (1.8%), *C. poicilipes* (1.2%), *An. maculipalpis* (1.1%) and *An. funestus* (1.1%). *An. arabiensis*, *An. pharoensis* and *C. quinquefasciatus* were mainly associated with rice cultivation occurring in significantly higher densities in the village with the planned rice cultivation than in the unplanned one while *An. funestus* and *An. maculipalpis* were significantly higher in the non-rice village. The mosquito species diversity (H) and evenness (E_H) in the non-rice growing site (Shannon diversity Index, $H = 1.507$, $E_H = 0.503$) was much higher than in the sites with rice cultivation ($H = 0.968$, $E_H = 0.313$, Kiamaciri; and $H = 1.040$, $E_H = 0.367$ Mbuinjeru)

Conclusions: Mosquito diversity is impacted by rice cropping strategies and it is critical to understand mosquito community structure for targeting control strategies in rice agroecosystems.

The southern African lepidopteran fauna in a regional and global context

Martin Krüger

Transvaal Museum, NFI, Pretoria, South Africa

Among the major holometabolous orders, Lepidoptera are thought to have radiated most recently, largely during the Cretaceous and Early Tertiary. Consequently, mesozoic geological events such as the breakup of Gondwana are considered to have had comparatively little influence in shaping biogeographical patterns within the order. After the breakup, Africa underwent a prolonged period of geographical isolation before repeatedly being connected to Eurasia during the Tertiary. The afrotropical Lepidoptera fauna accordingly consists mainly of autochthonous elements resulting from intrinsic post-Gondwanan speciation, with Gondwanan relicts and descendants of Tertiary immigrants being much less numerous.

In keeping with the global pattern, Non-Glossatans and Non-Heteroneuran Glossata are fairly well represented at temperate latitudes in Southern Africa, but are virtually unrecorded further north. Examples include the *Sabatinca*-lineage of Micropterigidae, *Prototheora* (Prototheoridae), *Antihepialus* and *Afrotheora* in the Hepialidae and *Scyrotis* in the Cecidosidae (Incurvarioidea).

Some evidence for a Gondwanan distribution of basal ditrysians notwithstanding, currently accepted chronologies for the fragmentation process are incompatible with the existence of austral disjuncts among higher ditrysians. In addition to the larentiine geometrid tribe Trichopterygini, for which a Gondwanan distribution type of distribution has been tentatively suggested, evidence is presented for the existence in Southern Africa of the ennomine tribe Nacophorini, previously recorded from Australia and temperate South America. The putative Afrotropical members of the tribe are primarily associated with Fynbos, which dates to the Cretaceous; their occurrence in other biomes is considered to be secondary in nature.

Pymetrozine for brown planthopper control overcomes neonicotinoid resistance

Robert Lind, Russell Slater, Domingos Pedroni, Robert Senn

[1]Syngenta, Bracknell, Berkshire, United Kingdom, [2]Syngenta, Basle, Switzerland

Introduction: Resistance to neonicotinoid insecticides has been reported in field populations of the brown planthopper (*Nilaparvata lugens*) in many of the rice growing regions of South East Asia. Resistance factors of 5000 and 500 can be reached for imidacloprid and thiamethoxam respectively. Thus, compounds with novel modes of action such as pymetrozine are needed to combat resistance.

Methods: Neonicotinoid resistant strains were field collected from India and Vietnam and lab bioassays against nymphs and adult egg lay were used to evaluate the potential cross resistance to pymetrozine. To complement this study, the biokinetics of resistance were compared between susceptible and resistant strains by quantifying the rate and levels of metabolites of the archetypal neonicotinoid, imidacloprid using liquid chromatography mass spectrometry (LCMS).

Results: No differences in laboratory pymetrozine dose response in nymph mortality or egg lay was observed between susceptible and resistant strains. In agreement, there was no marked differences in the uptake of pymetrozine or between the rate or amount of the major hydroxy metabolite produced by the susceptible and resistant strains as determined by LCMS. Conversely, there was marked differences in imidacloprid metabolite production in resistant strains of approximately 25-fold compared to susceptibles. The major metabolite was formed by hydroxylation indicating the involvement of cytochrome P450 in the mechanism of resistance.

Conclusions: Laboratory and field studies have proved that pymetrozine can offer effective control of brown planthoppers, with no evidence of cross resistance to neonicotinoids thus providing it utility in resistance management programs providing long term, effective control.

Analysis of Japanese oak wilt spread using aerial photography and GIS

Ryotaro Komura[1], Naoto Kamata[2], Ken-ichiro Muramoto[3], Andrew Liebhold[4], Kojiro Esaki[5]

[1]Ishikawa National College of Technology, Tsubata, Ishikawa 929-0392, Japan, [2]University of Tokyo, Bunkyo, Tokyo 113-8657, Japan, [3]Kanazawa University, Kanazawa, Ishikawa 920-1192, Japan, [4]Northern Research Station, USDA Forest Service, Morgantown, WV 26505, United States, [5]Ishikawa Forest Experiment Station, Hakusan, Ishikawa 920-2114, Japan

In Japan, Japanese oak wilt (JOW) has been known since the 1930s. In the decades directly following its initial discovery, JOW epidemics were only a few years in duration and were confined to only a few areas on the Japan Sea (western) coast of Japan. However, in the last ten years epidemics have intensified and spread to the island's western coastal areas. The symbiotic ambrosia fungus *Raffaelea quercivora* is the causal agent of oak dieback, and is vectored by *Platypus quercivorus* (Murayama). This is the first example of an ambrosia beetle fungus that kills vigorous trees. We provide here an analysis of the historical distribution and spread of JOW previously recorded at the regional scale. Additionally of mortality caused by JOW at the stand scale level was investigated using aerial photographs. In this study, statistical analysis of spread of the oak diebacks was done conducted using a geographical information system (GIS) and rates of JOW spread were among different spatial scales. Results suggest that spread is the result of long, middle and short distance movement by adult beetles.

Evaluation of effect of sunlight on insecticide impregnated fabrics against vector species of mosquitoes under laboratory conditions

Neera Kapoor

IGNOU, New Delhi, India

Introduction: Insecticide treated curtains (ITC) play an important role in controlling vector-borne diseases in urban areas as plain curtains are normally used in majority of urban houses. After impregnating curtains with insecticides they are dried in shade. This implies that sunlight influences the efficacy of impregnated curtains. Since impregnated curtains are expected to be occasionally exposed to sunlight, tests were done under laboratory conditions to determine the residual activity at the interval of 1 week after the treatment.

Methods: Effect of sunlight was studied by exposing impregnated fabric panels to sunlight for 8-10 hours a day till the insecticide activity was observed and bioassay tests were conducted daily by exposing females to treated surface. Bioassay tests were carried out with WHO susceptibility test kits. The experiments were pursued till 0% mortality of the test mosquitoes was observed.

Results: On cotton impregnated with deltamethrin at 40 mg/m^2, there was approximately 50% reduction in *An. stephensi* mortality in 8 weeks and in 10 weeks there was 90% reduction in *An. stephensi*. Similar trend was observed for other two species of test mosquitoes. On nylon and plastic also at 40 mg/m^2, all the insecticides showed drastic reduction in mortality after 4 weeks and complete loss after 8 weeks of exposure to sunlight. At 80 mg/m^2, deltamelthrin showed its residual effect till 12 weeks on cotton and jute against all the three mosquito species tested on nylon. The complete loss of all the insecticides on exposure to sunlight was observed in 8 weeks. At 100 mg/m^2, complete insecticidal loss was observed in 16 weeks against *Cx. quinquefasciatus* on all fabrics and against *Ae. aegypti* on nylon and plastic. The residual effect of insecticide was observed even till 16 weeks against *An. stephensi* on all the fabrics. Lambdacyhalothrin, cyfluthrin and etofenrox impregnated fabrics on exposure to sunlight showed the residual effect for 8-16 weeks with the increase of dosage from 40 to 100 mg/m^2.

Conclusions: Our experiements confirm the earlier findings of Elliot etal, (1978) that sunlight causes rapid degradation of synthetic pyrethroids so it is recommended that curtains should be dried with air driers. Alternatively they can be rolled in daytime and hung at night to escape the effect of sunlight.

Genetic diversity of *Thaumastocoris peregrinus* (Hemiptera: Thaumastocoridae) in South African and South American *Eucalyptus* plantations

Ryan L. Nadel[1], Bernard Slippers[1], Mary C. Scholes[2], Juan Pedro Bouvet[3], Michael J. Wingfield[1]

[1]Department of Genetics, Forestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, Gauteng, South Africa, [2]School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, Johannesburg, Gauteng, South Africa, [3]INTA-Estación Experimental Agropecuaria de Concordia, CC34, Sección Entomología, Entre Ríos, Argentina

Thaumastocoris peregrinus (Hemiptera: Thaumastocorisdae) is a *Euclayptus* pest recently introduced into South Africa and South America. It is a short-lived, gregarious, sap-sucking insect that cause leaf discoloration and defoliation of infested *Eucalyptus* trees. Intensive, countrywide surveys for *T. peregrinus* were conducted in South Africa, spanning several *Eucalyptus* species, hybrids and their clones, and various geological and climatic regions. The main species or hybrids found to be infested by the insect were *E. grandis* x *camaldulensis* and *E. grandis* x *urophylla* clones, although *E. camaldulensis, E. macarthurii, E. grandis, E. tereticornis* and *E. smithii* were also heavily infested. The distribution of *T. peregrinus* in South Africa had no obvious climatic or altitudinal limits. Analysis of mitochondrial cytochrome *c* oxidase I (CO I) DNA sequence diversity was used to characterise the population diversity and distribution of the pest in South Africa, Argentina and Uruguay. The results confirmed that it is the same species of the insect that occurs in South African and South American plantations. Three CO I haplotypes were found amongst *T. peregrinus* individuals from South Africa, Argentina and Uruguay. Two of these haplotypes were found in South Africa, one of which is widely distributed in individuals from both summer and winter rainfall areas. The other South African haplotype is dominant in a small area of the sub-tropical summer rainfall zone. The Argentinean and Uruguayan populations displayed a distinct haplotype. The data suggest that there have been two separate introductions of *T. peregrinus* into South Africa and that the insect in South America represents an introduction without any connection to South Africa. This relatively large number of separate introductions emphasises the ease with which the pest is able to move and it also suggests relatively ineffective quarantine measures in areas where it has appeared.

Association of fungus-growing termites (Isoptera: Macrotermitinae) with *Termitomyces* in Kenya

Zipporah B. Osiemo[1], Andreas Marten[1], Manfred Kaib[2], Linus M. Gitonga[3], Hamadi I. Boga[4], Roland Brandl[1]

[1]Department of Animal Ecology, University of Marburg, Marburg, Germany, [2]Department of Animal Physiology, University of Bayreuth, Bayreuth, Germany, [3]Department of Zoology, Jomo Kenyatta University of Agriculture & Technology, Nairobi, Kenya, [4]Department of Botany, Jomo Kenyatta University of Agriculture & Technology, Nairobi, Kenya

Fungus-growing termites of the subfamily Macrotermitinae are abundant in African and Asian tropics where they play a major role in the decomposition of plants. The obligate mutualism between fungi of the genus *Termitomyces* and termite species within the Macrotermitinae seems to be the result of a long co-evolutionary process, with a single phylogenetic origin in African tropical forests during the early Tertiary. However, there are still some uncertainties about the level of the host specifity in fungi (host genera *versus* host species). To address this question we sampled fungi within 40 colonies of termite species from four genera (*Macrotermes*, *Odontotermes, Pseudacanthotermes*) in humid to arid ecosystems across Kenya. We sequenced the nuclear ITS region and used these sequences as well as ITS sequences from African samples from Genbank to construct a phylogeny of the fungi applying parsimony as well as maximum likelihood methods.

ITS sequences formed several clusters with strong sequence divergence between clusters. Each cluster was exclusively associated with one host genus. Sequences of *Termitomyces* samples available in Genbank corroborate this pattern indicating specificity at the level of host genera. On the other hand, within the cluster associated with the host genus *Macrotermes*, strains occurred in several species indicating a low host specificity. Strains may occur across steep environmental gradients e.g. from Magadi to Thika. Therefore, the association of strains with several host species is not the result of an allopatric distribution of strains between climatic regions.

Impact of a formulation of *Beauveria bassiana* conidia on varroa mites and on honeybee colony health

William Meikle[1], Guy Mercadier[1], Vincent Girod[2], Niels Holst[3]

[1]European Biological Control Laboratory, Montferrier sur Lez, France, [2]Association de Développement Apicole pour les Professionnels – Languedoc Roussillon (ADAPRO-LR), Lattes, France, [3]Danish Institute of Agricultural Sciences, Slagelse, Denmark

Introduction: Varroa mites are among the most important bee pests worldwide, and they are usually controlled using chemical miticides or plant-based compounds. In an effort to develop a biological control program against varroa, strains of an entomopathogenic fungus, *Beauveria bassiana*, were isolated from varroa mites found in beehives in France and were tested in lab bioassays.

Methods: *B. bassiana* conidia were formulated with plant-based wax powder and used to treat hives in 4 field experiments. The main response variables measured over time were: 1) mite fall onto sticky boards; 2) infection rate of mites; and 3) number of fungal conidia per bee. Bee colony health was also monitored in terms of total colony weight, brood surface area, adult population weight and food reserves.

Results: Mite fall was significantly affected by fungal application, and repeated applications resulted in significantly lower mite fall among treated hives. All the mites collected immediately after application in treated hives were infected, and the proportion of infected mites declined thereafter, usually faster in the spring than in the fall. The number of conidia per bee declined rapidly from about 10^4 conidia per bee to fewer than 10 per bee in 7-14 days. No adverse effects were observed among the bee colonies

Conclusions: Progress has been made in developing a biopesticide against varroa mites. Issues remain concerning the most economically effective dosage, and the number and timing of applications. The role of *B. bassiana* in hive ecology is largely unknown.

An IGF-like peptide regulates adult development of the silkmoth, *Bombyx mori*

Naoki Okamoto[1], Naoki Yamanaka[2], Hiroshi Kataoka[2], Akira Mizoguchi[1]

[1]Nagoya University, Nagoya, Aichi, Japan, [2]The University of Tokyo, Kashiwa, Chiba, Japan

Introduction: Bombyxin is an insulin family peptide produced by the brain neurosecretory cells of the silkmoth *Bombyx mori*. Our recent analysis of bombyxin-immunoreactive materials in *Bombyx* hemolymph has revealed that a remarkably high amount of 8kDa-bombyxin-like peptide (8K-BLP) with a little larger size than bombyxin is present during pupa-adult development.

Methods: 8K-BLP was purified from the hemolymph of female developing adults by using anti-bombyxin-II antibody affinity chromatography, ion exchange HPLC and reversed phase-HPLC. The structure of the purified peptide was determined using a combination of MALDI-TOF MS, amino-acid sequencing and EST data base analysis. Spatial and temporal expression patterns of 8K-BLP mRNA and peptide were analyzed by quantitative RT-PCR, western blotting and immunocytochemistry. The function of 8K-BLP was investigated *in vitro*.

Results: 8K-BLP was a single-chain polypeptide belonging to the insulin family, indicating that 8K-BLP is structurally similar to insulin-like growth factors (IGFs) rather than insulin. Expression analysis showed that 8K-BLP is produced predominantly by the fat body during pupa-adult development. 8K-BLP secretion by the fat body was strongly stimulated by 20-hydroxyecdysone *in vitro*. When genital disks were cultured in the presence of 8K-BLP, they grew larger and their protein content became higher than the controls. 8K-BLP also promoted BrdU labelling of genital disks and other adult-specific tissues such as sperm ducts, flight-muscle anlagen and wing disks. Overall, these results strongly suggest that 8K-BLP is a *Bombyx* counterpart of vertebrate IGFs and serves as a potent growth factor to regulate adult development in *B. mori*.

Non-target effects of biological control – could there also be implications for agriculture?

Colleen Seymour, Ruan Veldtman

South African National Biodiversity Institute, Cape Town, South Africa

Introduction: Recently, there has been a call for the effectiveness of biological control to be viewed within the context of the ecological consequences of this strategy of controlling alien plants. We investigated whether or not the presence of a biological control agent of *Acacia saligna,* the gall-forming fungus, *Uromycladium tepperianum,* in the citrus-producing area of Citrusdal, South Africa, was providing alternative habitat for the crop pest *Cryptophlebia leucotreta* (False codling moth).

Methods: We established pheromone-baited traplines out into natural vegetation from the centre of 4 patches each of *A. saligna* only, *A. saligna* and orchard, and orchard only. We also collected 2500 cm^3 of gall created by *U. tepperianum* at each site, keeping these in a growing room for two months, to ascertain which invertebrates are using these galls.

Results: Three *C. leucotreta* were trapped in alien only sites, 151 in orchard sites, and 83 in alien and orchard sites. After two months, 90 *C. leucotreta* had emerged from galls collected from alien only sites, and 137 from orchard and alien sites.

Conclusions: Although traps should be able to attract moths over distances of up to 200m, our traps did not capture nearly as many moths as emerged from the relatively small amount of gall collected for the emergence study. That said, it is clear that *C. leucotreta* uses galls on alien plants as nursery sites, and this information could be used to encourage farmers to keep their lands free of *A. saligna,* to minimize refuges for this crop pest.

Effects of *Chilo partellus* Swinhoe (Lepidoptera: Crambidae) and *Sesamia calamistis* Hampson (Lepidoptera: Noctuidae) sublethally fed on Bt maize on the biology of *Cotesia flavipes* and *Cotesia sesamiae* Cameron (Hymenoptera: Braconidae)

Dennis Obonyo[1], Josephine Songa[2], Gabor Lovei[3], Florence Oyieke[1], Gideon Nyamasyo[1], Stephen Mugo[4]

[1]School of Biological Sciences, University of Nairobi, Nairobi, Kenya, [2]Biotechnology Centre, Kenya Agricultural Research Institute, Nairobi, Kenya, [3]Department of Integrated Pest Management, Faculty of Agricultural Sciences, University of Århus, Århus, Denmark, [4]International Maize and Wheat Improvement Centre, Nairobi, Kenya

Introduction: *Chilo partellus* and *Sesamia calamistis* are important maize stem borer species in Kenya. Transgenic maize transformed with delta-endotoxin genes from *Bacillus thuringiensis* (Bt maize) is being developed in Kenya for stem borer control. Two braconid parasitoids, *Cotesia sesamiae* and *Cotesia flavipes* are important natural enemies of lepidopteran larvae in Kenya, and the possible effects of Bt maize on these biological control agents have to be investigated. As a first step in the biosafety evaluation of this Bt maize, laboratory experiments were conducted to assess the potential effect of *C. partellus* and *S. calamistis* sublethally fed on Bt maize on the biology of the two parasitoids.

Methods: Fourth instar *C. partellus* and *S. calamistis* larvae were sublethally fed on Bt (and non Bt as control) maize and subsequently exposed to the parasitoids.

Results: There were no significant differences in host acceptance and host acceptance time by the parasitoids between Bt exposed and control larvae. Pre-cocoon and total development times were significantly longer for *C. flavipes* on Bt exposed *C. partellus*. Proportions of *C. flavipes* female progeny were significantly lower on Bt exposed *C. partellus* while sex ratio for *C. sesamiae* from *C. partellus* varied. The number of *C. sesamiae* cocoons, cocoon mass and progeny numbers were significantly higher on Bt exposed *S. calamistis*.

Conclusions: Response to Bt maize varied between host and parasitoid species and generalisation is not yet possible. Longer term studies are warranted to determine how Bt maize would affect host-parasitoid systems.

Ecophysiology of respiration in dung beetles – a comparative study

Frances Duncan

University of the Witwatersrand, Johannesburg, South Africa

Environmental aridity may be important in explaining the different respiratory strategies used by dung beetles. Previous research on dung beetles has found a general ecological pattern of changing discontinuous gas exchange patterns, from CFO (closed, flutter, open) cycles to CV (closed, ventilation) cycles in species from mesic to arid habitats. Dung beetles inhabiting the arid regions of South Africa are flightless. The fused elytra create a sealed air space called the subelytral cavity. The respiratory function of this cavity into which the posterior pair of metathoracic spiracles and six pairs of abdominal spiracles open is not completely understood. Previous work on the arid adapted flightless beetle, *Circellium bacchus* (Canthonini), showed that CO_2 is stored in the subelytral cavity and later released through the anterior mesothoracic spiracles which open to the exterior (Byrne & Duncan, 2003). The pattern of respiratory gas exchange, as well as the relative contribution of the spiracles to CO_2 release in four arid adapted dung beetles species (Scarabaeinae), was determined using flow-through respirometry for comparison. Carbon dioxide emission was measured from the mesothoracic spiracles and from around the elytral case. The results show that the emission varies from the subelytral cavity and can be altered by the beetles. Pressure changes within the subelytral cavity and tracheal system is specifically described for *C. bacchus* to explain the respiratory patterns observed.

Heteropteran juvenile hormone unveiled: a novel type of juvenile hormone identified in a stink bug, *Plautia crossota stali*

Toyomi Kotaki[1], Kanako Kaihara[2], Tetsuro Shinada[2], Yasufumi Ohfune[2], Hideharu Numata[2]

[1]National Institute of Agrobiological Sciences, Tsukuba, Ibaraki, Japan, [2]Osaka City University, Sumiyoshi, Osaka, Japan

Introduction: Heteropteran insects have been used as model animals for insect endocrinology since the pioneer work by Wigglesworth in 1930's. In a previous study, we reported the evidence for a novel juvenile hormone (JH) in a stink bug, *Plautia crossota stali*. However, the structure of JH of heteropterans has not been identified yet. The purpose of the present study is to elucidate its structure.

Methods: A combination of highly sensitive GC/MS analysis, bioassay-guided analysis, and synthetic methods involving combinatorial and asymmetric synthesis was adopted for structure determination.

Results: Hexane extracts of the incubation medium of the corpora allata (CA) from *P. c. stali* were subjected to GC/MS analysis to estimate the molecular formula. Based on the molecular formula, we constructed a molecular library of the JH candidates by the synthesis of all possible stereoisomers. Preliminary bioassay of the mixture of the library compounds exhibited potent inhibitory effects on the metamorphosis of nymphs. The compounds were then separated into >20 fractions by HPLC to identify the potent compound. NMR analysis of the potent compound provided a proposed structure of the JH that was found to be novel. The relative and absolute stereochemistry of the JH was determined by comparison of the GC/MS and biological profiles of the natural CA product with those of the optically active JHs prepared by the asymmetric synthesis.

Conclusion: The structure of JH in *P. c. stali* was unambiguously determined and found to be novel. Our discovery opens the new door to further progress in JH biochemistry.

The chrysomelid leaf beetle *Diabrotica virgifera virgifera* LeConte as an alien invasive maize pest in the Ticino canton, Southern Switzerland

Hans E. Hummel[1], Mario Bertossa[2]

[1]Justus-Liebig-University Giessen, Organic Agriculture, Giessen, Germany, [2]Swiss Federal Research Station Cadenazzo, Contone, Switzerland

Diabrotica virgifera virgifera (Coleoptera:Chrysomelidae), the western corn rootworm (WCR), is an immigrant from North America and one of the top ten global agricultural pest species. Within the last 15 years, WCR invaded Europe at a minimum of 3 focal points at Belgrade, Milan and Paris and is a severe threat to commercial maize production. The progress of WCR from Italy to North Central Europe via Switzerland has been under scrutiny and of major concern to European quarantine officers. Geographic concentration of transport routes along river valleys of Ticino and Misox necessitated careful observations of these routes by pheromone and kairomone monitoring traps. Experiences with WCR monitoring whose population dynamics are still incompletely understood, may be briefly summarized for 2005 to 2007:

1. WCR moves in south–north direction preferably along major freeways, railroads and associated trading centers for goods and services. 2. WCR densities further remote from these strategic thoroughfares are generally lower than those in their immediate vicinity. 3. WCR likes to hitchhike with *Homo sapiens* using his established traffic technologies, 4. Mandatory crop rotation in the canton Ticino slowed the previous spreading and densities of WCR significantly. After introduction of mandatory crop rotation in the canton Ticino, no further WCR infestations were detectable north of the main Alpine mountain chain during 2005 to 2007. 5.Traps in the side valley of Misox situated in the neighboring canton of Grisons (with delayed obligation for mandatory crop rotation) show a population increase, but WCR counts now stagnate at a higher level than in the canton Ticino. 6. Metcalf sticky traps baited with sex pheromones and kairomones as attractants are highly effective and early indicators of WCR populations. 7. Switzerland with its rigorous crop rotation program may serve as an example and a role model for prudent WCR pest management in the European context.

Movement strategies and plant structure: a modeling system for analyzing foraging insect development

Ezekiel Glaze[2], Jim Hanan[2], Stefan Maetschke[2], Marie-Louise Johnson[1], Bronwen Cribb[3], Lynda Perkins[1]

[1]University of Queensland - School of Integrative Biology, St. Lucia, Australia, [2]University of Queensland - Advanced Computational Modelling Centre, St. Lucia, Australia, [3]University of Queensland - Centre for Microscopy and Microanalysis, St. Lucia, Australia

Introduction: Insect foraging behavior is influenced by many factors. The influence of all factors on foraging, the distribution of damage, and caterpillar survival is difficult to quantify experimentally but can be addressed within a modeling framework. We use an agent-based modeling approach to compare 3 different movement "strategies". We explore the effect of explicit rules for caterpillar movement on caterpillar fitness using realistic 3D "virtual" plant structures with and without induced defenses.

Methods: The three movement strategies implemented in our study are: (1) Implicit - in which movement does not take plant geometry into account, (2) Random - a randomly moving animal constrained to a virtual plant, and (3) Realistic - as in (2) but with more realistic movement rules based on our observations of *Helicoverpa* caterpillars. Each movement strategy is simulated with and without plant induced defenses.

Results: We rank the scenarios (by total development) thus: 1 Implicit movement – no induced defenses 2 Realistic movement - no induced defenses 3 Implicit movement – with induced defenses 4 Random movement – no induced defenses 5 Realistic movement – with induced defenses 6 Random movement – with induced defenses

Conclusions: We show that restricting the insect's movement to plant structures has a marked effect on insect development. Virtual insects develop fastest when their movement simulation does not follow plant topology, as is sometimes done in simplified models. Insects restricted to plant topology develop more slowly but, of these, those with a realistic movement biased toward the top of the plant do better.

Insect pest management with 2-(4-Hydroxybenzyl)cycloalkanol derivatives: A 30-year story

Zdenek Wimmer[1], Martina Wimmerova[1], Ondrej Jurcek[1], Hana Svobodova[1], Blanka Bennettova[2], Ivan Hrdy[3], Jelena Kuldova[3], David Saman[3], Erkki Kolehmainen[4]

[1]Laboratory of Chemistry, Institute of Experimental Botany AS CR, Videnska 1083, 142 20 Prague 4, Czech Republic, [2]Institute of Entomology, Biology Centre AS CR, Branisovska 31, 370 05 Ceske Budejovice, Czech Republic, [3]Institute of Organic Chemistry and Biochemistry AS CR, Flemingovo namesti 2, 166 10 Prague 6, Czech Republic, [4]University of Jyväskylä, Department of Chemistry, Laboratory of Organic Chemistry, Survontie 9, 40500 Jyväskylä, Finland

Derivatives of 2-(4-hydroxybenzyl)cycloalkanols were designed in late 1970's. Since that time, numbers of compounds have been synthesized and tested as insect juvenile hormone bioanalogs (JHAs). Considering a novel way to implement their practical application, we have elaborated the idea of juvenogens (hormonogenic substances) as novel types of insect pest management agents. Juvenogens are biochemically targeted complex substances, which usually display low biological activity upon topical application, and may be activated either through *in vivo* biochemical pathways (enzymatic system of living organisms) or through the environmental conditions (humidity, acidity, UV light *etc.*). They can be synthesized as targeted structures depending on knowledge of the enzymic system of the target insect pests and/or their host plants. These compounds may be more convenient for external application against insects, but not persisting in the environment and displaying as low as possible environmental and/or health risk. In our team, designing and developing new structures has been performed by application of a number of chemoenzymic approaches to get mainly enantiopure compounds available. Subsequent investigation of the structure-activity relationship, and the studies in metabolomics of these compounds followed to get knowledge on potential ecotoxicity of the applied compounds and their metabolites.

However, the future of the insect pest management should be based on the principles of biology-oriented synthesis. An efficient combination of biology-derived compounds with naturally occurring insect pest control agents (mostly plant defense compounds) may result in designing biochemically targeted and species specific substances. Attention will be paid to supramolecular structures based on natural steroid molecules.

The establishment of *Cotesia flavipes* (Hymenoptera: Braconidae) in sugarcane fields of Ethiopia and the origin of the founding population

Yoseph Assefa[1], Andrew Mitchell[2], Desmond Conlong[3], Katherine Muirhead[4]

[1]School of Biological and Conservation Sciences, University of KwaZulu-Natal, Private Bag X01, Pietermaritzburg, Scottsville, 3209, South Africa, [2]Wagga Wagga Agricultural Institute, NSW Department of Primary Industries,, PMB Wagga Wagga, NSW 2650, Australia, [3]South African Sugarcane Research Institute, Private Bag X02, Mount Edgecombe, 4300, South Africa, [4]Centre for Evolutionary Biology & Biodiversity, School of Earth & Environmental Science DP 418, The University of Adelaide, SA 5005, Australia

Introduction: *Cotesia flavipes* Cameron (Hymenoptera: Braconidae) is used as a classical biological control agent against *Chilo partellus* Swinhoe (Lepidoptera: Crambidae). This parasitoid has been introduced into several African countries for the control of *C. partellus* in maize and sorghum, but has never been released in Ethiopia. In recent surveys conducted in Ethiopia, *C. flavipes* was recovered from *C. partellus* in sugarcane at a site more than 2000 km from the nearest known release sites in Kenya and Somalia. These findings question published hypotheses which estimate the dispersal rate of *C. flavipes* to be 60 km per year in Africa, and suggest that since its release in Africa this parasitoid has developed strains adapted to searching particular host plants infested by particular stem borers. The anomalies between our results and previous reports evoked the hypothesis that *C. flavipes* in Ethiopian sugarcane might be a different strain.

Methods: COI gene sequences of *C. flavipes* collected from sugarcane in Ethiopia, from maize in other African countries and different host insect/plants in other continents to determine the origin of the Ethiopian population.

Results: *Cotesia flavipes* population established in Ethiopian sugarcane is most closely related to the populations released against *C. partellus* in maize in other parts of Africa, which were derived from the original population imported from Pakistan.

Conclusions: Maize/sorghum strains of *C. flavipes* can colonize sugarcane fields at least under Ethiopian cropping systems. The dispersal rate of the parasitoid was estimated to be more than 200 km per year.

The establishment of *Cotesia flavipes* (Hymenoptera: Braconidae) in sugarcane fields of Ethiopia and the origin of the founding population

Yoseph Assefa[1], Andrew Mitchell[2], Desmond Conlong[3], Katherine Muirhead[4]

[1]School of Biological and Conservation Sciences, University of KwaZulu-Natal, Private Bag X01, Pietermaritzburg, Scottsville, 3209, South Africa, [2]Wagga Wagga Agricultural Institute, NSW Department of Primary Industries,, PMB Wagga Wagga, NSW 2650, Australia, [3]3South African Sugarcane Research Institute, Private Bag X02, Mount Edgecombe, 4300, South Africa, [4]Centre for Evolutionary Biology & Biodiversity, School of Earth & Environmental Science DP 418, The University of Adelaide, SA 5005, Australia

Introduction: *Cotesia flavipes* Cameron (Hymenoptera: Braconidae) is used as a classical biological control agent against *Chilo partellus* Swinhoe (Lepidoptera: Crambidae). This parasitoid has been introduced into several African countries for the control of *C. partellus* in maize and sorghum, but has never been released in Ethiopia. In recent surveys conducted in Ethiopia, *C. flavipes* was recovered from *C. partellus* in sugarcane at a site more than 2000 km from the nearest known release sites in Kenya and Somalia. These findings question published hypotheses which estimate the dispersal rate of *C. flavipes* to be 60 km per year in Africa, and suggest that since its release in Africa this parasitoid has developed strains adapted to searching particular host plants infested by particular stem borers. The anomalies between our results and previous reports evoked the hypothesis that *C. flavipes* in Ethiopian sugarcane might be a different strain.

Methods: COI gene sequences of *C. flavipes* collected from sugarcane in Ethiopia, from maize in other African countries and different host insect/plants in other continents to determine the origin of the Ethiopian population.

Results: *Cotesia flavipes* population established in Ethiopian sugarcane is most closely related to the populations released against *C. partellus* in maize in other parts of Africa, which were derived from the original population imported from Pakistan.

Conclusions: Maize/sorghum strains of *C. flavipes* can colonize sugarcane fields at least under Ethiopian cropping systems. The dispersal rate of the parasitoid was estimated to be more than 200 km per year.

The importance of floral scent in the evolutionary shift from bird to beetle pollination in *Protea*

Sandy-Lynn Steenhuisen[1], Steven D. Johnson[1], Robert A. Raguso[2]

[1]School of Biological and Conservation Sciences, University of KwaZulu-Natal, Pietermaritzburg, KwaZulu-Natal, South Africa, [2]Department of Neurobiology and Behavior, Cornell University, Ithaca, New York, United States

Introduction: The majority of *Protea* species in South Africa occur in winter rainfall regions, and are pollinated by birds. They produce large, colourful and unscented inflorescences visited by sunbirds and sugarbirds that feed on copious amounts of nectar, accessed by their long bills. Rodent pollination systems have been investigated in a few geoflorous species that produce yeasty scented inflorescences. In contrast, the role of insects as pollinators in this genus has been controversial. In this study, we present evidence that four *Protea* species in the summer rainfall regions of South Africa employ an insect pollination system. These species produce open bowl-shaped, colourful and fruity scented inflorescences, most frequently visited by cetoniine beetles exploiting accessible nectar and pollen rewards.

Methods: We analysed the volatile components of the scent of these species using GC-MS, the source of scent production from dissected inflorescences, ontogeny of scent production in the field, and the change in scent of the inflorescences from microbial fermentation of the nectar. In addition we analysed GC-EAD responses of the most common beetle visitor, *Atrichelaphinis tigrina,* to whole flower scents and selected volatiles.

Results: Choice tests confirmed that *A. tigrina* shows a significant preference for the fruity scent of the flowers. The monoterpene linalool, a known attractant of cetoniine beetles, comprised more than 40% of all scent samples.

Conclusions: We suggest that the evolution of a fruity scent has accompanied the shift from an ancestral bird pollination system to a cetoniine beetle pollination system in this clade.

Invasions by *Bactrocera* spp.: Its implication on horticulture in Africa

Maulid Mwatawala[1], Amon Maerere[1], Marc De Meyer[2]

[1]Sokoine University of Agriculture, Morogoro, United Republic of Tanzania, [2]Royal Museum for Central Africa, Tervuren, Belgium

Two Asian *Bactrocera* species, *Bactrocera latifrons* (Hendel) and *Bactrocera invadens* Drew White and Tsuruta have been reported from Africa in 2004 and 2007 respectively. These two add to the earlier introduced *Bactrocera cucurbitae* (Coquillet) and *Bactrocera zonata* (Saunders). *B. invadens* and *B. cucurbitae* are widely distributed throughout the continent. *B. zonata* has been reported from Indian Ocean islands and Egypt, while the African distribution of *B. latifrons* is still unclear but so far only known from Tanzania and Kenya. The impact of these pests is hereby examined based on the fact that introduced *Bactrocera* species are known to cause heavy losses in the fruits they attack, they are quick to establish themselves and become numerically dominant and in some cases they have been shown to competitively displace the pre-established species from their fundamental niches. Additionally, these pests are of quarantine importance since the presence of larvae in fruit shipments could lead to rejection of consignment and loss of international markets. Most countries will have to design viable management programs in order to meet export standards of importing countries, whereas the countries that have not recorded these pests need to have strong quarantine measures to avoid introduction of these pests and subsequent loss of markets. Experiences, challenges and limitations in achieving these are the main focus of this paper. Specific references will be given on the detection surveys and host range studies of *B. latifrons* in Tanzania.

Ambrosia beetles as affected by environmental factors: Are these phenomena changes or just new findings?

Naoto Kamata[1], Jean-Claude Gregoire[2]

[1]University of Tokyo, Bunkyo, Tokyo 113-8657, Japan, [2]Free University of Brussels, 50 avenue F.D. Roosevelt,B-1050 Brussels, Belgium

Ambrosia beetles are generally recognized as insects that infest weakened, dying, or dead trees, and logs. A few species were known to attack healthy living trees. However, recently reports on ambrosia beetles that infest apparently healthy living trees have been increasing as follows: *Platypus quercivorus* and *P. koryoensis* both accompanied with fungi that kills oak trees in Japan and Korea, respectively. *Platypus mutatus* attacking poplar trees in Argentina and Italy. *Trypodendron domesticum*, *T. signatum*, *Xyleborus dispar* and *Xylosandrus germanus* attacking beech trees in Europe. We would like introduce several examples of ambrosia beetles infesting healthy living trees from all over the world. Ecological and evolutionary aspects of this increase will be discussed in relation to environmental changes and globalization.

Mechanism of multiple functional coupling of a *Bombyx mori* octopamine receptor

Yoshihisa Ozoe, Jia Huang

Shimane University, Matsue, Japan

Introduction: The phenolic biogenic amine octopamine (OA) is derived from tyrosine and is widely distributed in the insect nervous system and peripheral tissues. OA regulates or modulates various physiological processes of insects as a neurotransmitter, neuromodulator, or neurohormone. OA receptors (OARs) belong to the rhodopsin-like family of G protein-coupled receptors. We cloned a cDNA encoding an OAR from the silkworm *Bombyx mori* (BmOAR1) and heterologously expressed it to examine its functional and pharmacological properties.

Methods: The cDNA was prepared using mRNA from the brain and ganglia of *B. mori*, and the wild type and variants of BmOAR1 were stably expressed in HEK-293 cells. Five variants of BmOAR1 with mutation(s) in the putative OA binding site (a crevice formed by transmembrane domain (TM) 3, 5, and 6) were generated by site-directed mutagenesis. The expressed receptors were examined for their ability to change intracellular Ca^{2+} and cAMP levels as well as that to bind [^{3}H]OA.

Results: BmOAR1 was identified as an α-adrenergic-like OAR, which was linked to OA-stimulated elevation of Ca^{2+} and cAMP levels. The S202A (TM5) mutant increased cAMP levels in response to OA as did the wild type, but such a function was abolished in the D103A (TM3), S198A (TM5), and S198A/S202A mutants. Significant [^{3}H]OA binding and OA-induced Ca^{2+} mobilization were also not observed in the case of D103A, S198A, and S198A/S202A mutants, whereas the S202A mutant retained both functions. These findings indicate that D103 and S198 are involved in both G_s- and G_q-protein couplings of BmOAR1 through electrostatic and hydrogen bond interactions with OA, but that S202 does not participate in these processes. In contrast, the Y412F (TM6) mutation eliminated the cAMP response to OA, but was without effect on the Ca^{2+} response and [^{3}H]OA binding. This finding suggests that Y412 is an amino acid residue necessary for G_s-protein coupling, which leads to cAMP production, but not for G_q-protein coupling.

Conclusions: The results lead to the proposal that BmOAR1 exists in three major conformations, and that Y412 plays a key role in transition from a semi-active conformation that favors G_q protein to a fully active one that favors both G_q and G_s proteins.

Can botanical pesticides be used safely and reliably in stored product protection?

Steven Belmain[1], Phillip Stevenson[1], Monique Simmonds[2], Brighton Mvumi[3], Gudeta Sileshi[4], Phosiso Sola[5], Stephen Nyirenda[6], John Kamanula[7], David Hall[1]

[1]Natural Resources Institute, University of Greenwich, Central Avenue, Chatham Maritime, Kent ME4 4TB, United Kingdom, [2]Jodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AB, United Kingdom, [3]Department of Soil Science & Agricultural Engineering, Faculty of Agriculture, University of Zimbabwe, P. O. Box MP167, Mt Pleasant, Harare, Zimbabwe, [4]World Agroforestry Centre (ICRAF), SADC-ICRAF Agroforestry Program, P.O. Box 30798, Lilongwe, Malawi, [5]Southern Alliance for Indigenous Resources, P.O. Box BE 398 Belvedere, Harare, Zimbabwe, [6]Department of Agricultural Research Services, Lunyangwa Research Station, P.O. Box 59, Mzuzu, Malawi, [7]Mzuzu University, P/Bag 201 Luwinga, Mzuzu, Malawi

Introduction: Poor farmers continue to use pesticidal plants to protect stored grain from insect pests. However, there can be problems associated with their use. Although natural, botanical pesticides are potentially toxic with compounds such as rotenone (classified by the World Health Organisation as a moderately hazardous, Class II) present in many plants currently promoted for stored product protection. Reliability of control is affected through the temporal and spatial variability of bioactive constituents produced by plants as well as poorly understood modes of action such as repellency that may differentially affect different insect species. Despite a growing number of publications on pesticidal plants, key questions on reliability, ecological sustainability and safety remain unanswered. A better understanding on the ecology of pesticidal plants and their interactions with stored product insects will help to optimise their sustainable use by poor farming communities.

Methods: The SAPP[1] research project takes a multi-dimensional approach to optimise the use of pesticidal plants by increasing scientific research on the knowledge gaps and constraints that currently limit their safe and reliable use. Research activities relate to phytochemical characterisation, vertebrate toxicity trials, sustainable harvesting and cultivation, mode of action and bioactivity trials, on-farm trials in poor farming communities and exploration of indigenous knowledge.

Results: Some well known pesticidal plants used commonly in Africa may be inactive against many target insect species. This may be explained by phytochemical analysis which has shown that some of these species, e.g. *Tephrosia vogelii*, do not contain the expected bioactive compounds. Insect behavioural bioassays assessing pesticidal plants for repellent properties indicate that repellency is modulated by the host orientation/finding strategies adopted by different insect species, e.g. *Sitophilus zeamais* is susceptible to repellents whereas *Rhyzopertha dominica* is not.

Conclusions: Promoting pesticidal plants without sufficient knowledge on their efficacy and safety can be dangerous for human health and lead to unpredictable levels of pest control which may diminish confidence in their use.

[1] Southern African Pesticidal Plants – http://www.nri.org/sapp

Can botanical pesticides be used safely and reliably in stored product protection?

Steven Belmain[1], Phillip Stevenson[1], Monique Simmonds[2], Brighton Mvumi[3], Gudeta Sileshi[4], Phosiso Sola[5], Stephen Nyirenda[6], John Kamanula[7], David Hall[1]

[1]Natural Resources Institute, University of Greenwich, Central Avenue, Chatham Maritime, Kent ME4 4TB, United Kingdom, [2]Jodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AB, United Kingdom, [3]Department of Soil Science & Agricultural Engineering, Faculty of Agriculture, University of Zimbabwe, P. O. Box MP167, Mt Pleasant, Harare, Zimbabwe, [4]World Agroforestry Centre (ICRAF), SADC-ICRAF Agroforestry Program, P.O. Box 30798, Lilongwe, Malawi, [5]Southern Alliance for Indigenous Resources, P.O. Box BE 398 Belvedere, Harare, Zimbabwe, [6]Department of Agricultural Research Services, Lunyangwa Research Station, P.O. Box 59, Mzuzu, Malawi, [7]Mzuzu University, P/Bag 201 Luwinga, Mzuzu, Malawi

Introduction: Poor farmers continue to use pesticidal plants to protect stored grain from insect pests. However, there can be problems associated with their use. Although natural, botanical pesticides are potentially toxic with compounds such as rotenone (classified by the World Health Organisation as a moderately hazardous, Class II) present in many plants currently promoted for stored product protection. Reliability of control is affected through the temporal and spatial variability of bioactive constituents produced by plants as well as poorly understood modes of action such as repellency that may differentially affect different insect species. Despite a growing number of publications on pesticidal plants, key questions on reliability, ecological sustainability and safety remain unanswered. A better understanding on the ecology of pesticidal plants and their interactions with stored product insects will help to optimise their sustainable use by poor farming communities.

Methods: The SAPP[1] research project takes a multi-dimensional approach to optimise the use of pesticidal plants by increasing scientific research on the knowledge gaps and constraints that currently limit their safe and reliable use. Research activities relate to phytochemical characterisation, vertebrate toxicity trials, sustainable harvesting and cultivation, mode of action and bioactivity trials, on-farm trials in poor farming communities and exploration of indigenous knowledge.

Results: Some well known pesticidal plants used commonly in Africa may be inactive against many target insect species. This may be explained by phytochemical analysis which has shown that some of these species, e.g. *Tephrosia vogelii*, do not contain the expected bioactive compounds. Insect behavioural bioassays assessing pesticidal plants for repellent properties indicate that repellency is modulated by the host orientation/finding strategies adopted by different insect species, e.g. *Sitophilus zeamais* is susceptible to repellents whereas *Rhyzopertha dominica* is not.

Conclusions: Promoting pesticidal plants without sufficient knowledge on their efficacy and safety can be dangerous for human health and lead to unpredictable levels of pest control which may diminish confidence in their use.

[1] Southern African Pesticidal Plants – http://www.nri.org/sapp

[1] Southern African Pesticidal Plants – http://www.nri.org/sapp

Biological control-based IPM for citrus in Japan

Masami Takagi

Kyushu University, Fukuoka, Japan

We had no serious citrus pest in Japan before 1900s because the international trade was not very much carried out before 1858. All most of the serious citrus pests were introduced into Japan after that. Classical biological control was very effective against those adventive pests, which are well controlled by introduced natural enemies now. The first attempt of introduction of forging natural enemies into Japan to control citrus pests was that of the vedalia beetle to the cottony cushion scale in 1911. This attempt was very successful like as the cases of many other countries. The second successful case was biological control of the red wax scale, *Ceroplastes rubens* by *Anicetus beneficus*. The last successful classical biological control was that of the arrowhead scale, *Unaspisi yanonensis* by two parasitoids, *Aphytis yanonensis* and *Coccobius fulvus*, introduced from China. The arrowhead scale was the most serious citrus pest in Japan before the introduction of these two parasitoids. All the classical biological control of these pests was very successful and they are no more serious scale pests in Japan. Although we have many native species of scale insects which infest citrus trees, native natural enemies control those pests at noneconomic level. At present several mites such as the citrus red mite and the pink citrus rust mite were the most important pests. Serious outbreak of the citrus red mite is induced usually by pesticide spray for control other pests and diseases which destroy natural enemies of citrus red mite. So conservation of natural enemies is very important for IPM of these pests.

Natural enemies of *Plodia interpunctella* and *Ephestia* spp. in cereal and dried fruit facilities

Consuelo Belda, Maria José Pons, Rosa Gabarra, Jordi Riudavets

IRTA Plant Protection, ctra Cabrils Km2, Cabrils, Barcelona, Spain

Biological control could be an important tool for pest control of Lepidoptera on stored cereals and dried fruits. Population dynamics of Lepidoptera with pheromone traps and their natural enemies with yellow sticky traps and light traps was assessed during one year on six food facilities. Monthly samples of the different products were also taken randomly. Depending on the companies, *Plodia interpunctella*, *Ephestia* spp. or a mix of both species were found. Pest population occurred all year around, but was more abundant from April to September. Regarding natural enemies, Lepidoptera parasitoids *Venturia canescens* and *Habrobracon* spp. were the main species trapped both with yellow sticky traps and light traps. Both parasitoid species were found in all facilities, regardless the pressure of chemical treatments. Mean number of adult parasitoids trapped reached a maximum of 137 individuals per light trap and 64 per yellow sticky trap. Parasitoid individuals were captured in every sampling date, with higher populations in summer till early autumn. The high number of natural enemies seems to indicate that natural biological control can be a complementary tool to be considered for Lepidoptera pest control in stored cereals and dried fruits facilities.

A multi-vector potential for transmitting African horse sickness virus (AHSV) in South Africa

Gert J Venter[1], Isabel M Wright[1], Theuns C Van der Linde[2], Janusz T Paweska[3]

[1]ARC-Onderstepoort Veterinary Institute, Onderstepoort, South Africa, [2]University of the Free State, Bloemfontein, South Africa, [3]National Institute for Communicable Diseases, Sandringham, South Africa

Introduction: During the last decade outbreaks of African horse sickness (AHS), caused by AHS virus (AHSV) (*Orbivirus*, *Reoviridae*), have increased dramatically in South Africa. The virus is transmitted between its equid hosts almost exclusively by the bites of certain species of *Culicoides* (Diptera, Ceratopogonidae). The availability of competent vectors is an important factor determining the occurrence and spread of AHSV. Of the approximately 120 *Culicoides* species in South Africa only *C. imicola* is a confirmed vector. The aim of this study was to determine which of the other *Culicoides* species, found near horses, are susceptible to infection and may therefore be potential vectors.

Methods: Field collected midges from three distinct geographical localities in South Africa were fed on sheep blood spiked with different isolates of one of the nine serotype of AHSV. After 10 days incubation at 23.5°C females were assayed individually on BHK-21 cells following a micro titration procedure.

Results: Oral susceptibility was found to differ significantly between various *Culicoides* species/ populations and different virus isolates. AHSV could replicate in eleven *Culicoides* species belonging to at least six subgenera. These *Culicoides* species are relative widespread in South Africa and in some the infection rate was significantly higher than that found in the confirmed vector *C. imicola.*

Conclusion: Our results indicate that oral susceptibility to infection with AHSV, however it is restricted to certain species, and is widespread in the genus *Culicoides*, thereby implying a multi-vector potential for its transmission in South Africa.

An awkward age for butterflies: when did Nymphalidae (Lepidoptera) diverge and diversify?

Niklas Wahlberg[1], Julien Leneveu[1], Carlos Peña[2], Ullasa Kodandaramaiah[2], Sören Nylin[2], André Freitas[3], Andrew Brower[4]

[1]Department of Biology, University of Turku, Turku, Finland, [2]Department of Zoology, Stockholm University, Stockholm, Sweden, [3]Instituto de Biologia, Universidade Estadual de Campinas, Campinas, São Paulo, Brazil, [4]Dept. of Biology, Middle Tennessee State University, Murfreesboro, TN, United States

Introduction: The phylogenetics of the species-rich butterfly family Nymphalidae has been under close scrutiny for the past 10 years. The major lineages and their relationships are now quite clear and the time has come to infer the basic components of the evolutionary history of the family. Here we investigate the times of divergence of the major lineages.

Methods: A dataset composed of 236 morphological characters and DNA sequences from 10 gene regions (7747 bp) was analysed for 429 taxa (399 genera out of 540, plus outgroups). A relaxed molecular clock was used to infer times of divergences.

Results: Phylogenetic relationships of the major lineages were nearly identical to previous analyses of smaller datasets. Libytheinae was sister to the rest of Nymphalidae, with Danainae being next, then the satyrine clade and finally the heliconiine and nymphaline clades were sister to each other. Nymphalidae began diversifying between 100 and 90 million years ago. Apparently 12 lineages survived the K/T-event 65 million years ago and soon after diversified into the currently accepted subfamilies. The bulk of Satyrinae, the most diverse subfamily with close to 2000 species, diversified around 30 to 25 million years ago, coinciding with a general cooling of the Earth and the spread of grasslands.

Conclusions: Nymphalidae is older than previous speculations about the age of butterflies, in agreement with several recent studies on smaller groups of butterflies. The temporal scale that is now available for Nymphalidae will allow more detailed studies of the evolutionary history of the many model systems being studied, such as *Bicyclus*, *Heliconius* and *Melitaea*.

Population dynamics and within plant distribution of *Megalurothrips sjostedti* and *Frankliniella occidentalis* (Thysanoptera: Thripidae) in a French bean agroecosystem

Linus Gitonga, Bernhard Lohr

Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya

Introduction: The temporal, spatial and within plant distribution patterns of *Megalurothrips sjostedti* Trybom and *Frankliniella occidentalis* Pergande on French beans was determined so as to come up with appropriate sampling methods through development of constant precision sequential sampling plans.

Methods: Fieldwork was carried out at three localities. French beans were sown on a monthly basis at each location. Beans parts, namely leaves, flower buds, flowers and bean pods were sampled twice a week and thrips larvae and adults extracted and enumerated. Spatial distribution of larvae and adult thrips was assessed using Taylor's power law, whose constants were used to develop constant-precision level sampling plans.

Results: Both larvae and adult thrips were present in the crop all year round, with population peaks for both species occurring at different times of the year. *Megalurothrips sjostedti* peaked during the period following the rains and in the absence of *F. occidentalis*. The latter peaked during the hot and dry months of the year. There was clear displacement of *M. sjostedti* by *F. occidentalis* in the crop during the hot and dry months of the year and in the hot and drier parts of French bean growing. Both larvae and adults were aggregated, but higher aggregation was observed for larvae than adult thrips in the flowers.

Conclusions: These findings on alternation of occurrence, displacement, habitat partitioning and sampling have implications on thrips control in the context of IPM. *Megaluthrips sjostedti* and *F. occidentalis* have well defined preferred oviposition sites.

Insecticide resistance frequencies in *Bemisia tabaci* in Omani and UAE vegetable farms

Farid Talukder[1], Walid Kaakeh[2], Michael Deadman[1], Jaber Al-Dahmani[2]

[1]Sultan Qaboos University, Al-Khod, Muscat, Oman, [2]UAE University, Al-Ain, Abu Dhabi, United Arab Emirates

The frequency of insecticide resistance in different populations of sweet potato whitefly (*Bemisia tabaci*) were investigated in 40 different vegetables growing farms in the Al-Batinah, Oman and Al -Ain, U.A.E. areas through a joint research program. Field populations of whiteflies were collected, preserved and analyzed through the *in-vitro* insecticide resistance assays. Results showed that enzyme inhibition rates (IR) varied from 35% to 52% in case of different Omani whitefly populations, and from 46% to 74% in case of different UAE populations. When the IR values in different insecticides were compared, the different degrees of insecticide resistance were found in both Omani and UAE insect populations.

A review of the Palaearctic genus *Apodiphus* Spinola (Heteroptera: Pentatomidae: Halyini) and a key to its world known species

Dr. Nasreen Memon, Dr. Imtiaz Ahmed

University of Sindh,, Jamshoro, Pakistan

Introduction: The genus *Apodiphus* Spinola is widely distributed from Eastern Europe – Asia and more than 100 years have been passed, since the 1st description of the genus was made. But only 10 species are described to date. Before Ghauri (1977) most of the literature consists of isolated description, fauna or catalogue. Here we have described and illustrated the new species with allied species and presented a key of 11 world known species and discuss their phylogenetic relationship.

Method: We have examined the external morphology and male and female genitalia of specimen under the dissecting compound microscope. Male and female genitalia were dissected and boiled in Potassium Hydro Oxide (KOH) for 20-30 minutes, examined and the drawings were made on graph paper by using ocular graph.

Results: Our study reveals that our new species *A. iraqiensis* is a new record of the genus from Iraq, although most of its species have been recorded from its neighbouring countries. Within the genus this is the only species that has very indistinct basal angular spots, lateral margins of head much curved upwardly and ventro posterior margin of pygophore with deep v-shaped cavity. This particular combination of character states indicates that these states are autapomorphic.

Conclusion: Here we have described the new species *A. iraqiensis* sp. n. particularly on the basis of male genitalia and discuss its phylogenic relationship within the genus, and presented a key of 11 species.

Action spectrum for the suppression of arylalkylamine *N*-acetyltransferase activity in the two-spotted spider mite *Tetranychus urticae*

Takeshi Suzuki, Makio Takeda

Kobe University, Kobe, Japan

An action spectrum was obtained for the suppression of arylalkylamine *N*-acetyltransferase (NAT) activity in the two-spotted spider mite *Tetranychus urticae* by irradiating the mite with monochromatic lights of various wavelengths using the Okazaki Large Spectrograph at the National Institute for Basic Biology, Okazaki, Japan. Fluence-response curves were obtained for wavelengths between 300 and 650 nm by irradiating the mite for 4 h d^{-1}. The samples were frozen after the third exposure. A negative correlation between the fluence rate and NAT activity was detected in the range of 0.01–1 μmol m^{-2} s^{-1} for wavelengths between 300 and 500 nm and in the range of 0.1–10 μmol m^{-2} s^{-1} for wavelengths between 550 and 650 nm. The constructed action spectrum indicated that the photoreceptors mediating the circadian and/or photoperiodic systems might be ultraviolet (UV)-A- and blue-type photoreceptors with absorption peaks at 350 and 450 nm.

Host location by the braconid paraisitoid *Cotesia flavipes* and suitability of 'wild' and 'cultivated' stemborer species

Meshack Obonyo, Paul-André Calatayud, Johnnie van den Berg

North-West University, Potchefstroom, South Africa

Intoduction: Maize fields in Africa are usually surrounded by land occupied by wild plants many of which harbor lepidopteran stemborer species not found on crops. It is not known if the exotic braconid parasitoid *Cotesia flavipes*, which was released in Kenya in 1993 against the invasive crambid stemborer *Chilo partellus* (the economically most important pest of maize and sorghum in the lowlands of East and Southern Africa) searches for and attacks these borers in their natural habitats and whether they are suitable for parasitoid development.

Methods: The objective of this study was to assess the relationship between acceptance and suitability of six stemborer species attacking cultivated sorghum (*C. partellus, Busseola fusca, Sesamia calamistis, and S. nonagrioides*) or Napier grass (*Busseola phaia* and *Sciomesa piscator*) to *C. flavipes*.

Results: Although all stemborer species were equally accepted for ovipositor probing by *C. flavipes*, only *C. partellus* and *S. calamistis* were suitable and produced parasitoids. In olfactometric bioassays, *C. flavipes* females were more attracted to stemborer-infested than uninfested plants. Analyses of the volatile compounds showed that they produced richer volatile profiles, mainly comprising C5–C6 alcohols, terpenoids, aromatic and aliphatic compounds, than uninfested plants.

Conclusion: It can be concluded that stemborer species, that were accepted for oviposition but were unsuitable for parasitoid development, form a reproductive sink and that the exotic parasitoid would not establish in areas where these are the predominant species.

Climate change and new cultural practices affect incidence and management of sugar cane pests in Mauritius

Seelavarn Ganeshan

Mauritius Sugar Industry Research Institute, Reduit, Mauritius

Management of sugar cane pests in Mauritius relies essentially on biological control and cultural practices, the latter not generally being antagonistic to the former. Insecticides have never been applied on a routine basis or on a large scale for the control of sugar cane pests. To reduce production costs, the Mauritian sugar industry is currently undergoing major changes, such as removal of rock heaps, mechanization and improved irrigation systems. These changes necessitate increasing the size of fields. Also, the scarcity of labour has led to abandoning certain traditional practices like trashing. With mechanization of cane harvest, the dry cane leaves and /or plant residues, which were previously raked and aligned in every alternate interrow, are now being left *in situ* (trash blanketing) in the field. Localised but severe infestations by several pests have as a result occurred recently. For example armyworm *Mythimna* spp. (Lepidoptera: Noctuidae) infestations have been found in machine-harvested fields, while the white borer *Tetramoera schistaceana* Snellen (Lepidoptera: Eucosmidae) and the maize webworm *Angustalius malacellus* (Dup.) (Lepidoptera: Crambidae) have been associated with the presence of weeds, the soft scale *Pulvinaria iceryi* Signoret (Homoptera: Coccidae) is attributed to loss of habitat of natural enemies by removal of natural vegetation in and around sugar cane areas. Prolonged drought periods and lower rainfall have increased the incidence of the armoured scale the *Aulacaspis tegalensis* Zehntner (Homoptera: Diaspididae), thrips *Fulmekiola serrata* (Kobus) (Thysanoptera: Thripidae) and white flies *Neomaskellia bergii* (Homoptera: Aleyrodidae).

The potential of crop borders to reduce incidence of aphid-transmitted *Potato Virus Y*

Michelle L. Fourie, Kerstin Krüger

Department of Zoology and Entomology, University of Pretoria, Pretoria, South Africa

Introduction: Potato Virus Y (PVY), one of the most important viruses of potato, is transmitted to new crops via seed tubers or non-persistently through aphid species. The control of the spread of PVY relies largely on measures that incorporate biological traits of aphid vectors (e.g. flight behaviour) and virus transmission characteristics. PVY incidence can be reduced by aphid vectors' losing the ability to transmit PVY when feeding on a non-virus host before moving into the field proper. Four crops were evaluated as potential border plants by determining host-plant preference of aphids in a semi-field trial.

Methods: Five crops (lucerne, maize, potato, soybean, and wheat,) were planted in a randomized block design. Aphids were sampled using different methods (leaf counts, sweep-netting, and green bucket traps to determine landing rates) in order to avoid sampling bias caused by any specific method.

Results: Based on leaf counts, the highest number of aphids was recorded on maize, whereas lucerne had the highest aphid numbers using sweep net samples. Potato had more species in common with maize and wheat than with lucerne or soybean. Further, the landing patterns of alate aphids in the trial plots were not random but showed a clear preference for specific crops. Although aphid species differentiated between crops when landing, there was no relationship between aphid abundance in the green bucket traps and leaf counts.

Conclusions: Maize and wheat showed the greatest potential as a border crop, based on aphid abundance and species composition

The effect of semiochemicals and aphid resistant cultivars on Russian wheat aphid control.

Goddy Prinsloo[1], Velemir Ninkovic[2], Theuns Van der Linde[3], Amie Van der Westhuisen[4], Robert Glinwood[2]

[1]ARC-Small Grain Institute, Bethlehem, South Africa, [2]Department of Ecology,Swedish University of Agricultural Sciences, Uppsala, Sweden, [3]Department of Zoology and Entomology, University of the Free State, Bloemfontein, South Africa, [4]Department of Plant Sciences, University of the Free State, Bloemfontein, South Africa

Introduction: Behaviour modifying semiochemicals are known to have repellent properties to the grain aphids *Rhopalosiphum padi* and *Sitobion avenae* in Sweden. Possible repellency by these semiochemicals to Russian wheat aphid (*Diuraphis noxia*) was investigated under dryland production conditions in South Africa during a collaborative project between the two countries.

Methods: During the study, olfactometer tests with methyl salicylate and other chemicals from plant essential oils were conducted for *D. noxia* behavioural activity. The semiochemicals were also tested for effects on *D. noxia* population development in field trials in 2004 and 2005 using a *D. noxia* resistant cultivar (Elands) and a susceptible cultivar (Betta). Methyl salicylate was compared with a commercial produced formulation Nocoron which is a slow releasing wax pellet formulation consisting out of three different volatile substances.

Results: Methyl salicylate and Nocoron repelled *D. noxia* significantly during olfactometer tests. *D. noxia* settled less on Elands plants that had been exposed to volatiles, whereas the effect on *D. noxia* settling on Betta was less obvious. In 2004, semiochemicals reduced aphid populations in Elands, but led to increased aphid populations in Betta. Further, the impact of the chemicals on aphid numbers and grain quality varied according to plant variety indicating an interaction between semiochemicals and aphid resistant plant varieties.

Conclusion: The results suggest that differential effects of semiochemicals on insect populations in resistant and susceptible plant varieties can occur, possibly due to complex interactions between the chemical, plant variety and growing environment.

Balancing benefits and risks of biological control

Franz Bigler[1], Dirk Babendreier[2]

[1]Agroscope ART, Zurich, Switzerland, [2]CABI Bioscience, Delémont, Switzerland

Risks of environmental effects from releasing exotic biological control organisms is of increasing concern, and regulatory authorities have taken a more risk-averse attitude for biological control during the last years. Awareness of risks related to biological control has attained a disproportionate attention by governments and sometimes by the public. A more balanced discussion of risks has to take into account the benefits of biological control and the risks of not applying biological control organisms. However, risk-cost-benefit assessment of a biological control agent is a complex task given that it should take into account expected risks, costs and benefits of economic values, human health, and the environment. Environmental impacts can usually not be valued in absolute monetary terms, therefore they are analysed in a qualitative manner. Proposed procedures for environmental risk-benefit assessment consist of identifying, analysing, and evaluating (weighing-up) risks and benefits of monetary and non-monetary values. Procedures that are ranking risks and benefits separately in decreasing order of significance are discussed and examples are given. Even though adverse effects of biological control agents are mostly limited to effects on non-target arthropods, uncertainties about potential long-term and area-wide impacts greatly complicate risk-benefit assessments. Examples demonstrate that the benefits of replacing insecticides by releasing biological control agents outweigh the environmental risks posed by such organisms.

Malaria vector control: Dealing with non-vector species

Richard Hunt[1], Belinda Spillings[2], Lizette Koekemoer[2], Basil Brooke[2], Christophe Kinkanke[2], Maureen Coetzee[3]

[1]School of Animal, Plant & Environmental Sciences, University of the Witwatersrand, Johannesburg, South Africa, [2]Vector Control Reference Unit, National Institute for Communicable Diseases, NHLS; Division of Virology & Communicable Disease Surveillance, School of Pathology of the University of the Witwatersrand, Johannesburg, South Africa, [3]NRF Chair in Medical Entomology & Vector Control, School of Pathology, University of the Witwatersrand, Johannesburg, South Africa

Introduction: There has always been the general assumption that mosquitoes found resting inside houses have fed on the residents and are responsible for any malaria transmission taking place. Before the recognition of the *Anopheles gambiae* complex, there was no reason to doubt this assumption. However, with modern methods for identification of groups or complexes of anophelines, it has become increasingly common for species resting inside houses to be identified as non-vectors. This presentation details recent work carried out in Malawi where modern technology failed to provide an adequate identification of what looked like *Anopheles funestus.*

Methods: Mosquitoes were collected resting inside houses near Karonga, northern Malawi, and returned to the laboratories at the NICD in Johannesburg. Wild females were set up for egg-laying and each egg batch was treated as an individual family. Morphological, cytogenetic, cross-mating and molecular studies were carried out on all samples.

Results: Preliminary morphological studies showed the presence of distinct pale bands at the joints of tarsomeres 1-3, unlike *An. funestus*. All other morphological characteristics were as in the *An. funestus* subgroup. The larvae reared under standard insectary conditions showed a distinct reddish coloration compared with the normally dark grey larvae of *An. funestus*, but with no other morphological differences. None of the 84 wild-caught females were found infected with malaria parasites. Chromosomal banding patterns of the X chromosome were homosequential with *An. funestus*, but a unique polymorphic inversion was seen on autosome arm 2. The population appears to be homozygous for inverted arrangements 3a, 3b and 5a. Cross-mating produced hybrid males from the cross between Malawi females and funestus colony males. The hybrid testes and spermatozoa were apparently normal. The reciprocal cross produced >900 eggs but very few hatched (0.22% - two females). Sequencing of a 740bp fragment of the ITS2 region showed a 4.5% (33/740bp) difference between the field caught samples compared with the laboratory strain of *An. funestus*. Four basepair changes (4/20bp) in the species-specific primer binding site for the *funestus* group PCR identification were seen in the field caught samples which explains why amplification failed.

Conclusions: This population of mosquitoes, while readily utilizing human habitations as a resting habitat, is apparently not involved in malaria transmission. Host preference studies and further molecular analyses are needed but at this stage we tentatively conclude that we are dealing with an undescribed species within the *An. funestus* subgroup.

Platypus quericovrus causing Japanese oak wilt disease in Japan: Why has JOW become epidemic recently?

Masahide Kobayashi[1], Naoto Kamata[2]

[1]Kyoto Prefectural University, Sakyo, Kyoto 606-8522, Japan, [2]University of Tokyo, Bunkyo, Tokyo 113-8657, Japan

In Japan, Japanese oak wilt disease (JOW) caused by a fungus *Raffaelea quercivora* vectored by an ambrosia beetle *Platypus quercivorus* has been spreading rapidly since late 1980s. Fagaceae trees were used as fuels in the past. However, these tree species were left unattended after the fuel revolution since early 1960s in Japan. We speculate that great increase of the number of large-diameter trees suitable for *P. quercivorus* reproduction is one of major causes of JOW epidemics. The number of the insect offspring that emerged from brood trees tends to be greater in trees with larger diameters because these trees provide larger space for the beetle reproduction and maintain necessary moisture for longer period. Other hypotheses on JOW epidemics are related to global warming. Mortality of *Quercus crispula* is approximately 40% but much lower for associated species of Fagaceae (< 5%). It is likely that other tree species resistant to the fungus evolved under a stable relationship between the tree, fungus and beetle during a long evolutionary process. *Q. crispula* was probably not part of this coevolution because *Q. crispula* is distributed in cooler regions than other host tree species. A warmer climate since the late 1980s made possible the fateful encounter of *P. quercivorus* with *Q. cripsula* by allowing the beetle to extend its distribution to more northern and higher altitudes. Tree stress caused by high temperature and by drought is also a likely cause of the epidemics because JOW incidences tend to increase greatly in hot summers.

Aquatic habitat productivity to adult *Anopheles arabiensis* and *Culex quinquefasciatus* in a rice agro-ecosystem, in Mwea, Kenya

Joseph Mwangangi[1], Ephantus Muturi[2], Joseph Shililu[3], Simon Muriu[3], Benjamin Jacob[2], Ephantus Kabiru[4], Charles Mbogo[1], John Githure[3], Robert Novak[2]

[1]Centre for Geographic Medicine Research - Coast, Kenya Medical Research Institute, Kilifi, Kenya, [2]Department of Medicine, William C. Gorgas Center for Geographic Medicine, Alabama, United States, [3]International Centre for Insect Physiology and Ecology, Human Health Division, Nairobi, Kenya, [4]Kenyatta University, Department of Pathology, Nairobi, Kenya

Between April and September 2005, studies were conducted to determine the contribution of diverse larval habitats to adult *Anopheles arabiensis* Patton and *Culex quinquefasciatus* Say production in a rice land agro-ecosystem in Mwea Kenya. Two sets of cages measuring 0.125 m^3 and 1 m^3 were placed in different habitat types to investigate the influence of non-mosquito invertebrates on larval mortalities and the contribution of each habitat type to mosquito productivities, respectively. The cages (emergence trap) were designed having a fine netting material cover to prevent adult mosquitoes from ovipositing in the area covered by the trap and immature mosquitoes from entering into the cage. The emergence for *An. arabiensis* in seeps, tire tracks, temporary pools, and paddies were 10.53%, 17.31%, 12.50%, and 2.14%, respectively while the corresponding values for *Cx. quinquefasciatus* were 16.85% in tire tracks, 8.39% in temporary pools and 5.65% in the paddies from 0.125 m^3 cages during the study. Cages measuring 1 m^3 were placed in different habitat types which included paddy, swamp, marsh, ditch, pools and seep to determine larval habitat productivity. *Anopheles arabiensis* was the most predominant anopheline species (98.0% n = 232) although a few *An. coustani* Laveran (2.0% n = 5) emerged from the habitats. The larval habitat productivity for *An. arabiensis* were 6.0 mosquitoes per m^2 for the temporary pools, 5.5 for paddy, 5.4 for marsh, 2.7 for ditch and 0.6 for seep. The *Cx. quinquefasciatus* larval habitat productivity was 47.8 mosquitoes per m^2 for paddy, 35.7 for ditch, 11.1 for marsh, 4.2 for seep, 2.4 for swamp and 1.0 for temporary pools. Pools, paddy and marsh habitat types were most productive larval habitat for *An. arabiensis* while paddy, ditch and marsh were the most productive larval habitats for *Cx. quinquefasciatus*. The most common non-mosquitoes invertebrates' composition in the cages included dytiscidae, notonectidae, belostomatidae and ephemerellidae, and their presence negatively affected the number of emergent mosquitoes from the cages. In conclusion, freshly formed habitats are most productive aquatic habitats while old and more permanent habitats are least productive due to natural regulation of mosquito immatures.

Using electron microscopy to define species within *Asthenopholis* Brenske, a genus of African leaf chafer beetles (Coleoptera: Scarabaeidae: Melolonthinae)

James Harrison[1, 2]

[1]Transvaal Museum, Northern Flagship Institution, Pretoria, South Africa, [2]Department of Zoology and Entomology, Forestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, South Africa

Introduction: Currently, seven described species comprise the beetle genus *Asthenopholis* Brenske, 1898. A taxonomic revision was initiated for the species placed within *Asthenopholis*, a genus which includes localised African endemics, some of which can become sporadic agricultural pests and consequently require accurate identification. However, although light microscopy could provide intuitive separation of the specimens into morphospecies, scanning electron microscopy (SEM) was used to look for consistent morphological characters to differentiate these into species.

Methods: All type and available specimens (n = 650) were examined. Once morphospecies were obtained via light microscopy and analysis of geographical distribution, representatives of each morphospecies were examined using SEM. Specimens were softened in boiled water, cleaned ultrasonically (50-60 Hz; 80 W), then set and dried. Thereafter, they were mounted on stubs and gold coated using a SEM Auto-coating Unit (E5200) and viewed with a JEOL (JSM-840) SEM. Digital micrographs were captured using Orion 6.60.4.

Results: In total, about 150 hours (or 22 SEM days) produced 1200 micrographs for interspecific comparisons. Diagnostic characters were observed especially in the form and position of setae around the eye and on the pronotum, scutellum, and pygidium.

Conclusions: The SEM morphological analysis provided definable species-specific characters. The analysis recognized seven species of *Asthenopholis* (i.e., five valid existing and two new species; two previous synonymies were confirmed). Specimens from a species complex within the genus require additional material and probably molecular analysis to differentiate them further into definable species, or a cline of a single variable species.

Six years of field trials with transgenic Bt-potato in South Africa - experiences and lessons learnt

Diedrich Visser[1], David Sehlola[1], Walter Pett[2]

[1]ARC-Vegetable and Ornamental Plant Institute, Pretoria, South Africa, [2]Department of Entomology, Michigan State University, East Lansing, MI, United States

Introduction: A Genetically modified potato containing the *Bacillus thuringiensis* gene for the control of the potato tuber moth, *Phthorimaea operculella* (PTM), was evaluated between 2001 and 2007 in South Africa.

Methods: Field trials comprising randomized block designs were conducted in six provinces. Efficacy studies were carried out at all locations, while environmental impact and non-target studies were carried out in three provinces.

Results: Six field trial permits, as well as a permit for the conducting of contained use experiments in laboratories and a greenhouse, were issued by the Registrar of Genetically Modified Organisms Act of South Africa. These permits also included permission to do storage trials in the relevant areas. Seed tubers for all field trials had to be produced in a specially adapted greenhouse modified to multiply mini tubers in a vermiculite substrate open hydroponic system. Movement of all seed tubers, planting, harvesting and storing was strictly monitored by inspectors of the Department of Agriculture. Regular inspections during the season of all field trials were also carried out. In some instances the strict requirements as stipulated in the permit were altered after written objections to the Registrar. At all locations where PTM occurred, the Bt-potato provided excellent control of PTM compared to the non-transformed potato. No PTM were found, nor was any PTM damage observed on the Bt-potato lines tested.

Conclusion: Six years of field trials with Bt-potatoes were conducted successfully in South Africa. However, strict regulations, instructions and inspections always impacted on the normal potato field trial processes.

Advantages, limitations and extrapolation to field situation of different laboratory test methods used to evaluate side-effects of plant protection products to non-target arthropods

Marco Candolfi

BASF SE, Agricultural Center, Limburgerhof, Germany

An overview on laboratory test methods used to access the side-effects of plant protection products on non-target and beneficial arthropods will be presented. Methodology used to access lethal and sub-lethal endpoints will be compared and discussed. Advantages and limitation of different test method approaches will be discussed in view of predictability of effects under field conditions.

Could semiochemicals enhance parasitism of aphids on Russian wheat aphid resistant cultivars?

Goddy Prinsloo[1], Robert Glinwood[2], Theuns Van der Linde[3], Amie Van der Westhuizen[4]

[1]ARC-Small Grain Institute, Bethlehem, South Africa, [2]Department of Ecology, Swedish University of Agricultural Sciences, Uppsala, Sweden, [3]Department of Zoology and Entomology, University of the Free State, Bloemfontein, South Africa, [4]Department of Plant Sciences, University of the Free State, Bloemfontein, South Africa

Introduction: Plants attacked by herbivores, produce herbivore-induced volatiles, which benefit the natural enemies by making the herbivores more vulnerable to the natural enemies. The behavioural response of two Russian wheat aphid parasitoids namely *Aphelinus hordei* and *Diaeretiella rapae* to methyl salicylate was tested in the laboratory. Methyl salicylate is known for its aphid repellent properties

Methods: The response of the parasitoids to an oil formulation of methyl salicylate was tested in a four-arm olfactometer in the laboratory. The resistant cultivar TugelaDN and the near isogenic susceptible cultivar, Tugela were then treated with methyl salicylate. The behavioural response of the parasitoids was then tested against treated and untreated plants.

Results: Both parasitoid species were significantly repelled by the methyl salicylate formulation but *A. hordei* was affected more than *D. rapae*. However, when plants were treated with the formulation the parasitoids were attracted to the plants. This effect was stronger with on resistant TugelaDn than on susceptible Tugela. Being known as a stress signal, methyl salicylate could induce the defence mechanism in the different cultivars, leading to the production of herbivore induced volatiles that were attractive to the parasitoids.

Conclusion: Methyl salicylate may have several beneficial effects when used in the control of Russian wheat aphid. Not only does it contribute to the lower aphid numbers in the wheat crop but could enhance the effect of parasitism in the field and improve the control of the aphids.

Data management and taxonomic applications for the Platygastroidea Global Biodiversity Inventory

Norman Johnson[1], Andrew Austin[2], Luciana Musetti[1]

[1]The Ohio State University, Columbus, Ohio, United States, [2]The University of Adelaide, Adelaide, SA, Australia

The Platygastroidea Global Biodiversity Inventory is an NSF-sponsored international project aimed toward increasing the sampling of these parasitic wasps in collections, development of a robust phylogeny for the group, and the rapid description of a large number of species within the superfamily. Current taxonomic practices are, we believe, insufficient to handle the scale and pace of this taxonomic enterprise, and new tools and paradigms are required to achieve the desired goals.

Data domains associated with taxonomy include nomenclature, literature, characters and their states, collecting data, and imagery. Several informatics tools used to manage these data are described. A complete electronic taxonomic catalog is used to manage names and literature. Access to these data is available through the Hymenoptera Name Server (purl.oclc.org/NET/hymenoptera/hns). A specimen-level database manages information derived from collecting events. This is accessible through Hymenoptera On-Line (purl.oclc.org/NET/hymenoptera/hol). An image management application, Specimage, archives images and provides mechanisms to rapidly compare pictures for diagnosis. A new application, vSysLab (purl.oclc.org/NET/hymenoptera/vsyslab), assists in the development of taxon by character matrices. vSysLab exports data in formats for import into identification software (Lucid interchange files and Structure of Descriptive Data XML format), phylogenetic analyses, and as natural language descriptions. This application links the character data to the specimen and taxonomic portions of the database. As a result, nomenclatural summaries and material examined sections of typical taxonomic descriptions are quickly and accurately produced.

Communication between project collaborators is an essential element of a large-scale taxonomic project. Wiki software provides the mechanism for real-time discussion and documentation of taxonomic research. A weekly newsletter is produced to coordinate activities and to maintain the interest in and momentum of the project. Project results may be viewed at purl.oclc.org/NET/hymenoptera/platygastroidea.

Identification of proteins found in fungus-growing ant fecal material

Morten Schiøtt, Henrik H. de Fine Licht, Jacobus J. Boomsma

University of Copenhagen, Copenhagen, Denmark

Ca. 50 million years ago a single ancestor of today's >210 species of fungus-growing ants committed herself irreversibly to farming fungi for food instead of being a hunter-gatherer as most other ants. However, the Leucocoprini (Agaricales) that were domesticated remained mostly uncommitted to the symbiosis until a single lineage evolved special "ant-feeding" hyphal tips (gongylidia). Recent work has shown that many fungal enzymes pass the ant intestines unharmed to be transferred to the actively growing parts of the fungus garden where the ants deposit their fecal droplets. However, not all of these compounds are benevolent promotors of new fungal growth. Some appear to function primarily as defenses of the resident clonal fungus against alien strains of symbiont that foraging ants might bring in. In order to identify the active compounds in fecal droplets, we have commenced a survey of the proteins present in *Acromyrmex echinatior* fecal droplets. The survey is based on separating proteins with SDS polyacrylamide gel electrophoresis followed by tandem mass spectrometry and PCR to determine the gene sequences encoding the fecal droplet proteins.

Food attraction and reproductive success of the Japanese burying beetle, *Eusilpha japonica*

Wakana Taki, Mamoru Watanabe

University of Tsukuba, Tsukuba city, Ibaraki prefecture, Japan

Introduction: The Japanese burying beetle, *Eusilpha japonica*, seems to search for carrion by walking around the forest floor throughout the day. In order to reveal the food requirement of adults in relation to the reproductive success, food attraction and feeding habits were studied in the field and in the laboratory, respectively.

Methods: Field survey included the consecutive capturing for two days, using pitfall traps with carrion and without carrion. When the adults were collected in the field, they were starved over 72 hrs in the rearing container and then allowed to feed on a meat of chicken to estimate the daily food intake.

Results: Females and males were captured in the pitfall traps with carrion probably due to the attraction of the meat odor, while the traps without carrion tended to have both sexes together. After 2 days starvation, females showed the significantly larger quantity of food intake (0.37±0.02g) than males (0.20±0.02g), and thereafter, their daily food intake decreased. The clutch size of the first brood increased with the cumulative quantity of food intake of the pair until the oviposition. The pairs successively produced 3.2±0.3 clutches for 20 days up to the end of the experiment, though each clutch size after the second brood was not affected by the food intake of the pair.

Conclusions: Because females in the fields required more food than males for egg production especially in their first brood, walking around the forest floor might be a searching behavior for food which appeared temporally and patchily on the ground.

Combining theoretical population ecology and practical biocontrol: Earwigs in fruit orchards

Rob Moerkens[1], Bruno Gobin[2], Gertie Peusens[2], Laurent Crespin[1], Herman Helsen[3], Herwig Leirs[1]

[1]University of Antwerp, Antwerp, Belgium, [2]Zoology Departement, Pcfruit TWO, Sint-Truiden, Belgium, [3]Wageningen UR, Zetten, Netherlands

Earwigs, *Forficula auricularia* (L.) (Dermaptera: Forficulidae) are beneficial predators in apple and pear orchards where they are capable of maintaining several pest species below economic thresholds. Earwigs thus play an important role in integrated fruit orchards and are essential in organic top fruit cultures. Numbers of earwigs show large interannual variations in densities in both organic and IPM orchards, this limits their practical use. All practical attempts for re-establishing earwig populations have failed. These problems indicated that a theoretical approach was necessary. In order to develop strategies for increasing earwig populations we have built a population model. This enables the prediction of earwig phenology throughout the season while a sensitivity analysis allows us to identify key factors and critical periods in the earwigs' life cycle.

It is well know that earwig development is temperature dependent. This allows us to make phenological predictions in a given year using daydegrees, which are the sum of daily temperatures above a certain threshold. Taking into account microclimates and different habitat temperatures we have validated the simulations with existing field data from several European and non- European earwig populations. Predictions of third and fourth instar nymphs produce excellent results, while adults show a considerable bias. First sensitivity analyses reveal that the numbers of nests during winter have a very big impact on the population in relation to spring or summer survival. However more knowledge about limiting and regulating processes is required for developing specific and effective orchard management strategies. Such work is underway.

Preliminary results of laboratory efficacy tests using registered insecticides against the potato tuber moth, *Phthorimaea operculella*, in South Africa

Diedrich Visser, Nolwazi Mkize, Sakhi Sambo

ARC-Vegetable and Ornamental Plant Institute, Pretoria, South Africa

Introduction: Potato tuber moth (PTM) is one of the most destructive potato pests in South Africa. Its larvae feed on foliage and also tunnel into tubers. Yield losses of between 5 and 30% are not uncommon. Poor control is regularly reported when using registered insecticides against the potato tuber moth. Although this could be attributed to many factors, insecticidal resistance is usually assumed. A laboratory study was initiated to elucidate the effectiveness of insecticides against, and possible resistance in, the potato tuber moth.

Methods: In phase one of the study, a diagnostic dose for each of the 15 insecticides tested was used against nine geographically different moth populations, including a susceptible laboratory population. The diagnostic dosages were calculated from the recommended field dosages and applied as a detached leaf dip bioassay. First instar larvae were collected from insectarium reared populations (collected previously in different production regions) and transferred to treated leaves with a fine camel hair brush. The treated leaves with the larvae were incubated in petri dishes for approximately ten days after which mortalities were noted.

Results: Preliminary evaluations showed that all insecticides killed all larvae in all treatments. The next phase of the study will include the use of cumulative half dosages until surviving figures differ from that of the susceptible laboratory population. Dose-response studies using LD50 values will then be instituted on the relevant populations/insecticides.

Conclusion: Thus far no severe insecticidal resistance could be proven using diagnostic dosages in the laboratory against nine geographically different moth populations.

Occurrence of *Wolbachia* in introduced populations of pharaoh ants: A case of enemy release?

Anna M. Schmidt, Jes S. Pedersen

University of Copenhagen, Copenhagen, Denmark

Introduction: Pharaoh ants (*Monomorium pharaonis*) are very successful invaders of human habitation in most parts of the world. Like their fellow tramp ant species pharaoh ants are small, polygynous and unicolonial; traits considered instrumental in their invasion success. Enemy release may likewise be important for their success. This study examines the presence of the intracellular bacterium *Wolbachia* in introduced populations of pharaoh ants from several localities around the world. *Wolbachia* has previously been found to be present in native, but lacking in introduced populations of the highly invasive fire ants (*Solenopsis invicta*) and Argentine ants (*Linepithema humile*); therefore the lack of *Wolbachia* has been implicated as a possible factor increasing the success of the invasive populations.

Methods: Workers from more than 50 populations were screened for the presence of *Wolbachia* using the wsp81F and wsp691R primers. High quality extractions and sequencing will be performed to identify the strains present in the pharaoh ants and to study the occurrence and strains in some of their close invasive and non-invasive relatives.

Results and conclusions: *Wolbachia* was found in about 10% of the populations representing laboratory reared as well as free living colonies. This relatively high frequency raises the question of how harmful *Wolbachia* really is for pharaoh ants, since release from the bacterium does not appear to be a prerequisite for successful invasion. Including more samples will potentially further the understanding of the phylogenetic and geographical relationship of invasive ants and their *Wolbachia* symbionts.

Biology of the egg parasitoid *Trichogrammatoidea lutea* (Hymenoptera: Trichogrammatidae) on three lepidopteran host species

Khethani V. Mawela[1], Kerstin Krüger[2], Rami Kfir[3]

[1]University of Pretoria, ARC-Plant Protection Research Institute, Pretoria, South Africa, [2]Department of Zoology & Entomology, University of Pretoria, Pretoria, South Africa, [3]ARC-Plant Protection Research Institute, Pretoria, South Africa

Introduction: *Trichogrammatoidea lutea* is a parasitoid of Lepidoptera eggs. The effects of ultraviolet (UV) radiated host eggs of three lepidopteran species on life history parameters of *T. lutea* were evaluated as part of developing a mass-rearing programme for this parasitoid. UV-radiation was used to arrest the development of the eggs in order to simplify mass-rearing and to avoid cannibalism by the newly hatched larvae.

Methods: Three lepidopteran host species, *Helicoverpa armigera, Chilo partellus* and *Ephestia cautella,* were used to evaluate the effect of UV radiation (15 min) on the duration of development, parasitism, number of progeny per host egg and sex ratio of *T. lutea*, and to determine the effects of hosts and temperature (18-30℃) on its biology.

Results: *T. lutea* parasitized and completed development on UV-radiated host eggs. Parasitism, number of progeny and sex ratio were not affected by UV-radiation. Developmental time was shorter on un-radiated compared to UV-radiated host eggs. Parasitism increased with temperature on all three hosts. The highest parasitism rate occurred at 27℃ on *H. armigera* and the lowest at 18℃ on *Chilo partellus*. The number of progeny was highest on *H. armigera* at all temperatures. Sex ratio of *T. lutea* was not affected by temperature. Rate of development increased with temperature on all hosts and was fastest on *H. armigera*.

Conclusion: UV-radiation of host eggs had negligible effects on life history parameters of *T. lutea.* Both *H. armigera* and *E. cautella* were found to be suitable hosts for mass rearing of *T. lutea.*

Neuro-endocrinology of reproduction and phase transition in the desert locust, *Schistocerca gregaria*

Jozef Vanden Broeck, Liesbeth Badisco, Elisabeth Marchal, Pieter Van Wielendaele, Heleen Verlinden, Gert Simonet

Animal Physiology and Neurobiology, Leuven, Belgium

The biological process that leads to locust swarm formation is termed 'phase transition'. Locusts can develop into two distinct 'phases', a solitary and a (swarming) gregarious one, which display very prominent differences in behavior, development, coloration, morphology and metabolism. These phases also show important differences in their reproductive physiology. Phase characteristics are likely to be influenced by factors derived from the central nervous system (CNS). Locusts are very suitable experimental models for physiological research. Major advantages are their big size compared to most other insects, their fascinating biology and the vast amount of physiological and endocrinological data that are already available. However, a major disadvantage is the huge size of their genome (several times the human genome). To compensate for this disadvantage, we recently initiated a project to generate an 'Expressed Sequence Tags' (EST) database representing a large number of transcripts expressed in the desert locust (*Schistocerca gregaria*) CNS. This research initiative is performed in collaboration with a specialized high-throughput sequencing center. The aim is to further explore the molecular information gathered in this locust EST database and to study the fundamental physiological mechanisms underlying the complex process of locust phase transition.

Increased habitat complexity to manage natural enemy community of the Colorado potato beetle, *Leptinotarsa decemlineata* (Say) (Coleoptera: Chrysomelidae)

Zsofia Szendrei[1], Matthew Greenstone[2]

[1]Rutgers, The State University of New Jersey, Chatsworth, NJ, United States, [2]Agricultural Research Service, USDA, Beltsville, MD, United States

Introduction: Habitat complexity influences predator efficiency and community structure. Molecular gut analysis is an effective tool to study predator-prey interactions under field conditions. Our goal in this study was to investigate the effects of habitat complexity on predator-prey interactions in potato fields.

Methods: Predators were collected from Maryland potato fields that were either tilled or mulched with winter rye or hairy vetch. Species-specific DNA primers were used to identify Colorado potato beetle (CPB) in predators gut contents. We performed molecular gut content analysis on almost 1700 individual CPB predators during the 2006 and 2007 field seasons. We used CPB-DNA half-lives derived under simulated field conditions to weight these raw proportions, and thereby to rank these predator species in order of their impact on the CPB population.

Results: Seven common and abundant foliar predator species in our experimental fields prey on different CPB life stages. This assemblage includes polyphagous species such as ladybeetles (Coleoptera: Coccinellidae) and *Podisus maculiventris* (Hemiptera: Pentatomidae); and specialists such as *Lebia grandis* (Coleoptera: Carabidae) and *Perillus bioculatus* (Hemiptera: Pentatomidae). Predator species were more evenly distributed in tilled plots than in cover-cropped fields. The most abundant species in all treatments was *Coleomegilla maculata*. The incidence of CPB DNA in the guts of the examined predator species ranged from 0 to 91%.

Conclusion: Our results indicate that habitat management is a potentially viable method of manipulating the CPB predator assemblage. The observed differences in predator species distribution, however, may not translate into better pest suppression.

The phylogeography of sex in the parthenogenic ant, *Platythyrea punctata*

Jon Seal, Katrin Kellner, Juergen Heinze

University of Regensburg, Regensburg, Germany

Parthenogenesis among animals is rather rare, but most animal taxa exhibit at least some members that produce diploid offspring from unfertilized eggs. The relative rarity is explained by some theory that indicates that parthenogenesis is not adaptive over long periods, and will eventually be replaced by sexual populations, owing to the greater variability among sexually produced offspring. The ponerine ant, *Platythyrea punctata*, is one of the six ant species that exhibits parthenogenesis. This species occurs from South Texas to at least Costa Rica on the American mainland and also occurs on nearly all Caribbean islands, south Florida and the Bahamas. Like many members of its genus, its colonies frequently lack queens and a worker (a 'gamergate') assumes queen behavior, but peculiarly, colonies on the islands and Florida can produce diploid eggs from unfertilized eggs by thelytokous parthenogenesis. Whether or not this occurs in mainland populations is unclear. This project documents the range of parthenogenesis in this species. Colonies have been collected from Barbados, the Bahamas, Grenada, Florida, Texas, Puerto Rico, Dominican Republic, Belize and Costa Rica. The data presented here will use a phylogeny constructed from a 1400 bp segment of mitochondrial CO I gene to test whether parthenogenesis is more common in young, rapidly expanding populations, as theory would predict. We will also compare genetic distances among the populations and thus provide their ages, the age of the parthenogenetic populations and perhaps the role of vicariance and dispersal in this population. Supported by DFG (He 1623/20-1).

Management studies against major insect pests of soybean (*Glycine max* (L.) Merrrill)

B. S. Thakur, Sandhya S.R.

Indira Gandhi Krishi Vishvavidhyalay, Raipur (Chhattisgarh), India

Pest succession and management studies against major insect pest of soybean (*Glycine max*) were conducted in Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.) India. In pest succession, out of twelve inset species observed *Obereopis brevis* S., *Ophiomyia phaseoli* Coq., *Melanagromyza sojae* and *Spodoptera litura* were the major pests and fourteen bioagent *viz.,* lady bird beetles, lace wing, Cantheconid bug, *Costesia sp.* and *Beauveria bassiana* were regulating the pest population of soybean.

June 25th recorded minimum incidence of girdle beetle, stemfly and *Spodoptera litura* and produced maximum for yield. Avoidable yield losses were higher in 8th and 15th July sown crop. Among the 20 cultivars screened, higher total phenol content varieties showed low incidence of stemfly and girdle beetle and with high level of chlorophyll succumbed to more incidence of *Spodoptera litura.* The carryover of girdle beetle was observed on several alternate hosts. Light trap catches of *Spodoptera litura* indicated its presence almost throughout the year. Pheromone trap population showed negative correlation of *Spodoptera litura* male moth with rainfall.

Combination of Nuclear Ployhedrosis Virus @ 1 lit/ha + Triazophos @ 800 ml /ha gave better result than other combinations against *Spodoptera litura*. The Phorate 10 G @ 1Kg a.i./ha reduced the stemfly infestation. On the basis of LC_{50} insecticides Fenvalerate and Profesophos were highly toxic against *Spodoptera litura* and Lindane & Endosulfan were observed as to least toxic. Integration of all the components studied has given good results in on farm and off farm studies against soybean pests.

Conservation biological control via unharvested enemy refugia: Coppicing willows, leaf beetles and predatory bugs

Christer Björkman

Dept of Ecology, Swedish University of Agricultural Sciences, Uppsala, Sweden

Introduction: Disturbances are common in natural systems and may affect important ecosystem processes (e.g. predation and hence biological control). If the perturbations, e.g. harvesting, are predictable they can be used to test ecological theories in large-scale field experiments.

Methods: Densities of leaf beetles (prey) and mirid bugs (predators) were compared in (i) coppicing willow plantations different years after harvest and (ii) in plantations with and without unharvested parts, expected to function as enemy refugia.

Results: Harvesting disrupts the biological control of leaf beetles in short rotation coppice willow plantations. The reason is that the main natural enemies (mirid bugs) are removed at harvesting, taking place in winter. The reason for this is that the bugs overwinter as eggs oviposited in willow tissue and we show that the density of mirid eggs increase with time after harvesting. The leaf beetles, overwintering outside the plantations, can thereby return to an enemy-free space in spring. We hypothesized that one way to conserve biological control would be to leave unharvested willows, functioning as enemy refugia. The results from a field experiment showed that (1) enemy densities and (2) predation pressure (but to a lower extent) was higher within than outside refugia, and (3) both leaf beetles and mirid bugs were positively affected by refugia on whole stand level.

Conclusions: Leaving unharvested refugia may affect the pest more positively than the predators. Our results illustrate the need to consider scale and basic biological knowledge before launching simple solutions to complex problems.

Insect rearing science opportunities at Mississippi State University

Frank M. Davis[1], Norman C. Leppla[2]

[1]Mississippi State University, Department of Entomology and Plant Pathology, Mississippi State, MS, United States, [2]University of Florida, Department of Entomology and Nematology, Gainesville, FL, United States

Introduction: In 2000 the Department of Entomology and Plant Pathology bought into the concept that insect rearing research and education is vital to the advancement of Entomology and that we would provide it. Fortunately, we had local entomologists who had rearing experience and were interested in developing an insect rearing center and its activities.

Methods: In the following seven years state-of-the-art rearing facilities were designed and constructed, rearing of insects for research was initiated, insect rearing research was begun utilizing staff and graduate students, an insect rearing library based on a gift from Dr. Pritam Singh was established, and a workshop for training insectary managers and rearing specialists was initiated.

Results: Our educational efforts have focused on a 5-day workshop titled “Principles and Procedures for Rearing Quality Insects”. It covers nine areas of rearing which are considered vital to have a successful rearing program. The workshop is team taught using local experts and those from other public and private institutions. Ten workshops have been sponsored. Occasionally two workshops were necessary per year to satisfy the demand for insect rearing education. Two hundred and twenty nine persons from twenty countries have participated in the workshop. A book based on workshop topics is scheduled to be available by the end of 2008.

Conclusions: An insect rearing center has been created with an educational and training component. Plans are being considered to offer an insect rearing course and perhaps the workshop by long distance educational means.

Warning and prognoses of insect pests and diseases in Norway with emphasis on two insect pests in apple orchards

Trond Hofsvang

Bioforsk Plant Health and Plant Protection, Aas, Norway

Introduction: VIPS is a web-based decision support system designed to assist Norwegian growers in the management of pests, diseases and weeds of cereals, vegetables and fruit crops. VIPS was established in 2001 as a collaborative project between Bioforsk and Norwegian Agricultural Extension Service (NAES) under a government-funded action for reducing risk connected to the use of pesticides. The aim of VIPS is to provide information to advisors and farmers to reduce reliance on pesticides.

Methods: Inputs to the forecasting models are weather data from the Bioforsk Agrometeorological Service consisting of a network of 80 automatic weather stations across crop production areas, weather forecasts from the Norwegian Meteorological Institute and biological/field observations collected by NAES.

Results: In 2008, five species of insect pests are included in VIPS. Two of these five insects, codling moth (*Cydia pomonella*) and apple fruit moth (*Argyresthia conjugella*), are important pests in Norwegian apple orchards. For both insects species climatic data and biological observations are used in the forecasting models. For codling moth day degrees (temperature at sunset), pheromone traps and flowering (petal falls) are included in the model. Day degrees (optimal treatment timing), abundance of rowan berries, per cent of berries with larvae, level of parasitism of the larvae and flowering are parameters used in the model for forecasting of apple fruit moth.

Conclusions: The service is open and free of charge at www.vips-landbruk.no and is an important tool for implementing IPM in Norway.

Conclusion: Insect rearing education and training support for advancements in entomology?

Frank M. Davis[1], Norman C. Leppla[2]

[1]Mississippi State University, Department of Entomology and Plant Pathology, Mississippi State, MS, United States, [2]University of Florida, Department of Entomology and Nematology, Gainesville, FL, United States

Introduction: The evolution of the science of rearing insects in the laboratory from the 1940's to now have been phenomenal as we moved from table top rearing of a few hundred insects per week to mega facilities producing millions per week. As a result, a solid foundation of insect rearing information was generated in the last half of the 20th century. During this era we observed the birth of private enterprises in rearing insects for a multitude of purposes to go along with public ventures which have traditionally focused on rearing for education and research purposes. What was obviously missing during this period was the lack of formal education and training opportunities for insect rearers.

Methods: Some entomologists involved in rearing insects today have recognized the need for formal education and training of insect rearing personnel and are making efforts to address this problem.

Results: Education and training for those interested in rearing quality insects at the lowest cost possible is now available through workshops, symposiums, books generated by these efforts, and visits to respected rearing facilities. Plans are being made to develop the first ever college/university course in insect rearing and expand its utility by long distance educational means.

Conclusions: The 21st century can be the "The Golden Years" of insect rearing if personnel are properly educated and trained in the critical areas of rearing. This will require investment in funding, time and commitment with the result being continued significant advancements in insect rearing science.

We are one but not the same: Population and colony structure of the thelytokous ant *Platythyrea punctata* in Puerto Rico

Katrin Kellner, Juergen Heinze

University of Regensburg, Regensburg, Germany

Although all female Hymenoptera are capable of laying haploid eggs that develop parthenogenetically into males (arrhenotoky), very few are capable of laying unfertilised eggs that turn into diploid females (thelytoky). Once such species is the neotropical ponerine ant, *Platythyrea punctata*. This species appears to be primarily clonal on Caribbean islands and may be sexual on the American mainland. Because the presence or absence of a sexual process is thought to determine the genetic structure at both the colony and population level, *P. punctata* has become a model system for understanding the relationship between reproductive mode and population structure. This talk presents data on the population genetics of this species on Puerto Rico. Previous work indicated that all colonies are queenless and the dominant mode of reproduction is thelytokous parthenogenesis. We used high polymorphic microsatellite markers from several sample sites distributed over the island further determine the genetic composition of colonies and population structure. We found that colonies do not exclusively consist of a single clone, but rather a mixture of genotypes. Genetic variation was surprisingly high between colonies and sample sites. Some of this could be due to fusion events or recombination due to the thelytoky mechanism this species employs. However, a laboratory experiment designed to investigate this mechanism, suggested that colonies produce diploid eggs by apomixis (meiosis does not occur), therefore the observed variation would appear to come from fusion events.

New developments in the rearing and the management of quality control for tsetse flies for AW-IPM

Andrew Parker, Idrissa Kabore

International Atomic Energy Agency, Vienna, Austria

Following the successful eradication of *Glossina austeni* from Unguja Island, Zanzibar and the launching of the AU-PATTEC there has been a considerable increase in interest in developing area-wide integrated pest management (AW-IPM) programmes, including the use of the SIT, for the creation of tsetse free zones. The Joint FAO/IAEA Programme of Nuclear Techniques in Food and Agriculture through its Insect Pest Control sub-programme continues to develop the technology and procedures for tsetse mass rearing to meet this increasing demand.

Principle amongst these has been the development of the Tsetse Production Unit 3, a semi-automated system for tsetse holding and feeding. To complement this we are now working on the development of an automated system to sex tsetse in the late pupal stage. This will lead to easier male handling and irradiation.

A second area that we are actively developing is improved techniques for the decontamination of blood diet for tsetse feeding. Up to now this has been achieved using gamma irradiation, but with the withdrawal from the market of the commonest irradiator an alternative is required. We are investigating both pasteurization and UV irradiation.

The Joint Programme is also running a five year Co-ordinated Research Project (CRP) on “Improved and Harmonized Quality Control for Expanded Tsetse Production, Sterilization and Field Application”. Included under this CRP is work on quality control of rearing, flight muscle development and blood diet processing. The Joint Programme is also offering a dose inter-comparison service to allow projects to check their dosimetry systems.

Developing IRM strategies for the next generation of insect-resistant maize

Richard L. Hellmich[1], Jarrad R. Prasifka[1], Blair D. Siegfried[2]

[1]USDA-Agicultral Research Service, Corn Insects and Crop Genetics Research Unit and Department of Entomology, Iowa State University, Ames, Iowa, United States, [2]Department of Entomology, University of Nebraska, Lincoln, Nebraska, United States

The high-dose/refuge strategy is commonly used to manage insect resistance to *Bacillus thuringiensis* (Bt) crops. This strategy should be effective as long as plants express a high dose of the toxin, genes conferring resistance are rare, and there are many insects from a refuge (structured or unstructured) available to mate randomly with resistant insects. These assumptions are met with many lepidopteran pests of maize throughout the world, but certainly not all. A new generation of transgenic crops, however, that combines two or more toxins with different modes of action (stacks and pyramids) could increase the spectrum of insect control and at the same time allow reduced refuge size and the possibility of seed mixtures. Interplant movement of larvae has been recognized as an important factor that could violate high dose assumptions and thus has limited the use of seed mixtures. Experiments are underway with colonies of resistant corn borers, *Ostrinia nubilalis*, to determine how resistance alleles influence larval movement among Bt and non-Bt maize plants. These experiments could help determine whether “refuge in the bag” is possible for Bt maize and *O. nubilalis* and establish methods to similarly test other insect pests of transgenic crops.

Capacity building for tsetse and trypanosomosis control in Africa by the sterile insect technique

Andrew Parker, Marc Vreysen, Udo Feldmann, Jorge Hendrichs

International Atomic Energy Agency, Vienna, Austria

The Joint FAO/IAEA Programme of Nuclear Techniques in Food and Agriculture is supporting Member States in their efforts to generate progress towards the ultimate objectives of the Pan African Tsetse and Trypanosomiasis Eradication Campaign of the African Union (AU-PATTEC). Various resources of the FAO/IAEA are used to support methods development, technology transfer and capacity building relevant to the integration of the sterile insect technique (SIT) for tsetse and trypanosomosis control in Africa.

Our capacity building activities cover both training and assistance with facility design, construction and equipping. The training is organised under the Agency's Technical Cooperation programme by fellowships to develop the skills of individuals, by means of on the job training in specific fields, formal university courses and regional training courses. Recent training courses have covered baseline data collection, GIS and population genetics, and a course on tsetse rearing and sterile male handling will be held shortly. We are now working with the other mandated UN organizations and the AU-PATTEC to identify Regional Designated Centres (RDCs) for training relevant to addressing the tsetse and trypanosomosis problem. Selected RDCs will be assisted to develop their facilities and training capabilities, and to resolve any limitations in their capacities.

Another area of our assistance to capacity building is through Co-ordinated Research Projects (CRPs). CRPs bring together participants from developing and developed countries through a number of Research Coordination Meetings (RCMs) to plan and coordinate the work. Through these RCMs collaborations are set up between researchers in developing and developed countries.

Spiracular fluttering is not a steady state behaviour

Thomas D. Förster, Stefan K. Hetz

Humboldt Universität, Berlin, Germany

Using an automated perfusion system we investigated the steady state spiracle behaviour of diapausing *Attacus atlas* pupae in response to fixed enforced tracheal gas mixtures.

No mixture resulted in steady fluttering of the spiracles. We conclude that the intermittent opening of single spiracles during the flutter phase results from internal oscillations of the endotracheal gas composition caused by an on-off type feedback control of the spiracles.

The p_{CO2}/p_{O2} phase space consists of 2 distinct regions corresponding to fully open resp. closed spiracles. The boundary between the regions is bilinear. For small p_{CO2} values an oxygen partial pressure of approximately 1-2 kPa marks the trigger for spiracle opening. This terminal p_{O2} is positively correlated with carbon dioxide partial pressure. p_{CO2} values above 2.5 kPa resulted in spiracle opening regardless of the oxygen content of the tracheal air.

The bilinear nature of the regions boundary provides support to the emergent property hypothesis, which postulates discontinuous gas exchange as the result of two coupled feedback control systems.

Development of sex pheromones for management of cocoa mirids in West Africa

Joseph Sarfo[1], David Hall[2], Colin Campbell[2]

[1]Cocoa Research Institute of Ghana, New Tafo, Ghana, [2]Natural Resources Institute, Chatham Maritime, Kent, United Kingdom

Introduction: Approximately 70% of the world's cocoa comes from West Africa. Recent studies indicate that 25-30 % of cocoa in Ghana has significant mirid damage, the main species being *Sahlbergella singularis* and *Distantiella theobromae.* The mirids damage pods and attack young stems and branches with an annual crop loss estimated at 100,000 tonnes. Currently mirid control relies heavily on the use of insecticides, especially older, more toxic compounds, and the potential for use of pheromones and biopesticides in management of these pests is being explored. Two sex pheromone components produced by females were identified and blends of these shown to attract males of both species.

Methods: The pheromone components were synthesised on large scale by a two-step process at NRI. Experiments to optimise the pheromone lure and trap design and to develop the traps for monitoring and control by mass trapping are being carried out on-station and in growers' farms in Ghana.

Results: Experiments to optimise the pheromone lure and trap design have highlighted the difficulties in working with these pests because of their highly aggregated distribution. Both pheromone components are required for attraction of the main species, *S. singularis*, but the exact blend does not seem to be critical. Both sticky and water traps are effective and small-scale trials have shown an apparent effect on mirid populations at 150 traps/ha. A replicated trial is in progress to determine the effect of mass trapping on mirid damage.

Conclusions: Pheromone traps show promise for monitoring and control of the main cocoa mirid species in West Africa.

Molecular detection of predation: opportunities and challenges

William O.C. Symondson

Cardiff University, Cardiff, Wales, United Kingdom

Predator-prey interactions are fundamental to our understanding of invertebrate community dynamics. Whether we are interested in food webs, control of crop pests by natural enemies or the conservation of endangered species, an understanding of the mechanistic links driving change in populations, and of the many factors affecting prey choice by generalist predators, is of great value.

There is a long tradition of molecular analyses to determine the diets of insects using enzyme electrophoresis, polyclonal antisera and monoclonal antibodies. However, since 1999 this field has experienced a quantum leap forward with the utilisation of PCR-based analyses. It has now been clearly demonstrated that prey DNA can still be detected in the guts of arthropod predators after many hours (even days) of digestion. The precision and speed with which new DNA primers can be designed is leading inexorably to the extinction of earlier technologies. We can now simultaneously detect a broad range of different prey in the guts of predators using multiplexing with a library of prey-specific primers. As sequences databases expand, and primer information is published, this process is becoming ever simpler and more rapid. Great challenges lie ahead. How can predation rates using different primers, in the same or different predators, be compared? Can qPCR be used effectively to improve estimates of predation rates? Can new technologies (microarrays, pyrosequencing) help us? The important message is that these molecular techniques are simply tools; as entomologists and ecologists we now need to start using them to address exciting new questions.

Genomic analyses of behavior in *Polistes* wasps: Insights into social evolution

Amy L. Toth, Gene E. Robinson

University of Illinois, Urbana-Champaign, IL, United States

Genomic studies can provide a wealth of information for testing long-standing evolutionary hypotheses. We used 454 pyrosequencing to generate an EST (expressed sequence tag) set for the paper wasp *Polistes metricus*, a non-model genetic organism which is an important species for the study of social evolution. Using this genomic resource, we performed two studies of brain gene expression in *P. metricus*. First, quantitative PCR analyses of genes previously known to be associated with honey bee division of labor showed large expression differences between wasp queens, workers, maternal founding females, and future reproductive gynes. Expression patterns were most similar between workers and maternal females, supporting the idea that worker behavior evolved from maternal behavior. Second, we used the EST sequence data to develop *P. metricus* microarrays representing over 3000 different genes. We will present the results of ongoing brain microarray analyses comparing wasps in different behavioral castes. This study will allow us to identify major pathways and networks associated with wasp social behavior, and via comparison to honey bee transcriptomic data, to highlight conserved pathways underlying division of labor across multiple social insect lineages.

Changes in plant attributes: a possible cause for alterations in insect host-plant selection in laboratory host-specificity tests

Tsedal Ghebremariam[1], Kerstin Krüger[1], Carl Reinhardt[2], Arne Witt[3], Stefan Neser[3]

[1]Dept. of Zoology & Entomology, University of Pretoria, Pretoria, South Africa, [2]Department of Plant Production & Soil Science, University of Pretoria, Pretoria, South Africa, [3]ARC-Plant Protection Research Institute, Pretoria, South Africa

Introduction: The biocontrol programme against *Solanum mauritianum* (Solanaceae), an invasive alien weed from South America, has been hampered by unexpected host-plant selection behaviour of candidate insect biocontrol agents during quarantine laboratory evaluations, which is in conflict with the narrow host ranges observed in the native range of potential agents. It is suggested that changes in plant attributes are causing these differences.

Methods: The morphology and chemistry of four *Solanum* species (*S. lichtensteinii* (natural host)*, S. mauritianum, S. tuberosum* and *S. melongena*) grown in open air and under controlled environments (glasshouse, growth chamber and shade-net) were examined using microscopy, elemental analysis, reaction with stains and reagents, and other techniques. Multiple-choice trials with plants grown under different conditions was undertaken to compare host-plant choice by a native South African beetle (*Conchyloctenia hybrida* Boheman (Coleoptera: Chrysomelidae)) reared on its natural host plant, *S. panduriforme*.

Results: Considerable differences in the morphology and chemistry of plants grown in open-air and controlled environments were found in terms of plant height, leaf area, leaf thickness, cell-wall and cuticle thickness, trichome density, phenol-containing glands, CaCo3 cystoliths, silica, alkaloid and glycoside content. In line with this, multiple choice trials identified differences in feeding and oviposition behaviour between plants grown under different growth conditions.

Conclusions: Morphological and chemical differences between plants grown under controlled conditions and in the field may contribute to the alteration in host selection patterns of insect herbivores under laboratory vs. field conditions.

Plant-animal mutualistic networks: The architecture of biodiversity

Jordi Bascompte

Estación Biológica de Doñana, Sevilla, Spain

The mutualistic interactions between plants and their insect pollinators have molded the organization of Earths's biodiversity. Recently, it has been shown that these interactions can form complex networks involving dozens and even hundreds of species. These coevolutionary networks are highly heterogeneous, nested, and asymmetric**.** Some Hymenoptera and Diptera species act as network hubs and have an important role as the glue that keeps these networks together. These network patterns highly determine the robustness of the network to species extinctions or habitat destruction. I will follow by exploring to what extend past evolutionary history conveyed in the phylogenies of plants and insects can explain these network patterns and the robustness of the network to species extinctions. Because pylogenetically similar species tend to play similar roles in the network, extinction events trigger non-random coextinction cascades. This implies that taxonomic diversity is lost faster than expected if there was no relationship between phylogeny and network structure. These results illustrate how the simultaneous consideration of phylogenetic information and network structure can aid in the conservation of biodiversity.

Groundnut leafminer, *Aproaerema modicella* (Deventer) (Lepidoptera: Gelechiidae), a pest of groundnuts in South Africa

Hannalene du Plessis

ARC - Grain Crops Institute, Potchefstroom, South Africa

Introduction: The groundnut leafminer (GLM), *Aproaerema modicella* is an important pest of groundnut and soybean in South and South-east Asia. Since 1998, it has been reported from Uganda, Malawi, Mozambique and also South Africa. Since it is a new pest in this country and no integrated pest management programme (IPM) exists for this insect, it was, therefore, investigated.

Methods: Moth flight activity was monitored with pheromone traps at four localities over a period of two years. The efficacy of different insecticides for control of GLM on groundnut was evaluated as none is currently registered for this purpose in South Africa. To determine host plants of GLM, weed species with GLM infestations were collected inside and around groundnut fields at Tsiombo irrigation scheme. Parasitoids reared from GLM infested soybean and groundnut leaves (larvae and pupae) from one and four localities respectively, were identified.

Results: Flight activity patterns corresponded with the productive phase of groundnut. Differences in efficacy of insecticides for the control of GLM were determined. Eleven weed species infested with GLM were collected. Nine possible biological control agents of GLM were sampled from GLM larvae and pupae.

Conclusions: Timing of planting will largely affect both the severity and onset of GLM infestation, irrespective of locality. For effective chemical control of GLM, a high volume of water is essential for more efficient covering of plants. Host status of plants identified and the role it could play during the off-season survival of the pest still needs verification. Key components for an IPM strategy for GLM in South Africa were identified by this research. The next challenge is to put all these together in a sustainable and economical pest-control strategy.

G protein-coupled receptors and their signaling properties in flies and locusts

Jozef Vanden Broeck, Tom Van Loy, Heleen Verlinden, Boris Van Hiel, Hans Peter Vandersmissen, Pieter Van Wielendaele, Jeroen Poels

Animal Physiology and Neurobiology, Leuven, Belgium

For the analysis of insect G protein-coupled receptors (GPCRs), the *Drosophila* genome project represented a major breakthrough. Since then, the genomes of several other insect species, such as the malaria mosquito, *Anopheles gambiae*, the honeybee, *Apis mellifera*, the silkworm, *Bombyx mori*, and the red flour beetle, *Tribolium castaneum*, most of which are of economic (positive or negative) or medical value, have been sequenced; and more sequence information is becoming available from novel genome and EST data. Some insect receptors are even believed to be potential targets for pest control agents. *In silico* analyses revealed the presence of a few hundred genes coding for putative heptahelical transmembrane (7TM) proteins in these insect genomes. These can be classified into at least four distinct evolutionary conserved families. Insect genomes also encode a multitude of putative neuropeptide and peptide hormone precursor genes. In addition, an important fraction of the insect GPCRs shows sequence similarities with mammalian peptide receptors. Many of these receptors have been deorphanized in recent years, while others still remain orphans. *In vitro* (*e.g.* cell-based assays, reverse pharmacology) as well as *in vivo* (*e.g.* analysis of fruit fly mutants) approaches will further contribute to the discovery of specific receptor ligands and to the elucidation of insect GPCR signaling function(s), respectively. We will further discuss results we have obtained with fly and locust GPCRs.

Biogeography of the Tachinidae (Diptera) of China

James O'Hara, Hiroshi Shima, Chun-tian Zhang

[1]Invertebrate Biodiversity, Agriculture and Agri-Food Canada,, Ottawa, Ontario, Canada, [2]2-11-1-406 Kusagae, Chuo-ku, Fukuoka, Kyushu, Japan, [3]Liaoning Key Laboratory of Evolution and Biodiversity, Shenyang Normal University, Shenyang, Liaoning, China

The Tachinidae are a huge and cosmopolitan family of parasitic flies with an estimated 10,000 described species. There are believed to be thousands more undescribed species, mostly in the understudied Neotropical, Afrotropical, Australasian and Oriental regions. Within these understudied regions, tachinid research is progressing most rapidly in China. This vast country is uniquely positioned at the transition between the Palearctic and Oriental regions. We have reviewed all the primary literature and nearly all the regional faunal studies on the Tachinidae of China to catalogue the species and record their known distributions by province. The *Flies of China* (1998) documented a tachinid fauna of 754 species and 191 genera, but now ten years later those numbers have climbed to roughly 1100 species and 260 genera. The tachinid fauna of China consists of a mix of Palearctic and Oriental species, with the former dominating in the northern half and west of the country and the latter dominating in the south and southeast. There is also an endemic fauna comprising species of both limited and widespread distribution within China. The level of endemicity within China is currently 37% of the tachinid fauna but this level will undoubtedly decrease as more species described from China are discovered outside the country. Patterns of distribution, areas of endemicity, and the boundary between the Oriental and Palearctic regions are discussed in relation to earth history, the age of the Tachinidae, and the landforms and ecoregions of China.

Variation in induced plant responses and parasitoid foraging behaviour

Tibor Bukovinszky, Erik Poelman, Georgios Prekatsakis, Andre Kamp, Marcel Dicke

Laboratory of Entomology, Wageningen University, Wageningen, The Netherlands

Introduction: Trophic relationships between species can be indirectly mediated by other species, with consequences for species coexistence. Host-induced plant volatiles may aid parasitoids in host location, but indiscriminate use of host and non-host induced volatiles in a diverse community can reduce foraging efficiency. The behavioral mechanisms underlying parasitoid foraging efficiency when herbivore-related cues and plant volatiles are varied are poorly understood.

Methods: Parasitism rates were compared in a semi-field set-up, where parasitoids (*Cotesia glomerata*) were presented with a plot of plants that were (1) only infested by hosts (*Pieris rapae*), or also non-hosts (*Mamestra brassicae*) were placed (2) either on plants with the hosts, or (3) on plants next to host-infested plants. We studied parasitoid foraging behavior in a greenhouse bioassay, where the composition and density of hosts and non-hosts on plants were varied.

Results: When non-hosts were present on the same or on different plants as hosts, parasitism rates were lower than when only hosts were present. In bioassays parasitoids flew indiscriminately towards host and non-host infested plants. Upon encountering a non-host patch, parasitoids readily discriminated and left shortly. However, in mixed patches of hosts and non-hosts, parasitoids could not discriminate and left later.

Conclusions: Variation in induced plant responses may reduce parasitism, depending on whether long distance (infochemical) or short distance (patch related) cues are scrambled. This affects time-allocation of parasitoids in different ways with implications for the spatial distribution of attacks.

Forecasting tools for the management of the grapevine moth *Lobesia botrana* (Lepidptera, Tortricidae) in SW Spanish vineyards.

Antonio Gallardo Cano[1], Lara Maistrello[2], Rafael Ocete Rubio[1], M. Angeles Lopez Martinez[1], Francisco Javier Soria Iglesias[1]

[1]Laboratory of Applied Zoology, Department of Physiology and Zoology, Faculty of Biology, University of Seville, Seville, Spain, [2]Department of Agricultural & Food Sciences, University of Modena and Reggio Emilia, Reggio Emilia, Italy

Introduction: The European grapevine moth, *Lobesia botrana* (Denis & Schiffermüller) (Lepidoptera, Tortricidae), represents the main pest of vineyards in the Mediterranean area. The highest population levels and heaviest economic damages are recorded in areas with annual average temperature and relative humidity around 20ºC and 70%, respectively, which are the best eco-climatic conditions for this insect.

Methods: This study was developed during 12 years in the South West of Spain. Male flights of *L. botrana* were monitored using synthetic sex pheromone baited delta traps from the beginning of March to the end of October, checking all traps once a week. In order to achieve a reliable prediction model, data from temperature accumulations (degree-days) were plotted against conveniently transformed data from males captures.

Results: Correlation coefficients obtained from log-probit linear equations were high, especially for data related to the second generation. Results showed the existence of a linear relationship between temperature accumulations and male trap catches. Moreover, average linear regressions were calculated for the second and third generations and the obtained correlation coefficients were similar for both.

Conclusions: Obtained equations have shown to be acceptable in order to be considered as useful tools in the prediction of emergencies and in the future design of models to improve the effectiveness of the integrated management of *Lobesia botrana* in the studied area.

Link between the circadian clock and metabolism in *Drosophila melanogaster*

Kanyan Xu, Xiangzhong Zheng, Amita Sehgal

Howard Hughes Medical Institute, University of Pennsylvania School of Medicine, Philadelphia, PA, United States

Studies in mammals have indicated a relationship between circadian clocks and nutrient metabolism, but little is known about how circadian effects on metabolism impact overall physiology and behavior. Circadian regulation of metabolism has not been investigated in *Drosophila* although clock proteins are expressed in many metabolically important tissues in the fly, including the fat body. We have found that *Drosophila* feeding behavior exhibits a strong 24-hour circadian rhythm which is regulated by a clock in the fat body.. Flies lacking a fat body clock also display increased food consumption, but have decreased levels of energy stores, accompanied by a higher sensitivity to starvation, indicating that the clock in the fat body is required for the storage of energy reserves. At least some of these metabolic phenotypes may be mediated by effects of clock proteins on the expression of specific metabolic genes. Interestingly, the metabolic parameters mentioned above are also affected by clocks in neuronal cells but the effects of neuronal clocks oppose those of the fat body. We propose that the input of neuronal clocks and clocks in metabolic tissues is coordinated to provide effective energy homeostasis.

We have also identified effects of metabolic activity on the central clock that controls behavior. We previously showed that oxidative stress dampens molecular and behavioral rhythms driven by central clock cells, an effect that is manifest in flies lacking the *foxo* gene product. In recent work we have identified effects of other metabolic pathways on the periodicity and light response of behavioral rhythms.

Serotonin receptors in the control of circadian rhythms and sleep in *Drosophila*

Quan Yuan, Amanda Crocker, Amita Sehgal

Howard Hughes Medical Institute, University of Pennsylvania School of Medicine, Philadelphia, PA, United States

Despite the well-known role of monoamines in behavioral processes in mammals, there is limited information on how these molecules impact behavior in Drosophila. In part, this is because the basic characterization of Drosophila monoamines and their receptors has been relatively under-studied. We have identified effects of serotonin on both circadian rhythms and sleep in Drosophila. We find that serotonin modulates the light response of the circadian clock, thereby decreasing the ability of the clock to respond to light under normal day:night conditions. The mechanism underlying this effect involves the d5-HT1B receptor, which promotes the phosphorylation and thereby decreases the activity of GSK3-β. This leads to reduced phosphorylation of the clock protein TIM by GSK3-β and a decrease in the TIM response to light. In extended darkness, levels of serotonin are low in the fly head, which may account for increased light sensitivity under these conditions.

In other work, we found that serotonin acts through the d5-HT1A receptor to promote sleep in flies. In the absence of this receptor, flies have reduced sleep, but more strikingly, the sleep is fragmented. The mutant phenotype is rescued by driving expression of the receptor in mushroom bodies, supporting a role for this structure in Drosophila sleep. Interestingly, although the d5-HT1A and 1B receptors are quite similar, d5-HT1B can not substitute for 1A in rescue experiments. More recently we have also initiated studies of octopamine and octopamine receptors in the regulation of sleep in Drosophila.

Leafminer insects trigger the host plant physiology through an unexpected association with endosymbiotic bacteria

Wilfried Kaiser[1], Elisabeth Huguet[1], Nadine Imbault[2], Jérôme Casas[1], David Giron[1]

[1]CNRS - University of Tours, Tours, France, [2]University of Tours, Tours, France

Introduction: Gall-inducer arthropods are usually distinguished from other insect-generated shelters by the fact that they involve active differentiation of highly nutritive tissues. However, plant manipulation appears not to be restricted to gall-inducers only, as shown by the autumnal formation of 'green-islands' around mining caterpillars. This study aims at understanding the underlying mechanisms of the host-plant physiological manipulation.

Methods: Using ELISA assays and colorimetric techniques the amount of phytohormones and nutrients in mined areas were recorded. Isopentenyl transferase gene expression (key enzyme of the cytokinin biosynthetic pathway) was investigated using RT-PCR and the role played by endosymbionts was studied using antibiotic treatments.

Results: Our results show a large accumulation of cytokinins in the mined tissues which are responsible for the preservation of functional nutrient-rich green tissues at a time when leaves are otherwise turning yellow. All individuals analyzed so far are closely associated with *Wolbachia* and a key enzyme of the cytokinin biosynthetic pathway has been isolated, cloned and sequenced from the *Wolbachia* genome (tRNA-ipt Wo). This key enzyme is expressed in *Wolbachia*-infected insects leading to a clear alteration of the plant physiology. A manipulative study allowed us to show that insects cured of endosymbionts are not able to influence the host plant physiology showing the pivotal role played by endosymbionts in the host plant manipulation.

Conclusions: These results clearly show the ability of leafminer insects to manipulate their host plant physiology and to create an "optimal" nutritional micro-environment through cytokinin production by their endosymbiotic partners.

Phylogenetic analysis of Encyrtidae (Hymenoptera: Chalcidoidea): Are there un-concerted copies of 28S rDNA in Hymenoptera?

James B. Woolley[1], John S. Noyes[2], Donald Quicke[3], Joe Gillespie[4], Matt Yoder[5]

[1]Texas A&M University, College Station, Texas, United States, [2]Natural History Museum, London, United Kingdom, [3]Imperial College, Silwood Park, Ascot, United Kingdom, [4]University of Maryland, Baltimore, Maryland, United States, [5]Ohio State University, Columbus, Ohio, United States

Phylogenetic Analysis: D2 and D3 expansion segments of 28S ribosomal DNA were sequenced for 110 species in 69 genera of Encyrtidae and 11 outgroups from Tanaostigmatidae, Eupelmidae, Aphelinidae, Pteromalidae and Eulophidae. Data were partitioned into stem regions in which alignment was unambiguous due to base pair covariation, and loop regions, in which alignment was ambiguous. Data were also aligned using CLUSTAL. Data from both alignments were analyzed using parsimony and Bayesian methods, and POY in which optimization alignment and parsimony analyses were performed together. Results support monophyly of Encyrtidae, but not a sister group relationship to Tanaostigmatidae. Neither Encyrtinae nor Tetracneminae are consistently recovered as monophyletic, although some tribes are recovered as monophyletic under all analytical conditions. Other tribes are recovered under some conditions only or are either paraphyletic or polyphyletic.

Broader Significance: Of more general significance, results suggest the presence of two different, un-concerted copies of rDNA in Chalcidoidea. This was first apparent as a short insertion in the D2 region in sequences published by Heraty's lab not present in sequences from Quicke's lab. When analysis is restricted to unambiguously aligned regions only (mostly stems), sequences from congeneric species both with and without the insertion are grouped together. When regions of ambiguous alignment are included (for example using CLUSTAL), sequences with the insertion are not grouped with congeneric species without the insertion, indicating considerable sequence divergence between the two copies in the structurally less conserved loop regions. Thus, methods for sequence alignment are of paramount importance in data analysis.

Road-building and use in the western Amazon Basin, Part 1: Impacting the rainforest and its entomofauna, or not?

Terry L. Erwin[1], Christy Jo Geraci[1], Valeria Aschero[2]

[1]Smithsonian Institution, Washington, DC, United States, [2]Instituto Argentino de Investigaciones en Zonas Aŕidas, Mendoza, Argentina

Introduction: In the western Amazon Basin, oil deposits support local and regional economies, but certain methods of extraction can be harsh on the rainforest ecosystem and its fauna. We present data from the Ecuador Canopy Biodiversity Project (ECBP), a long-term study presently underway in an area of Yasuni National Park (Ecuador) that has been impacted by road construction for oil extraction. We compare data taken from impacted and control sites to examine the effects of road construction and use on canopy insect biodiversity.

Methods: Samples of the entomofauna were taken using standard canopy fogging protocols. Two macroplots of 1 km in length were established: one adjacent to the road, and one 21 km away. One-hundred sampling stations arrayed in 10 plots in each macroplot were each sampled 12 times over a period of 4 years. We examined changes in the abundances of target taxa across seasons and years, and compared data from the impact versus the control sites.

Results and Conclusions: Nearly 10 million specimens were collected, of which 3.8 million belonged to our target taxa. Each hectare of pristine Amazonian rainforest contains up to 3.2 x 10^{10} individuals of terrestrial arthropods representing some 100,000+ species. Relative abundances and adult-immature ratios did not significantly change over the course of the study (ANOVA: $F=0.39$, $P>0.05$). Our results suggest that management practices followed by oil extractors and road-building did not affect canopy entomofauna during the study period. Further research and monitoring will be needed to assure that this ecosystem will remain healthy and diverse.

Development of Spinetoram: A new spinosyn insecticide from Dow AgroSciences

Aris Chloridis, Paul Downard, James Dripps, Katsuya Kaneshi, Leng Choy Lee, Yi-Ki Min, Luis Pavan

Dow AgroSciences, Indianapolis, United States

Spinetoram (XDE-175) is a new spinosyn insecticide being developed by Dow AgroSciences. It is derived from two naturally occurring spinosyns that are chemically modified to increase insecticidal activity and duration of control. Spinetoram offers a unique mode of action and is effective against a broad spectrum of insect pests. It controls key top fruit and vine pests such as codling moth, *Cydia (Carpocapsa) pomonella*; oriental fruit moth, *Grapholita molesta*; pear psyllids, *Psylla (Cacopsylla*) spp; and grape berry moth, *Lobesia botrana*. In vegetable crops, spinetoram controls *Spodoptera* spp. and most other pest Lepidoptera. Spinetoram is also highly effective against thrips, (*Frankliniella* spp., *Thrips* spp., *Scirtothrips* spp.), dipterous leafminers (*Liriomyza* spp.) and certain coleopterans (*Leptinotarsa decemlineata*). Spinetoram conserves most beneficial arthropods in vegetables and tree fruits, and will be an effective and compatible control option for integrated pest management programs. In addition to fruits and vegetables, use in a number of other crops is being explored. Spinetoram was accepted for evaluation by US EPA under its reduced risk pesticide initiative and was granted US federal registration in October 2007. It is being marketed as Delegate WG (250 gai/kg) and Radiant SC (120 gai/L). It is also registered in Canada, New Zealand and in Pakistan for use in crops such as pome fruit, vegetables, and cotton. In EU, spinetoram is currently under evaluation for annex I inclusion. More registrations in other parts of the world are being pursued and anticipated from 2008 onwards.

Synomones induced by egg deposition in herbaceous plants.

Stefano Colazza[1], Ezio Peri[1], Eric Conti[2], Gianandrea Salerno[2], Ferdinando Bin[2]

[1]Department S.EN.FI.MI.ZO, Università di Palermo, Palermo, Sicilia, Italy, [2]Department of DSAA – Section of Entomology, Università di Perugia, Perugia, Umbria, Italy

The knowledge of the mechanisms of communication between plants, herbivores and parasitoids, mediated by volatile infochemicals, can provide more insights into the co-evolution of these tri-trophic systems. Recently, it has been demonstrated that egg parasitoids are able to detect plant synomones induced by egg deposition, indicating that these synomones are used to locate host eggs. Such "early alert" communication has been evidenced both in trees and in herbaceous plants. Relative to herbaceous plants, detailed evidences for defensive plant responses to oviposition, directed towards egg parasitoids, are available for the tri-trophic systems "bean plants – *Nezara viridula* – *Trissolcus basalis*" (bean system), "cabbage plants – *Murgantia histrionica* – *Trissolcus brochymenae*" (cabbage system) and "corn plants - *Sesamia nonagrioides* - *Telenomus busseolae*" (corn system). The bean system and the cabbage system present several analogies on the phenomenon of induction itself, its mechanisms, and its chemistry. However, females of *T. basalis* are able to perceive oviposition plant synomones as volatile compounds from a long/medium range, whereas *T. brochymenae* only after they have contacted the plant surface. The corn system shows more distinctive mechanisms, but it is also characterized by the emission of synomones that act on contact. The different strategies adopted by the egg parasitoids to explore these induced synomones are discussed, with respect to the possible manipulation of adult parasitoid behaviour, aiming at the enhancement of pest control, and to their implications for host selection by egg parasitoids.

Ancestral reconstruction of ancient insect allatostatins: a novel approach to the study of allatostatin function and evolution

Ekatarina Hult, C.J. Weadick, Belinda S.W. Chang, Stephen Tobe

University of Toronto, Toronto ON, Canada

Allatostatins (ASTs) are a class of regulatory neuropeptides, with diverse functions, found in an array of invertebrate phyla. ASTs have complex gene structure, in which individual ASTs are cleaved from a precursor peptide sequence. Little is known about the molecular evolution of AST peptides and functions, even in extensively studied groups such as cockroaches. We describe the application of a novel technique for the analysis of this system, using ancestral reconstruction, whereby ancestral amino acid sequences are resurrected in the laboratory. We inferred the ancestral sequences of a well-characterized peptide, AST7 at the insect ancestor and several cockroach ancestors. Peptides were assayed for *in vitro* inhibition of JH production in *Diploptera punctata* and *Periplaneta americana*. Our results, surprisingly, indicate that the ancestral insect peptide was a more potent inhibitor of JH production compared to ancient cockroach peptides in both species and peptides inferred at more recent cockroach ancestors had increased potency. We believe this decrease in potency at the cockroach ancestor is related to the increased copy number of peptide in these lineages. This model is supported by current physiological data and maybe linked to the increased role of ASTs in the regulation of reproductive processes in the cockroaches.

Does asymmetric specialization differ between mutualistic and trophic networks?

Colin Fontaine, Elisa Thebault

Center for Population Biology, Imperial College, London, United Kingdom

Introduction: Recently, plant-pollinator networks have been found to be highly structured in a nested pattern in which specialists interact with generalist species. This structure is often assumed to be particular to mutualistic interactions in opposition to the compartmentalized pattern expected for antagonistic networks.

Methods: We investigated the presence of asymmetric specialization in a data set assembled from the literature of 20 highly resolved plant-insect herbivore networks and compared them with 24 plant-pollinator networks.

Results: Our results indicate that these two types of networks differ, but not in the way it is generally assumed. Asymmetric specialization is present in plant-herbivore networks even if it appears less frequently than in plant-pollinator networks. Indeed, mean and median percentages of species showing asymmetric specialisation in herbivory webs are 33% and 14% respectively, compared to 57% and 60% in pollination webs. Furthermore, the amount of asymmetry is linked with species diversity and not to connectance in plant-pollinator networks whereas the opposite pattern is found in plant-herbivore networks.

Conclusion: Our results offer promising perspectives for understanding both the mechanisms that structure ecological communities and their impact on community dynamics depending on the type of interaction.

The role of juvenile hormone in parental care by burying beetles: A comparative perspective

Michelle Scott

University of New Hampshire, Durham, NH, United States

Introduction: Burying beetles (*Nicrophorus* spp.) provide lengthy biparental care. They bury and prepare small vertebrate carcasses as food for their young. Juvenile hormone (JH) in both males and females rises quickly upon the discovery of a suitable carcass and reaches high titers in females when larval care is most intense (e.g. *N. orbicollis* and *N. defodiens*).

The role of juvenile hormone: JH does not act primarily as a gonadotropin in burying beetles. It may regulate some parental behavior; it increases aggression directed toward conspecific competitors, and, in young larvae, appears to be correlated with begging intensity. Conversely, social stimuli affect JH titers. Males respond to the loss of a mate with increased JH and increased feeding behavior. JH of males caring for larger broods is higher than those with smaller broods. Both females and males respond physiologically to the intensity of larval begging.

Comparative endocrinology: In other carrion beetles, this hormone pattern varies and depends on life history. *Necrophila americana*, a species that uses large carcasses and provides no parental care, has no such hormonal response to the discovery of a carcass. *Ptomascopus morio*, a nicrophorine beetle, remain with their brood but provides only rudimentary care and has only a weak endocrine response to the arrival of larvae. *Nicrophorus pustulatus*, utilizes snake eggs as well as carcasses to provision their young and this host shift is reflected in JH titers. In burying beetles, the most dramatic changes in JH correlate with the most elaborate parental care.

Unusual challenges, unusual rewards: Introduction of insect-protected biotech cotton in Burkina Faso, West Africa

John Greenplate

Monsanto Company, St. Louis, Missouri, United States

Since 2003, Monsanto has been working with the government of Burkina Faso to assess the potential value of transgenic insect control technology in cotton, the country's leading export crop (>50% of export dollars), and its leading industry in terms of employment. Five years of confined field trials have determined that the technology can raise grower profits substantially, largely by increasing yields and saving caterpillar insecticide input costs. The road to commercial release of biotech cotton has been challenging, due mainly to the lack of enabling regulatory structures to assess, approve, and market biotechnology products. This presentation will describe the many partnerships forged and their efforts to build a robust regulatory framework to ensure grower access to the benefits of biotech cotton and to future safe, effective biotech products.

Augmentative biological control of sugarcane moth borers with *Cotesia flavipes* (Cameron) (Hymenoptera: Braconidae) in Thailand

Wiwat Suasaard, Kittiya Suksen, Oraphan Kernasa

[1]National Biological Control Research Center, Centsl Regional Center, Nakhon Pathom, Thailand, [2]Department of Entomology, Faculty of Agriculture at Kamphaeng Saen Kasetsart University, Kamphaeng Saen Campus, Nakhon Pathom, Thailand

Introduction: Investigation on biological control of sugarcane moth borers *Chilo infuscatellus* Snellen, *Chilo sacchariphagous* (Bojer), *Chilo tumidicostalis* Hampson and *Sesamia inferens* (Walker) with *Cotesia flavipes* (Cameron) was conducted in the central region of Thailand.

Methods: *Cotesia flavipes* were mass-reared at NBCRC-CRC. Augmentative field releases of *C. flavipes* (1000 per hectare) were made every month during 2003-2005 in Nakhon Pathom,Suphan Buri and Kanchanaburi provinces where were located in the central region of Thailand. Higher augmentative release rate (2000 per hectare) were made during 2006-2007 in the areas of heavy infestation occurred in Suphan Buri.

Results: Percent parasitization of sugarcane moth borers was higher in plots of cane where parasites were released than in plots of cane where parasites were not released in every year and every location. Overall parasitization averaged 18.33±8.42 and 4.4±3.12% in release plots and in non-release plots and overall percent infestation averaged 9.11±4.32 and 18.97±5.48 in release and non-released plots respectively during 2003-2005,. The infestation of sugarcane moth borers both in release and non-release plots was very high (23.98±13.61 and 42.98±6.73%) while percent parasitization was only 14.85±12.38 and 4.15±1.20 in release and non release plots during 2006-2007.

Conclusions: Augmentative release boosted biological control but the levels achieved were insufficient for reducing infestation of damage when heavy infestation occurred. Higher levels of control might be possible using higher release rate. This indicated that *C.flavipes* should be a key component in IPM program for sugarcane moth borers.

Heredity and fitness cost of resistance to granulosis virus in French populations of *Cydia pomonella*

Benoit Sauphanor, Marie Berling, Lionel Legros, Miguel Lopez Ferber, Antoine Bonhomme, Joel Chadoeuf

INRA, Avignon, France

Background: Control failures of the codling moth, *Cydia pomonella* , with the *Cydia pomonella* Granulovirus (CpGV) were recorded since 2004 in a few orchards of South-eastern and Centre France. Diapausing larvae of ten field populations were collected in these areas to be assessed in the laboratory for susceptibility to CpGV.

Results: Neonates of individual progenies of adult moths of these populations paired with a moth of a susceptible laboratory strain (Sv) were submitted to a diagnostic concentration of the virus, lethal for 95% of the Sv larvae. Over 90% survival was recorded in a part of individual progenies of field males paired with Sv females, while all individual progenies of field females paired with Sv males had only partial survival. The mortality distribution among these F1 progenies supported the hypothesis of a dominant and sex-linked resistance already demonstrated in German populations of *C pomonella*. Half of the ten analyzed French populations were proved to own a majority of resistant individuals. Inside each population, the resistant and susceptible moths did not significantly differ in weight, longevity, rate and numbers of mating, fecundity and fertility.

Conclusion: Due to its low reproductive cost, this resistance to CpGV is likely to be stable in time and also to spread easily out of the orchards under selection with virus formulations. Special attention has thus to be turned to resistance management strategies in organic orchards, in which CpGV is the only efficient way to control of the high *C pomonella* populations of southern Europe.

Cospeciation in the triplex symbiosis of termites, gut protists, and their bacterial endosymbionts

Osamu Kitade

Ibaraki Unibersity, Mito, Ibaraki, Japan

Introduction: A number of co-phylogenetic relationships between two organisms namely a host and a symbiont or parasite have been studied to date. However, biological interactions in nature usually involve multiple members. We investigated the cospeciation of a triplex symbiotic system comprising a hierarchy of three organisms - termites of the family Rhinotermitidae, cellulolytic protists of the genus *Pseudotrichonympha* in the guts of these termites, and intracellular bacterial symbionts of the protists.

Methods: The phylogeny was inferred based on two mitochondrial genes of the termites and nuclear ssu rRNA genes of the protists and their endosymbionts, and these were compared.

Results and Discussion: Although intestinal microorganisms are generally considered to have looser associations with the host than intracellular symbionts, the *Pseudotrichonympha* protists showed almost complete codivergence with the host termites, probably due to strict transmissions by proctodeal trophallaxis based on the social behavior of the termites. Except for one case, the endosymbiotic bacteria of the protists formed a monophyletic lineage in the order Bacteroidales, and the branching pattern was alsmost identical to those of the protists and the termites. However some non-codivergent evolutionary events were evident. The members of this triplex symbiotic system appear to have cospeciated during their evolution with minor exceptions.

Cospeciation in the triplex symbiosis of termites, gut protists, and their bacterial endosymbionts

Osamu Kitade

Ibaraki Unibersity, Mito, Ibaraki, Japan

Introduction: A number of co-phylogenetic relationships between two organisms namely a host and a symbiont or parasite have been studied to date. However, biological interactions in nature usually involve multiple members. We investigated the cospeciation of a triplex symbiotic system comprising a hierarchy of three organisms - ternites of the family Rhinotermitidae, cellulolytic protists of the genus *Pseudotrichonympha* in the guts of these termites, and intracellular bacterial symbionts of the protists.

Methods: The phylogeny was inferred based on two mitochondrial genes of the termites and nuclear ssu rRNA genes of the protists and their endosymbionts, and these were compared.

Results and Discussion: Although intestinal microorganisms are generally considered to have looser associations with the host than intracellular symbionts, the *Pseudotrichonympha* protists showed almost complete codivergence with the host termites, probably due to strict transmissions by proctodeal trophallaxis based on the social behavior of the termites. Except for one case, the endosymbiotic bacteria of the protists formed a monophyletic lineage in the order Bacteroidales, and the branching pattern was alsmost identical to those of the protists and the termites. However some non-codivergent evolutionary events were evident. The members of this triplex symbiotic system appear to have cospeciated during their evolution with minor exceptions.

Homology of the wing base sclerites and flight muscles of basal Pterygota

Jana Willkommen[2], Thomas Hoernschemeyer[1]

[1]Georg-August-University, Goettingen, Germany, [2]Staatliches Museum für Naturkunde, Stuttgart, Germany

Presently, there is no generally accepted hypothesis about the evolution of the different forms of the flight systems of Ephemeroptera, Odonata and Neoptera from a common winged ancestor. Usually, Ephemeroptera are regarded as the sistergroup of the remaining Pterygota, because they are the only insects moulting in a winged stage.

In this context we examined the flight apparatus of Ephemeroptera and compared it with those of Odonata and Neoptera. To be able to study as many species as possible, we supplemented dissections and serial sectioning with high resolution X-ray tomography. Finally, the ground plan of the wing base of Pterygota is reconstructed.

Our results show that most elements of the neopteran wing base are also present in Ephemeroptera and Odonata. Probably, the ground plan of the wing base of Pterygota was much more similar to the wing base of extant Neoptera than to that of extant Ephemeroptera. In the ground plan of Pterygota the wing base presumably is composed of three axillaries and the proximal median plate. Two muscles are attached to the first axillary and the third axillary is equipped with one short muscle. A most likely autapomorphic character of Neoptera is a second muscle that inserts on the third axillary and originates from the episternum. Consequently, the wing bases of Ephemeroptera and Odonata must be modified and stiffened secondarily and independently from each other. Nevertheless, the basalare of Ephemeroptera and Odonata is possibly not homologous to the basalare of Neoptera.

Land use intensity and landscape composition determine native bee diversity in agricultural landscapes

Andrea Holzschuh, Teja Tscharntke

Agroecology, Georg-August University, Göttingen, Germany

Introduction: Bees may connect noncrop habitats providing nesting sites and arable fields providing food resources via foraging. The agricultural intensification during the last decades may disrupt those bee movements thereby threatening biodiversity and ecosystem services.

M**ethods:** We studied effects of crop and noncrop habitats at local and landscape scales on bee diversity in 21 agricultural landscapes differing in land-use intensity.

Results: Organic farming of crop fields and heterogeneous landscapes both contributed to higher bee diversity. Our results suggest that organic farming may reach highest relative effectiveness in homogeneous landscapes with few remaining flower-rich habitats. Food subsidies from weeds in organic crop fields may have landscape-wide effects on bee communities even in noncrop habitats. An increase of the proportion of organic crop fields from now 5 % on average in Germany to 20 % as aimed by the government may enhance species richness of bees in fallow strips by 50 %.
Bee abundance in mass-flowering oil seed rape fields without seminatural habitats in the vicinity was low suggesting little contribution of bee pollination to seed set in isolated rape fields.

Conclusions: According to our data, cross-habitat fluxes between crop and noncrop habitats are important for maintaining high bee diversity in agricultural landscapes. Conservation management plans and studies assessing biodiversity patterns have to consider factors at both local and landscape scales, because they have the potential to modify or to complement effects of each other.

Density dependent effects of predator species-richness on herbivore supression

Georgianne Griffiths[1], Andrew Wilby[2], Michael Crawley[1], Matthew Thomas[3]

[1]Imperial College, London, United Kingdom, [2]University of Lancaster, Lancaster, United Kingdom, [3]Penn State University, Pennsylvania, United States

Introduction: Mechanisms driving the diversity-function relationship have implications for the optimal management of biodiversity for ecosystem services. With biological control, prevalence of the selection effect supports augmentation of the single most effective natural enemy, whilst dominance of complementarity supports augmentation of natural enemy richness. Few empirical studies however, explicitly consider changes in function with relative or absolute changes in abundance, and may confound the relative importance of richness and density through experimental designs (additive or substitutive).

Methods: Using the natural enemies of cereal aphids we test the relative contributions of predator richness and abundance on pest suppression to contrast accumulation of net effects between con- and heterospecifics. Mechanisms are identified by comparing observed patterns with those predicted by the additive and multiplicative risk model and their associated biological assumptions.

Results: We show that the effects of species richness are density-dependent, and mechanisms underlying those effects are diversity-dependent. We illustrate how density-dependent effects can be detected using a substitutive (or replacement) series design, but argue that greater understanding of mechanism and optimal management will be obtained by examining community assembly along a richness-abundance gradient from substitutive to additive.

Conclusion: Where natural enemy abundance is low, greater increases in function can be achieved by augmenting the most effective natural enemy. However, where natural enemy populations are intermediate or high, it may be more advantageous to increase the richness of functionally complementary species. This will reduce intraspecific interference between functionally equivalent species, and enable new species to occupy unique, and complementary niche space.

Studies on pediculosis in Poland

Aleksandra Gliniewicz[1], Bozena Sawicka[1], Elzbieta Kedra[2]

[1]National Institute of Public Health-National Institute of Hygiene, Warsaw, Poland, [2]Institute of Parasitology, Polish Academy of Sciences, Warsaw, Poland

Introduction: In XX century studies on occurrence of *Pediculus humanus capitis* (P.h.c.) were carried out in 60's and 70's in several localities in Poland. Infestation levels reached this time 0.6-11%. The goal of our study was the evaluation of pediculosis occurrence among schoolchildren in chosen localities and the comparison with the results from the past.

Methods: A questionnaire was elaborated to obtain data about: occurrence of pediculosis, pediculicides used, age of infested children, persistent infestation. Data were collected in 2006 and 2007 in a big city and a province in Poland.

Results: Data from 24 primary schools (9778 pupils), 9 orphanages (562 children) from a city and 100 schools (45235 pupils), 23 orphanages (1012 children) from province were analysed. The infestation levels ranged from 0.65% (primary schools, province) to 17.2% (orphanages, city). In the group of

7–12 yrs old children pediculosis was often observed than among different groups of age. In more than 65% schools from province it was necessary to use a pediculicide more than twice to eradicate infestation. In Poland most of pediculicides contained permethrin as active ingredient, numerous – herb extracts.

Conclusions: The occurrence of pediculosis among schoolchildren from chosen localities in 2006 and 2007 did not significantly differ from the previous data. Several difficulties in P.h.c. eradication could be resulted in improper use of pediculicides; possible development of permethrin resistance in P.h.c. populations could be also considered.

(This work was partly supported by Project No 40407232/2198 of Polish Ministry of Scientific Research and Information Technology)

Distribution of stress in beetle mandibles analysed with finite element analysis and µCT-data

Thomas Hoernschemeyer

Georg-August-University, Goettingen, Germany

The distribution of stress in the mandibles of a beetle (Coleoptera: Archostemata: *Priacma serrata*) was investigated with finite element analysis (FEA) of high resolution computed tomography data (µCT) under different load scenarios. The µCT-data allowed for reconstructing a very precise model of the mandible morphology. This model could be used for the finite element analysis. The investigation shows that the mandible-muscle apparatus of the species investigated is build very robust. The power that the muscles are able to generate is not sufficient to damage any part of the mandible or its attachment to the head capsule. The weakest part of the system is the point where the tendon of the adductor muscle is attachment to the mandible. If failure of the system should occur, it most likely would be at this point.

The design of the mandible maximises the pressure that is applied to the substrate. Thus, the species is enabled to cut even comparatively hard material. Since *P. serrata* always occurs in the vicinity of conifers, this material may be wood or conifer seeds and cone material. SEM investigation of the functional surfaces of the mandibles also shows that *P. serrata* really makes use of them. This example shows that the combination of µCT and FEA allows for reconstructing parameters of the biology even for species for which no real life observations are available.

How glyphosate pesticide residues affect the behaviour of agrobiont spiders and beetles

Veronika Michalkova, Stano Pekar, Stanislav Korenko

Masaryk University, Brno, Czech Republic

Introduction: Current production of GM corn includes application of high rates of non-selective herbicides. Aim of the study was to assess the effect of the glyphosate residues on the behaviour of epigeic spiders and carabid beetles under laboratory conditions.

Methods: Specimens of *Pardosa agricola* (Araneae: Lycosidae) and *Poecilus cupreus* (Coleoptera: Carabidae), collected in the field, were exposed for 2 hours to the fresh, 1-day or 5-day old residues of the herbicide glyphosate (Roundup Biaktiv, Monsanto, API 480 $g.l^{-1}$) applied on the dish surface. The control group of spiders and beetles were exposed to water. Specimens were kept at constant climate conditions and used in one of three behavioural experiments: consumption efficiency, avoidance and speed of locomotion.

Results: Consumption of prey (*D. hydei*) was similar for all treated specimens of both spiders and beetles. Neither spiders nor beetles avoided surface treated with herbicide residues more than the control surface. The speed of locomotion of spiders was not affected by herbicide residues. But in beetles exposed to residues the speed of locomotion was significantly lower than of those exposed to water, due to longer time spent grooming.

Conclusions: All types of herbicide residues studied here did not affect consumption and avoidance in both spiders and beetles. Speed of locomotion was, however, affected negatively in beetles.

Synthesis of information in phylogenetics, evolution, biogeography, and megadiverse taxa

Mark Westneat, Torsten Dikow

Biodiversity Synthesis Center, Field Museum of Natural History, Chicago, Iliinois, United States

Biodiversity informatics is changing the speed of problem solving and also the kinds of hypotheses that are testable in a wide range of biological disciplines. The Biodiversity Synthesis Center (BioSynC) of the Encyclopedia of Life (EOL) helps to facilitate scientific discovery in biodiversity, evolution, and conservation biology by hosting synthesis meetings. Funded by the MacArthur Foundation, synthesis meetings for the EOL can bring together experts on a wide range of scientific and public issues to encourage progress towards specific goals proposed by the scientific community. Meetings focus on biodiversity informatics involving large data sets, the formulation of novel scientific ideas, and building new bridges among disciplines. In particular, synthesis meetings deal with timely issues in biodiversity or conservation research that have a direct relation to the Encyclopedia of Life or develop new ways of using the growing content of the EOL web-pages for scientific discovery. Of particular interest are megadiverse groups such as many insect lineages, novel research questions in biogeography, evolution, systematics, and taxonomy, visualization of large data sets, and study of biodiversity hotspots. In addition, the BioSynC synthesis meetings can help to highlight public benefits to informatics such as new educational materials and citizen science approaches. Here we present the results of the first year of synthesis meetings, including advances in taxonomy and searchable web resources on insects, contributions to browsing insect phylogenies and related informatics, and a general tool for visualization of large data sets in taxonomy and phylogenetics.

The biology and impacts of Argentine ants: An overview

Andrew Suarez

University of Illinois, Urbana, IL, United States

Argentine ants are recognized as one of the world's most widespread and damaging invaders. Native to northern Argentina, Paraguay and southern Brazil, they have been spread by humans to over 30 countries on 6 continents. Research on Argentine ants has historically concentrated on their consequences and methods for their control. However, in addition to providing insight into the study of biological invasions, they are rapidly becoming a model system for understanding processes in a variety of fields in ecology, evolution and behavior. These include nestmate recognition, facilitation and mutualism, competition, population genetics, and sociality. In the introduction to the symposium, I discuss the history of Argentine ant research, introduce the speakers and suggest some future directions of study.

HIRA and the paternal chromatin assembly at fertilization in *Drosophila*

Benjamin Loppin, Emilie Bonnefoy, Guillermo Orsi, Pierre Couble

Université Claude Bernard Lyon 1, Villeurbanne, France

In sexually reproducing animals a crucial step of zygote formation is the decondensation of the fertilizing sperm nucleus into a replication-competent male pronucleus. In sperm DNA packaged with male germline specific chromosomal proteins, including protamines, these non histone proteins are replaced with maternally provided histones to form the male pronucleus. By studying a point mutation allele of the *Drosophila Hira* gene, we could show that HIRA, a conserved chromatin assembly factor, is essential for the assembly of paternal chromatin at fertilization. During this process, HIRA deposits nucleosomes containing the histone variant H3.3 on the decondensing male pronucleus, in agreement with its general role in assembly pathways independent of DNA synthesis that specifically involves this H3.3 histone variant. The exclusive H3.3 marking of paternal chromosomes could represent a primary epigenetic distinction between parental genomes in the zygote.

To further understand the functions of HIRA during early development, a loss-of-function allele of *Drosophila Hira* was generated by homologous recombination. Surprisingly, the phenotypic analysis of this mutant revealed that the only essential function of HIRA is the assembly of paternal chromatin during male pronucleus formation. Moreover, analysis of this mutant established that protamines are correctly removed at fertilization in the absence of HIRA, thus demonstrating that protamine removal and histone deposition are two functionally distinct processes. The observation that H3.3 deposition is apparently not affected in *Hira* mutant embryos and adults, suggests that different chromatin assembly machineries could deposit this core histone variant.

Transgenic crops, pest resistance, and outbreaks

Bruce Tabashnik[1], Aaron Gassmann[2], David Crowder[1], Yves Carrière[1]

[1]University of Arizona, Tucson, AZ, United States, [2]Iowa State University, Ames, IA, United States

Transgenic crops producing insecticidal proteins from the bacterium *Bacillus thuringiensis* (Bt) have grown on more than 200 million ha since 1996. Evolution of pest resistance to transgenic crops threatens the continued success of this approach. The theory and evidence regarding evolution of pest resistance to transgenic crops will be reviewed and evaluated for the potential of such resistance to cause pest outbreaks. Contrasts will be made with the effects on outbreaks of pest resistance to broad-spectrum insecticides. In principle, because transgenic crops producing Bt toxins have narrow specificity and cause little or no direct harm to natural enemies of pests, such crops are less likely than broad-spectrum insecticides to trigger outbreaks of insect pests.

The causes of outbreak dynamics: A life history perspective

Toomas Tammaru

University of Tartu, Tartu, Estonia

Populations of some insects frequently reach outbreak densities while others never do so. Among Lepidoptera, outbreak dynamics appears to be associated with capital breeding strategy (Oikos 77: 561-564). In capital breeders, as opposed to income breeders, reproduction completely relies on resources derived during the larval life of the insects. For various, reasonably well understood reasons females of capital breeding moths typically display simplified adult behaviors which involves lack of selectivity in oviposition substrate selection. As a consequence, ovipositing females of capital breeders are unable to evaluate the quality of resources available for their offspring. This implies no opportunity for density-dependent regulation of population density by the mechanisms of adult behavior. This allows for carrying capacity of the environment to be easily exceeded. Additionally, many outbreaking income breeders are spring feeders with the larvae being able to develop only on young, developing foliage of their host trees. The ways how such a life history may contribute to outbreaks, as well as to regular population dynamics is discussed using the ecologically well studied *Epirrita autumnata* (Lepidoptera: Geometridae) as an example. The key aspects may include insensitivity of reproduction to weather conditions, as well as the timing of the occurrence of different developmental stages in relation to the breeding cycle of insectivorous birds.

Spatial dynamics of ground beetle assemblage in a mosaic fragmented landscape

Irena Bertoncelj, Paul M. Dolman

University of East Anglia, Norwich, United Kingdom

Understanding dispersal and population persistence in fragmented habitat network is essential to conserving biodiversity in anthropogenic landscapes. We examined spatial and temporal dynamics of ground beetle populations in a mosaic landscape, comprising different growth stages of conifer plantations, patches and linear strips of permanent open habitats and ephemeral open areas created by clear-felling. Conservation interests in Breckland SPA (UK) focus on heathland species. We investigated effects of habitat quality, area and spatial location (proximity to source) for community composition and abundance of heathland ground beetles within this open habitat network in the forest landscape. Under current management regime narrow strips of suitable habitat between younger plantations (permanent linear refugia) provide a sufficient source of colonisers for clear-felled areas.

The impact of sulfur on spider mite and predatory mite populations on grapes and hops in the Pacific Northwest of the United States

David James[1], David Gent[2], Deirdre Prischmann[1], Lawrence Wright[1], Deborah Brooks[1], Oscar Garcia[1]

[1]Washington State University, Prosser, Washington, United States, [2]Oregon State University, Corvallis, Oregon, United States

Data collected from field studies and experiments conducted in vineyards and hop yards in Oregon and Washington State during 2001-2007 indicate that the multiple use of sulfur as a powdery mildew management tool, has an adverse impact on biological control of spider mites. In vineyards there appears to be a positive correlation between the frequency of sulfur applications and spider mite population densities. Multiple (> 4) applications of sulfur can result in spider mite population outbreaks requiring control. Similarly, in replicated vineyard and hop yard experiments, multiple applications of sulfur increased spider mite populations. Conversely, predatory mite (Phytoseiidae) populations are generally smaller on sulfur-exposed hops and grapes than on non-exposed plants, and it is likely that suppression of phytoseiid populations by multiple applications of sulfur contributes to spider mite population outbreaks in some instances. However, multiple applications of sulfur increase spider mite populations even in the absence of predatory mites suggesting a more complex mechanism than just elimination of natural enemies.

Gall-inducing insects can evade host-plant defences that are triggered by other insect herbivores

John Tooker, Consuelo De Moraes

Pennsylvania State University, University Park, PA, United States

Gall-inducing insects are accomplished plant parasites that can profoundly influence host-plant physiology. We recently reported that the caterpillar *Gnorimoschema gallaesolidaginis* failed to trigger emissions of host-plant volatiles that often recruit natural enemies of feeding insect herbivores. Only one other caterpillar species has been shown to circumvent some of the feeding-induced indirect defenses of its host plant, and does so by feeding on linolenate-deficient fruits. We initiated this study to determine whether the absence of volatile responses to the gall-inducing *G. gallaesolidaginis* could be explained by a lack of linolenic acid (LNA) in galls. We screened interior and exterior tissue of galls and control stems of the host plant *Solidago altissima* for LNA, jasmonic (JA) and salicylic (SA) acids. Linolenate is a precursor of the octadecanoid pathway, which produces JA, a phytohormone that triggers volatile releases. In some cases, SA can interact antagonistically with JA. We found unexpectedly that *G. gallaesolidaginis* strongly increased amounts of LNA in gall interiors without corresponding increases in JA or SA. These and similar findings with *Eurosta solidaginis*, a gall-inducing fly, suggest that gall insects can nutritionally enhance their food source without concomitant increases in phytohormones and associated defence responses.

Is DGC a result of a mismatch between spiracular conductance and metabolic demand?

Stefan K. Hetz, Thomas D. Förster

Humboldt Universität, Berlin, Germany

The insect tracheal system is a unique respiratory system in the animal kingdom. Oxygen is delivered directly to the tissues. Closable spiracles control the exchange of respiratory gases between tracheal system and atmosphere.

Discontinuous gas exchange cycles (DGC) are a result of discontinuous spiracle activity leading to huge fluctuations in oxygen and carbon dioxide partial pressures. Possible reasons for these DGCs are summarized by Chown et al. (2006). Recent investigations have shown that moth pupae use more spiracles in an opening period than needed in order to release the actually produced carbon dioxide (Hetz 2007). Even if all but one or two spiracles are artificially closed, the discontinuous release of carbon dioxide persists.

The huge spiracular conductance in some insect species may be an adaptation to changing metabolic demand e.g. during flight. Thus, in active insects, the tracheal system and the spiracles are designed for maximum gas exchange capability.

In inactive insects or insect stages, however, this design leads to effects comparable to a respiratory alkalosis caused by hyperventilation. The maximum flow rate of CO_2 through the spiracles in an opening period can exceed the average CO_2 production rate by a factor of 20 or more. The amount of CO_2 released in an opening period may thus reach up to 30 per cent of the total CO_2 stored within the insect body. This results in dramatic changes of the carbon dioxide partial pressure and the hemolymph pH.

The accumulation of CO_2 in the interburst period may be considered as a recovery from a respiratory alkalosis caused by the CO_2-burst.

Aversive conditioning in the monarch butterfly, *Danaus plexippus* (L.) (Lepidoptera: Nymphalidae)

Daniela Rodrigues[2], Martha Weiss[1]

[1]Georgetown University, Washington, DC, United States, [2]Universidade Estadual de Campinas, Campinas, SP, Brazil

Introduction: Learning ability allows insects to respond to a variable environment, and to adjust their behaviors in response to positive or negative experiences. Pollinating insects readily learn to associate floral characteristics, such as color or pattern, with the presence of a sugar reward. However, in nature, pollinators may also encounter flowers that present opportunities for aversive conditioning; the flowers may, for example, contain distasteful or toxic nectar, or offer highly variable nectar volumes. Whereas some bees learn to avoid flowers with unpalatable nectar or variable nectar rewards, little is known about how lepidopterans respond to these aversive stimuli.

Methods and Results: We determined that monarch butterflies learn to discriminate against model flowers that contain salt solution, decreasing probing time on models of a preferred color and altogether avoiding models of a non-preferred color. In addition, when we offered butterflies flower models of two different colors, both of which contained the same mean nectar volume but which differed in variance (models of one color all contained 2 µl of sucrose; models of the other color contained either 4 µl sucrose or none at all), the monarchs probed the constant flowers significantly more than the variable ones, regardless of flower color or butterfly gender.

Conclusions: These results, taken together, demonstrate that monarchs can respond to aversive as well as appetitive stimuli, allowing them to track positive and avoid negative stimuli as they forage in the field.

Financial Support: CAPES

Factors affecting the incidence of intraguild predation

Annie-Eve Gagnon[1], George, E. Heimpel[2], Jacques Brodeur[3]

[1]Département de Phytologie, Université Laval, Québec, Québec, Canada, [2]Department of Entomology, University of Minnesota, St-Paul, Minnesota, United States, [3]Institut de recherche en biologie végétale, Département des sciences biologiques, Université de Montréal, Montréal, Québec, Canada

Introduction: Understanding of guild interactions between natural enemies is of great interest for ecologists and biological control practitioners. Intraguild predation (IGP) occurs when two predators that compete for a shared prey species also engage in predator-prey interactions with each other.

Methods: We describe a method for the detection of intraguild prey in predator gut contents using a molecular approach. PCR primers were designed for four abundant predators in Quebec soybeans: *Coccinella septempunctata*, *Propylea quatuordecimpunctata, Harmonia axyridis* and *Coleomegilla maculata* (Coleoptera: Coccinellidae). Primer specificity and prey detectability half-life following a meal were determined for all coccinellid species interactions. We used these primers to evaluate the incidence of IGP between individuals collected in soybean fields during four years.

Results: Prey detectability half-life differed between species associations and was then considered to correct data from field-caught coccinellids. IGP was a very common interaction (~40%) within the coccinellid community. The interactions were symmetric (mutual intraguild predation) as each species may become prey or feed on each other and were influenced by factors inherent to the predator and prey species, predator-prey densities and seasonality.

Conclusion: This molecular technique is a powerful tool to disentangle and quantify poorly understood and complex interactions among natural enemies under field conditions.

Phylogeny of the Chalcidoidea

John Heraty[1], James Munro[1], Jean-Yves Rasplus[2], Roger Burks[1], Johan Liljeblad[1]

[1]University of California, Riverside, CA, United States, [2]INRA - Centre de Biologie et de Gestion des Populations, Montpellier, France

Economically and ecologically, Chalcidoidea are one of the most important groups of insects. More than 500,000 estimated species are grouped into 19 families, 81 subfamilies and over 2000 genera. Relationships among these mostly parasitic wasps have remained untested, and so far are based solely upon intuitive ideas or studies of only a few closely related groups. The Hymenoptera Tree-of-Life project was focused on three important aspects of Chalcidoidea: their monophyly, their sister group relationships within Hymenoptera, and relationships within the superfamily. These questions are being addressed using morphological and molecular characters, although only the later results will be discussed. The molecular phylogeny of Hymenoptera as based on four gene regions (28S, 18S, COI and EF-1alpha) supports both monophyly of Chalcidoidea and a sister group relationship with either Diapriidae or Mymarommatidae. A more directed study using 31 outgroup Proctotrupomorpha and 504 Chalcidoidea representing all families and 69 subfamilies for portions of 28S (D2-D5) and 18S (E17-35) has been completed. Alignment is optimized by eye across all taxa and also using secondary structure analysis with ambiguous regions optimized in MAFT. Data are analyzed using RAxML and CIPRES. Monophyly of Chalcidoidea is supported, as is a sister group relationship between Diapriidae and Chalcidoidea, and Mymaridae and the remaining Chalcidoidea. Several important and diverse family groups are monophyletic, including Agaonidae, Encyrtidae, Eulophidae and Trichogrammatidae, as are most subfamilies. Several family groups are polyphyletic, including Aphelinidae and Chalcididae. The implications of the phylogeny for understanding morphological and behavioral evolution in the group will be discussed.

Electrical Penetration Graph (EPG) monitoring of feeding by glassy-winged sharpshooter and potential application of EPG to other pathogen vectors

Elaine Backus

USDA Agricultural Research Service, Parlier, CA, United States

Introduction: Recent findings on feeding of the glassy-winged sharpshooter, *Homalodisca vitripennis*, and the mechanism of its transmission (acquisition and inoculation) of *Xylella fastidiosa* (*Xf*) to grape will be used as an example of the utility of Electrical Penetration Graph (EPG) monitoring for vector studies.

Methods: A recently designed Universal AC-DC EPG monitor provides updated, high-quality amplifiers with a wider range of user-selectable adjustments, to tailor the monitor to any new species.

Results: A model will be introduced of four critical steps to assure success in the acquisition and inoculation process (i.e. vector efficiency), however only the third step will be discussed in detail. This third step is performance of a specialized inoculation behavior that consists of salivation, ingestion of mixed saliva and plant fluid, followed by two different types of egestion, each from a different area of the anterior foregut. Thus, the mechanism of inoculation is a combination of salivation and egestion. Specific EPG waveforms are correlated with each of these behaviors, and are used to measure how often these behaviors are performed and their durations.

Conclusions: Our goal is to develop a resistance index using EPG waveforms alone, for use in development of host plant resistance to the vector. Possible applicability of EPG technology to studies of blood-sucking arthropod vectors will be discussed.

An evolutionary context for the Argentine ant

Alexander Wild

University of Arizona, Tucson, AZ, United States

The Neotropical ant genus *Linepithema* is known for the invasive Argentine ant *L. humile*, but the group contains an additional 18 species. These are distributed across a variety of habitats from Mexico to Argentina. A multi-locus molecular phylogeny suggests a southern South American origin for *Linepithema*, supports a recent morphology-based division into four monophyletic species groups, and demonstrates a sister-species relationship between *L. humile* and an obscure Andean species *L. oblongum*. Too little is understood about the biology of most species to elucidate the evolution of traits implicated in ecological invasiveness, but I discuss what is known and suggest avenues for future research.

Parasitoid communities attacking leaf chewing Lepidoptera in New Guinea rainforest

Jan Hrcek

Faculty of Science, University of South Bohemia and Institute of Entomology, Biology Center of the Czech Academy of Sciences, Ceske Budejovice, Czech Republic

Introduction: Natural leaf chewing caterpillar - parasitoid communities are overly complex, which often leads researchers to concentrate on Macrolepidoptera and neglect Microlepidoptera hosts. This study presents results from a mass rearing survey, where the caterpillars were sampled in proportion to their natural abundance.

Methods: Our group (www.entu.cas.cz/png/) studied a community of leaf chewing Lepidoptera and their parasitoids on 45 locally common tree species in primary and secondary tropical rainforest near Madang, Papua New Guinea over five years. All free-living and semi-concealed (leaf-rolling, web-tying) caterpillars were quantitatively sampled from 1500m^2 of foliage of every tree species, morphotyped and reared. Hatched insects were morphotyped by parataxonomists and later identified by taxonomists.

Results: The rearing of 49.000 caterpillars yielded 15.000 Lepidoptera adults from 274 species and 1.600 Hymenoptera and Diptera parasitoids from ~260 species.

Most of the caterpillars were semi-concealed (78%), only 22% were free-living. Two thirds of the parasitoids were Hymenoptera (mostly Ichneumonoidea) and one third were Diptera: Tachinidae.

Semi-concealed hosts had significantly higher parasitism rate than free-living hosts. While Hymenoptera strongly preferred semi-concealed hosts, Diptera parasitised both free-living and semi-concealed caterpillars with similar intensity. Free-living hosts seem to be prone to apparent competition from semi-concealed host via shared parasitoids, as majority of their parasitoids attack both types of hosts.

Conclusions: I suggest that semi-concealed caterpillars (in contrast to free-living ones) are main hosts of parasitoids because of numerical dominance in natural communities, concealment from predators and apparency for parasitoids.

Further quantitative studies are needed to evaluate the generality of these results.

Biodiversity hanging by a thread: the invertebrate community of fungal litter-trapping systems

Jake Snaddon[1], Paul Eggleton[2], William Foster[1]

[1]University Museum of Zoology, Department of Zoology, University of Cambridge, Cambridge, United Kingdom, [2]Department of Entomology, The Natural History Museum, Cromwell Road, London, United Kingdom

Introduction: Tropical rainforests are among the most diverse terrestrial ecosystems on the planet, and yet the rainforest canopy and understorey are hostile environments due to their extremely variable microclimatic conditions. Despite this, rhizomorph-forming fungi are abundant and efficient litter-trapping systems in moist tropical forest canopies.

Methods: We present research from a study in Sabah, Malaysia, where the influence of the fungal litter-trapping systems on the invertebrate community was experimentally assessed by removing the rhizomorph networks and associated leaf-litter from the forest understorey.

Results: The fungal litter-trapping systems were found to provide a valuable resource for a distinct invertebrate community within the forest. Affecting the diversity, abundance and composition of the invertebrate community.

Conclusion: The litter-trapping fungi and associated leaf-litter provide an important component of the forest structure and in doing so enhance invertebrate diversity within rainforest canopies.

Gene discovery and functional genomics in the Mediterranean fruit fly, *Ceratitis capitata*

Ludvik Gomulski[1], George Dimopoulos[2], Zhiyong Xi[2], Marcelo Soares[3], Maria Bonaldo[3], Anna Malacrida[1], Giuliano Gasperi[1]

[1]University of Pavia, Pavia, Italy, [2]Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, United States, [3]Northwestern University's Feinberg School of Medicine, Chicago, IL, United States

The medfly is a highly invasive agricultural pest that has become a model insect for the development of biological control programmes. Despite research into the behaviour and classical and population genetics of this organism, the quantity of sequence data available is limited. We used an expressed sequence tag (EST) approach to obtain detailed information on transcriptome signatures that relate to a variety of physiological systems in the medfly. Given that the study was based on normalized cDNA libraries from embryos and adult heads we have obtain information relating to reproduction, sex determination, and chemosensory perception.

Over 21,000 high-quality ESTs were obtained from the embryo and head libraries. Clustering analyses resulted in almost 12,000 unique sequences or transcripts. These assembled sequences represent a wide range of biological processes and molecular functions. Of particular interest are the sequences that share homology with *Drosophila* genes involved in sex determination, olfaction, and reproductive behaviour.

The sequences obtained in this study represent the first major dataset of expressed genes in a tephritid species of agricultural importance. This resource provides essential information to support the investigation of numerous questions regarding the biology of the medfly and other related species and also constitutes an invaluable tool for the annotation of complete genome sequences. Our study has revealed intriguing findings regarding the transcript regulation of sex determination genes, as well as insights into the comparative genomics of genes implicated in chemosensory reception and reproduction.

Production of *Bacillus thuringiensis* based biopesticide using a commercial lab medium and raw material rich in carbon and nitrogen

Fernando Valicente[1], Lucas Mendes[2], Leandro Carvalho[2]

[1]Embrapa, Sete Lagoas, MG, Brazil, [2]UNIPAM, Patos de Minas, MG, Brazil

No abstract submitted, or incorrect abstract submitted, or submitted in an inaccessible format.

Molecular biology and functional biochemistry of olfaction in *Anopheles gambiae* and *Aedes aegypti*

LJ Zwiebel

Vanderbilt University, Nashville, TN,, United States

The ability to sense and discriminate a large collection of chemical and visual cues is central for several behaviors of insects that act as vectors for the pathogens that are responsible for many important human diseases. In particular, olfaction plays a major role in host seeking and selection behaviors of blood feeding female anopheline mosquitoes. A long-term objective of our research is centered on an examination of the molecular genetics of the chemosensory system in anopheline and other mosquitoes and its role in determining anthropophilic host preference in malaria vector mosquitoes. We have identified and continue to characterize the complete repertoire of 79 odorant receptor (OR) genes *An. gambiae* as well the complete set of 117 functional OR genes from the Dengue and Yellow Fever virus vector mosquito A*edes aegypti*. Together with our collaborators, we have completed a detailed analysis of the olfactory physiology, molecular neurobiology and odorant-binding characteristics of ORs on the adult maxillary palp and proboscis as well as behavioral and molecular elements of the larval stage olfactory system of *An. gambiae* and *Ae. aegypti* to begin to define the functional "odor space" for these vector mosquitoes. Progress will also be presented on ongoing efforts to design novel anti-malarial programs that target chemosensory pathways and the behaviors they control in vector mosquitoes.

This work has received generous support by grants from the Foundation for the National Institutes of Health through the Grand Challenges in Global Health Initiative as well as the U.S. National Institutes of Health.

Progress in the management of maize streak virus and its leafhopper vectors in sub-Saharan Africa

Nilsa Bosque-Perez

Department of Plant, Soil and Entomological Sciences, University of Idaho, Moscow, ID, United States

Maize streak virus (MSV) is the causal agent of the most economically important and widespread disease of maize in sub-Saharan Africa. MSV is persistently transmitted by leafhoppers in the genus *Cicadulina.* Of the 22 species of *Cicadulina* known, 18 occur in Africa. Nine species of *Cicadulina* are confirmed vectors of MSV in Africa. MSV epidemiology is closely linked to the ecology of its vectors. Both MSV and its vectors evolved with African grasses and adapted to maize after its introduction into the continent. Several cultural practices have been suggested for MSV control, including avoiding maize plantings downwind from earlier-planted cereal crops, areas of bare ground between early and late-planted maize fields, and crop rotation, to reduce leafhopper movement and subsequent virus spread. While insecticides have been used also to control vectors, resistant varieties are recognized as the most effective method for MSV management. Several breeding programs are active in the development of resistant varieties. Maize varieties differ in disease severity and incidence and subsequent yield loss. Resistant varieties exhibit higher yields when diseased and lower disease incidence than susceptible ones. Low disease incidence is partly due to insect resistance and the potential for disease spread is lower on varieties exhibiting this character. Although MSV was first studied in the 1920's and resistance transferred into maize in the 1960's, many farmers in sub- Saharan Africa still grow MSV-susceptible maize and continue to experience yield losses. Advances in the management of MSV and its *Cicadulina* spp. vectors will be discussed.

Biogeographic factors that determine the distribution of the Exapiini Alonso-Zarazaga, 1990 (Coleoptera: Apionidae) in the Iberian Peninsula (Spain)

Mª Pilar Gurrea[1], Mª José Sanz[2], José Martin[1], Edgar Camero[3]

[1]Universidad Autónoma de Madrid, Madrid, Spain, [2]Universidad SEK, Segovia, Spain, [3]Universidad Nacional de Colombia, Bogotá, Colombia

Introduction: There are a great variety of methods to explain the distribution of the species. The techniques based on the use of presence data species try to identify the ranks of certain environmental variables in which these species appear comparing its distribution with a random one. In this work, we have analyzed the factors that affect the Iberian distribution of the weevil species of the tribe Exapiini, some of them well known for its economic interest because they have been used for the biological control of weeds. This tribe of Apionidae includes nearly 50 species, 22 of them known from the Iberian Peninsula.

Material and methods: The data of the distribution of these species of Exapiini have been obtained from UTM grids of 10x10 km. The presence or absence of each species has been analyzed to determine the influence of the geographic variables as such as latitude, length, distance to the Pyrenees, maxima altitude, minimum altitude, altitudinal rank, environmental (temperature, precipitations, pluviometric irregularity, types of ground) and food plants. The analysis has been repeated for the set of the species of Exapiini to estimate the variables of greater significance in the species density populations.

Results: The results show that the maxima altitude of the grids and the altitudinal rank are the factors with greater level of significance, as much for the density of species as for each one of them. The distribution model is predictive, and allows us to indicate areas of the Iberian Peninsula with greater probabilities of finding these species.

Photoperiodic diapause in mosquitoes: A link to insulin signaling

David Denlinger, Cheolho Sim

Ohio State University, Columbus, Ohio, United States

Introduction: Short daylength is used to program adult diapause in the mosquito, *Culex pipiens.* The downstream endocrine event that halts ovarian maturation is a shut-down in juvenile hormone (JH) production, but little is know about the molecular events that occur between perception of short daylength and the cessation of JH production. Here we explore a potential role for insulin signaling as an intermediary in this pathway.

Methods: Genes encoding the insulin receptor and a downstream gene, FOXO, were suppressed using RNAi and such attributes as ovarian maturation, fat accumulation and longevity were monitored. JH rescue experiments were also conducted to evaluate the capacity for JH to reverse the RNAi induced phenotype.

Results: Knocking down the insulin receptor with RNAi in nondiapausing mosquitoes results in a cessation of ovarian development akin to diapause. Mosquitoes could be rescued from this this developmental arrest with an application of JH. When RNAi was directed against FOXO in mosquitoes programmed for diapause, fat storage was dramatically reduced and the mosquito's life span was shortened, results suggesting that a shut-down of insulin signaling prompts activation of the downstream gene FOXO, leading to the diapause phenotype.

Conclusion: The results are consistent with a role for insulin signaling in the short-day response that ultimately leads to a cessation of juvenile hormone production.

Insulin signaling and juvenile hormone in metamorphic commitment of imaginal primordia and discs in the tobacco hornworm

Takashi Koyama[1], Lynn Riddiford[2]

[1]University of Washington, Seattle, WA, United States, [2]Janelia Farm Research Campus, HHMI, Ashburn, VA, United States

Juvenile hormone (JH) maintains morphostasis of the eye and leg primordia and the wing discs during the early larval life of *Manduca*, but in final instar fed larvae JH cannot prevent pupal commitment and subsequent morphogenetic growth. Normally *broad* (*br*) mRNA (indicative of pupal commitment) appears in both the eye primordia and the wing discs between 12 and 24 hr of feeding. In both tissues this up-regulation of *br* could be stimulated in a dose-responsive manner in starved 5th larvae by injection of either *Manduca* bombyxin or bovine insulin and inhibited in fed larvae by wortmannin, a specific inhibitor of phosphatidylinositide-3 kinase. *In vitro* wing discs from freshly ecdysed larvae showed a 4-fold increase in *br* mRNA by 24 hr in hormone-free medium which was prevented by the JH analog methoprene. Either bombyxin or insulin prevented the suppression by JH. The presence of either wortmannin or Insulin Receptor dsRNA in the culture medium prevented this action of insulin. These data show that feeding in the 5th instar causes bombyxin (insulin) release which in turn overcomes the JH inhibition of pupal commitment of the imaginal discs and primordia. This effect of insulin was not seen in 4th instar wing discs. Thus, the hypothesized nutrient-dependent Metamorphosis Initiating Factor that overcomes JH suppression of the discs and primordia in the 5th instar to allow pupal commitment and the subsequent morphogenetic growth (Truman *et al., Science,* 2006) is *Manduca* insulin. Factors involved in the subsequent growth are under study. Supported by NSF.

Forest management and the conservation of boreal forest arthropod biodiversity

Jan Volney, John Spence, David Langor

[1]Natural Resources Canada, Edmonton, Alberta, Canada, [2]University of Alberta, Edmonton, Alberta, Canada, [3]Natural Resources Canada, Edmonton, Albert6a, Canada

The EMEND (Ecosystem Management Emulating Natural Disturbance) Experiment is a large-scale, replicated comparison of variable retention forest harvesting and fire-dominated natural disturbance in the western Canadian boreal forest. The intent is to provide an empirical evaluation of the natural disturbance paradigm in designing forest management approaches. Outcomes of 5 levels of strip retention harvesting (75%, 50%, 20%, 10% and 2% residual structure) in 4 mixedwood canopy cover types (deciduous dominated, deciduous dominated with coniferous understory, mixedwood and coniferous dominated) are being compared with data collected after whole compartment burns and slash burns in 10-ha compartments. Residuals have been left evenly distributed in strips throughout compartments and as aggregated elliptical patches of two sizes (0.20 and 0.45 ha). The set of response variables is wide-ranging, including productivity, dynamics of coarse woody material, soil nutrient dynamics, hydrology, fire effects, harvesting costs and regeneration. Pre-treatment arthropod biodiversity estimates of forest canopy-feeding Lepidoptera, epigaeic fauna (Coleoptera and Arachnida), and saproxylic insects (both in coarse woody debris and fire-killed wood) were made and continued periodically post-treatment. These estimates allow comparisons of trade-offs among various distributed retention harvesting systems, clear-cutting, and prescribed fire in standing timber and slash burns. Results to date indicate that variation in the responses seems paramount. Future management indicators have to be tailored to account for this finding. Thus the use of ecosite indicators, the understory vegetation, and related sub-stand features become essential in designing practices that conserve biodiversity on forested landscapes.

Flea beetle diversity of the Sierra Tarahumara, Copper Canyon, Mexico (Chrysomelidae: Alticinae).

David Furth

Smithsonian Institution, Washington, D. C., United States

Introduction: This is the product of a 4 year study of the diversity of Alticinae of the Sierra Tarahumara a mountainous area of the Sierra Madre Oriental of northern Mexico, especially in the states of Chihuahua and Sonora. It is part of a multi-disciplinary bio-cultural survey of this region involving indigenous people, especially the Tarahumaras. Chihuahua is the largest, but biologically least known state in Mexico.

Methods: There are few recorded data of Alticinae from this region, thus almost all the data is from fieldwork collected by sweeping. Fieldwork was done by the author during 4 collecting trips at different seasons over a 5 year period.

Results: Thus far 24 genera and 71 species of Alticinae have been identified from the Sierra Tarahumara. At least 2 species are new to science, 6 new to Mexico, ca 40 new to Chihuahua, 10 new to Sonora, and there arenew host records for several species. Species diversity increases at lower elevations (below 2000m) with a complete turnover of the species composition every ca. 850 meters. Biogeographic affinities are Nearctic at higher elevations and Neotropical at lower.

Conclusions: Chihuahua is more species rich than previously recorded and the biogeographic affinities are primarily Nearctic.

Inquilinism in ants: ecology, social organization, phylogenetics, and speciation

Riitta Savolainen

University of Helsinki, Helsinki, Finland

Introduction: Eusociality involves cooperation in caring for the offspring, reproductive division of labour, and overlap of generations of different life stages. Ant social parasites have, however, lost all or some traits of eusociality. In particular, workerless social parasites, inquilines, have reverted to selfish behaviour that maximizes sexual reproduction on behalf of their host. Social parasites occur in six ant subfamilies, though the majority of parasites have been found in Formicinae and Myrmicinae, inquilines mostly in Myrmicinae. Here, I explore the origins of inquilines.

Methods: I will review the literature on inquiline ants and their hosts, weaving together patterns of their ecology, social organization of the colony, and phylogenetics.

Results: Phylogenetic analyses suggest multiple origins of inquiline ant species. Some inquiline-host pairs are sister species; this raises the question: could a species give rise to its own parasite?

Conclusions: Occurrence of inquilines mainly in temperate regions may be a real phenomenon resulting from relatively species-poor ant community structures that allow locally high nest densities of potential hosts. I suggest that the evolution of polygyny and polycaly as a highly successful adaptive tactic in specific ecological contexts has predisposed colonies to exploitation by cheating queens – a starting point for the evolution of inquilinism. By analysing morphological and behavioural changes accompanying the polygyny-polycaly syndrome, I will show how loss of sociality and speciation of inquilines through intraspecific parasitism in sympatry, within their host colonies, is possible.

The evolution on inbred social systems in spiders—causes and consequences

Leticia Avilés

University of British Columbia, Vancouver, Canada

Social spiders are notable among social organisms for being highly inbred—male and female colony members remain within the natal nest to mate generation after generation. Social spider colonies, therefore, constitute more or less isolated population lineages that grow, proliferate and become extinct without mixing with one another. We present recent evidence that confirms such strong population subdivision even at fast evolving microsatellite loci in the neotropical social spider *Anelosimus eximius*. We review data showing that the inbred social spiders originated from outbred subsocial ancestors, a transition that we suggest was associated with a switch from environments where costs of dispersal are high and benefits of group living low to environments where the reverse holds. That ecological and demographic factors can often be sufficiently strong to overcome inbreeding depression during the initial phases of the transition to inbreeding is suggested by the repeated phylogenetic origins of inbred spider sociality. Social spider species lineages, however, appear as isolated terminal branches of the phylogenetic tree of spiders. Such spindly phylogenetic distribution, reminiscent of that reported for asexual taxa, suggests that although social spiders may have overcome the initial costs of inbreeding, in the long run, inbred spider sociality may represent an evolutionary dead end.

Foraging activity in stingless bees depends on the reproductive state of a colony (*Plebeia remota*)

Patrícia Nunes-Silva[1], Pérsio de Souza Santos Filho[2], Vera Lucia Imperatriz-Fonseca[1]

[1]Faculty of Philosophy, Science and Letters of Ribeirão Preto, University of Sao Paulo, Ribeirão Preto/São Paulo, Brazil, [2]Institute of Bioscience, University of Sao Paulo, São Paulo/São Paulo, Brazil

Colonies of the Brazilian stingless bee *Plebeia remota* show a reproductive diapause in autumn and winter. During this period, the colonies do not build brood combs, and, in consequence, no new individuals are produced. Colonies of this bee species, therefore, present two distinct reproductive states (oviposition period and reproductive diapause), during which colony-needs are putatively different. Consequently, resource collection should be adapted to the different needs. We recorded the foraging activity of two colonies for 30 days in both reproductive states, registering the number of foragers entering the colony with different resources (nectar or pollen), and the time of collection. Indeed, the foraging activity of *P. remota* presented different patterns during the reproductive diapause and the queen oviposition period. In the course of the reproductive diapause, the resource predominantly collected by the foragers was nectar. Here, the majority of the bees were nectar foragers, and the peak of collecting activity occurred around noon. Instead, in the queen oviposition period, the predominantly collected resource was pollen, and the peak of activity occurred around 10:00am. Although the majority of the foragers was not specialized in this period, there was a larger number of pollen foragers compared to the period of reproductive diapause. The temperature and relative humidity also influenced the foraging activity. Apparently, the presence of new brood - during the queen oviposition period - is important for the "decision" of stingless bee colonies to collect pollen. Both internal and external conditions of the colonies influence the foraging behavior of this species.

Effects of international movement on populations of *Sirex noctilio* and its symbiotic fungus *Amylostereum areolatum*

Bernard Slippers, Brett P. Hurley, Magriet van der Nest, Osmond X. Mlonyeni, Brenda D. Wingfield, Michael J. Wingfield

Department of Genetics, Forestry and Agricultural Biotechnology Institute, Pretoria, South Africa

Genetic bottlenecks and environmental variability can have a substantial influence on populations of introduced insects and their microbial symbionts. We have used genetic, phenotypic and biological data to consider the influence of these factors on populations of the woodwasp, *Sirex noctilio*, and its homobasidiomycetes fungal symbiont, *Amylostereum areolatum*. The data show that these organisms have most likely been introduced a limited number of times into southern hemisphere pine plantations, but that they have spread widely after each introduction to other areas in the region. Each introduction has left an apparently clonal, and unique population of the fungus over vast areas, and even across continents. This lack of diversity is also evident in the wasp populations. Where introduced natural enemies are not compatible with the large, genetically uniform populations of *S. noctilio* and *A. areolatum,* the success of biological control programs may be retarded. This might account for the poor levels of parasitism achieved with the parasitic nematode, *Deladenus siricidicola*, in some areas. Furthermore, the lack of genetic diversity and population fluctuations in the wasp could also have contributed to the significant variation in sex ratio, often with a severe male bias, observed across invasive populations of *S. noctilio*. Apart from genetic influence, there are also dramatic life cycle changes associated with environmental differences in invaded areas. These influence the population dynamics of the mutualism and the establishment of biological control agents alike. A sound understanding of the genetic and environmental effects on population dynamics in an invasive insect such as *S. noctilio* and its fungal symbiont is clearly essential for a successful biological control program.

The cuckoo fungus "termite ball" mimicking termite eggs: a novel insect-fungal association

Kenji Matsuura, Takashi Tamura, Toshihisa Yashiro, Norimasa Kobayashi, Ken Shimizu

Okayama University, Okayama, Japan

Mimicry has evolved in a wide range of organisms encompassing diverse tactics for defense, foraging, pollination, and social parasitism. Here we report an extraordinary case of egg mimicry by a sclerotium-forming fungus, whereby the fungus gains competitor-free habitat in termite nests. Egg protection is one of the most fundamental social behaviours in social insects. When termite workers recognize the eggs laid by queens, they bring the eggs together and heap them up in nursery cells to take care of them. *Reticulitermes* termites frequently harbor brown fungal balls, called termite balls, alongside their eggs. The termite ball was identified as the sclerotium of a parasitic corticioid fungus, an undescribed species of genus *Fibularhizoctonia*, which mimics termite eggs physically and chemically so as to be protected in termite nests. This phenomenon has been found for seven *Reticulitermes* species in Japan and the US.

The discovery of the chemical camouflage by the egg-mimicking fungus indicated that termites can be manipulated by using the termite egg recognition pheromone (TERP), which strongly evokes the egg-carrying and -grooming behaviours of workers. We found that the TERP also provided antibacterial activity against a gram-positive bacterium. We isolated the target protein, determined the molecular size of 14.5kDa and identified the antibacterial protein lysozyme as the TERP. RT-PCR analysis confirmed that mRNA of termite lysozyme was expressed in both salivary glands and eggs. This novel function of lysozyme as a termite pheromone illuminates the profound influence of microbes on the evolution of social behaviour in termites. In addition to the mechanism of egg mimicry, we discuss the evolutionary processes of this novel insect-fungus interaction.

Are the determinants of ant diversity invariant across spatial and taxonomic scales?

Nathan Sanders[1], Robert Dunn[2], Michael Kaspari[1]

[1]University of Tennessee, Knoxville, TN, United States, [2]North Carolina State University, Raleigh, NC, United States, [3]University of Oklahoma, Norman, OK, United States

Macroecologists want to know whether and why biodiversity varies geographically. But the biotic and abiotic factors that shape biodiversity gradients may vary with spatial resolution – the factors that determine the number of insects in meter square quadrat might differ from the factors that determine why there are more insects in the tropics than in the tundra. Similarly, the factors that determine the number of species may not predict the number of genera, tribes, or subfamilies. In this study, we examined whether the determinants of ant diversity are invariant across spatial and taxonomic scales, using data from an extensively sampled elevational and latitudinal gradient and from a new global database on ant biodiversity. Along the elevational gradient, the determinants of species diversity varied with spatial scale: at the smallest 1-m2 scales, diversity was a function of abundance. At the largest scale, diversity was a function of temperature and energy availability. Surprisingly, the patterns and processes along the latitudinal gradient were qualitatively similar to those along the elevational gradient. This suggests that local interactions, such as competition, might operate at small spatial scales, but climatic, evolutionary, or historical factors might operate at larger spatial scales. When we asked whether diversity patterns of species mirrored generic and tribe-level diversity patterns, we found strikingly similar patterns. Generic diversity peaked at mid-latitudes and at low elevations. Together, these results suggest that gradients in ants are shaped by both evolutionary and ecological processes, but the relative importance of these processes varies with spatial and taxonomic scale.

Patterns of introduction of *Pinus* and *Eucalyptus* pests in South Africa compared using mitochondrial DNA sequence data

Bernard Slippers, Brett P. Hurley, Ryan Nadel, Derian Echeverri, Michael J. Wingfield

[1]Department of Genetics, Forestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, South Africa, [2]Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, South Africa

During the past 100 years a number of invasive pests have had a significant negative impact on the productivity of commercial *Eucalyptus* and *Pinus* plantations in South Africa. In this study, mitochondrial cytochrome oxidase subunit I (CO I) sequences were used to characterize populations of some of these invasive insects in South Africa. These include *Sirex noctilio* (Hymenoptera), *Thaumastocoris peregrinus* (Hemiptera), *Bradysia difformis* (Diptera) and *Gonipterus scutellatus* (Coleoptera). Where possible, populations of these insects were compared with populations from potential regions of origin. *Sirex noctilio* showed very limited CO I diversity in the southern hemisphere as a whole, and appears to have been introduced into South Africa from South America. *Thaumastocoris peregrinus* also showed very limited CO I diversity, but seems to have been introduced into South Africa on two separate occasions over a short period, and independently once into South America. In contrast, *B. difformis* was highly diverse and has clearly been introduced in fairly large numbers or multiple times. In the case of *Gonipterus*, the South African populations are divided into two very distinct mitochondrial types. This might indicate that two distinct species occur in the country, contrary to previous reports. One of these types is shared between South African populations and those found in South America and Europe, while a third mitochondrial type only occurs in populations in South America. Where it was possible to examine these, the population diversity of biological control agents for *S. noctilio* (*Deladenus siricidicola*: Nematoda) and *G. scutellatus* (*Anaphes nitens*: Hymenoptera) display very limited genetic diversity. These studies have highlighted the fact that knowledge relating to genetic diversity in invasive forest pests in South Africa will be an important guide to predict future introductions and to manage associated biological control programs.

Genetic diversity, species phylogeny and historical biogeography of Lord Howe Island moss bugs (Hemiptera: Coleorrhyncha: Peloridiidae: *Howeria*)

Jakob Damgaard, Gerry Cassis

The Natural History Museum of Denmark, Copenhagen, Denmark

Introduction: Moss bugs are critical for understanding the basal evolution of Heteroptera, as well as for investigating the historical biogeography of the Southern Hemisphere continents and the supercontinent Gondwanaland. About 35 species are found in cool and humid habitats in Patagonia, New Zealand, New Caledonia and Australia. Among these, three species are found on the 27 hectare, plateau-like mountain-top of Mt. Gower of Lord Howe Island in the Tasman Sea. Lord Howe Island got considerable attention for hosting a possible case of sympatric speciation in palms (Howea), but the islands moss bugs may represent a comparable case.

Methods: The genetic diversity of the three species *Howeria coggeri* Evans, *H. kingsmilli* Evans, and *H. payteni* Evans are investigated on basis of body measurements and analyses of mitochondrial and nuclear DNA sequence data. A phylogenetic analysis of moss bugs from Australia, New Zealand and Patagonia is used to address the origin and diversification of the Lord Howe Island fauna.

Results: The results show a clear separation between the three species of *Howeria* on Lord Howe Island based on body size and DNA, and may indicate a sympatric speciation on the Mt. Gower plateau. Phylogenetic analyses of *Howeria* and other moss bugs give indices of the source and timing of the initial colonization of the island.

Conclusions: The presence of three congeneric species of moss bugs on Lord Howe Island is of great interest in understanding the evolution of biota on oceanic islands and specifically the historical biogeography of the southern Hemisphere.

Diversity and interactions of flower visitors of *Aechmea nudicaulis* and *Vriesea friburgensis* (Bromeliaceae)

Simone Grohme[1], Volker Schmid[2], Anne Zillikens[1], Josefina Steiner[3]

[1]Botanical Institute, University of Tuebingen, Tuebingen, Germany, [2]Department of Evolution, Behavior and Genetics, University of Regensburg, Regensburg, Germany, [3]Department of Embryology, Federal University of Santa Catarina, Florianópolis, SC, Brazil

Introduction: Bromeliads are terrestrial and epiphytic plants occurring almost exclusively in the neotropics. Although the most widespread bromeliad flower syndrome (ornithophily) favours bird visitation, inflorescences can be exploited by many insect species. We aimed to record spectrum and species richness of flower visitors and to document their temporal pattern, behaviour, and efficiency as pollinators.

Methods: In southern Brazil, the bromeliad species *Aechmea nudicaulis* and *Vriesea friburgensis* were observed throughout their flowering seasons from 2005 to 2008 to record flower visitors as well as interorganismic interactions. Flower bagging experiments allowed us to determine the pollinator efficiency of single species.

Results: 42 taxa were observed visiting *A. nudicaulis* flowers, 38 in *V. friburgensis*. Bees and ants appeared to be the most diverse groups, followed by butterflies in *A. nudicaulis* and beetles in *V. friburgensis*. Most visits were made by bees and hummingbirds; the latter were the most efficient pollinators. They patrolled inflorescences throughout the day, foraging for floral nectar. In contrast, bees were observed mainly in the morning, collecting first pollen and then nectar, while butterfly visits were recorded mostly in the afternoon. Further interactions comprise lycaenid caterpillars of the genus *Strymon*, eating *A. nudicaulis* fruits and associated to visiting ants, as well as eurytomid wasps parasitizing buds of *V. friburgensis*.

Conclusions: The bromeliad species *Aechmea nudicaulis* and *Vriesea friburgensis* are associated to a high diversity of animals, thus opening countless possibilities of interactions. This underpins the importance of bromeliads for tropical ecosystems, especially concerning insect-plant interactions.

Tribolium castaneum as a model organism for comparative pathology

Jeff Lord

GMPRC, USDA-ARS, Manhattan, Kansas, United States

The advantages of *Tribolium castaneum* as a model for host-pathogen interactions lie in the variety of disease organisms that may attack it and the apparent strength of its defenses against them. Unlike *Galleria mellonella*, which is a commonly used model that is highly susceptible to a wide array of opportunistic pathogens, *T. castaneum* is very tolerant of non-specific diseases. For example, we have found that the LC50 of *Beauveria bassiana* for larval *T. castaneum* is ca. 300 mg/kg of diet, approximately 10-fold of its LC50 for larvae of most stored-product beetles. Accordingly, it provides a system for assessing which defense mechanisms are most effective. Furthermore, it is subject to a small number of host-specific but slow developing pathogens, such as *Farinocystis tribolii*, a neogregarine, and *Paranosema whitei*, a microsporidium, to which it mounts no apparent defense reactions. This affords the opportunity to test evasive mechanisms of successful parasites and to do so on an experimentally advantageous schedule. The hardiness of this species is an advantage that should not be overlooked. Paucity of control mortality is a great aid in interpreting bioassay data.

Evidence of an interaction between host preference and endo/exophagy in the malaria mosquito *Anopheles arabiensis*

Inaki Tirados, Gabriella Gibson, Stephen Torr

Natural Resources Institute, University of Greenwich at Medway, Chatham Maritime, Kent, United Kingdom

Introduction: *Anopheles arabiensis* is variously described as 'more zoophilic than *An. gambiae s.s.*', 'opportunistic' (feeding on humans and cattle in proportion to availability), or 'anthropophilic', based mainly on bloodmeals and host-odour baited trap data. The effect of host availability on the behaviour of *An. arabiensis* was investigated experimentally in southern Ethiopia.

Methods: Human-landing catches and cattle-baited trap catches were used to assess the relative attractiveness of each of these hosts to *An. arabiensis* when the hosts were either on their own or surrounded by a ring of 5 cattle (5 m diameter ring), in a 4 X 4 Latin square design. The attractiveness of a human host indoors with and without a ring of cattle surrounding the dwelling was also tested.

Results: The ring of cattle had no significant effect on the human-landing catch or the cattle-baited trap catch, although > 10 times as many *An. arabiensis* were caught by the human bait than by the cattle bait, whether or not the bait was surrounded by cattle. When the human-landing catch was conducted indoors, however, significantly fewer *An. arabiensis* entered the dwelling when it was surrounded by a ring of cattle than when it was not.

Conclusions: *An. arabiensis* is more strongly attracted to humans than to cattle when there are no physical obstacles to reaching the host, but they are less likely to fly into an enclosure in response to human host cues if cattle are nearby, i.e. there is an interaction between host preference and endo-exophagy.

Using natural polymorphism and artificial selection to investigate the hormonal basis of phenotypic integration in a wing-dimorphic insect

Anthony Zera

School of Biological Sciences, University of Nebraska, Lincoln, Nebraska, United States

Wing polymorphism has been extensively discussed with respect to the evolution of systemic endocrine regulators that integrate the expression of suites of morphological, behavioral, and physiological traits to produce morphs adapted for flight versus reproduction. Detailed investigations of flightless/reproductive and flight-capable morphs of naturally-occurring wing polymorphisms have identified morph differences in both JH and ecdysteroid titers that potentially regulate aspects of morph development. The enzyme juvenile hormone esterase (JHE), a regulator of the blood JH titer, appears to play an important role in this process. Complementary artificial-selection studies on hemolymph JHE activity in a wing-monomorphic congener have provided experimental evidence concerning (1) the degree to which JHE activity must be changed to alter the JH titer sufficiently to modify the development of components of the flight apparatus, (2) the extent to which endocrine traits expressed in different life cycle stages are constrained to evolve in concert, and (3) the relative roles of JH and ecdysteroids in regulating variation in wing and flight muscle morphology. Recent molecular studies of JHE are identifying the mechanisms by which variation in JHE gene expression gives rise to variation in blood JHE activities, which, in turn regulate the expression of morphological traits involved in flight. Finally, recent studies of JH and ecdysteroid titers in adult wing morphs have demonstrated substantially more complex JH titer variation between morphs which necessitates a rethinking of basic models of the endocrine regulation of the expression of morph-specific traits in wing polymorphic insects.

Some challenges in modelling the potential distribution of invasive insects under climate change

Darren Kriticos

CSIRO Forest Biosciences, Kingston, ACT, Australia

CLIMEX is a modelling tool for exploring the relationship between a taxa and climate. This facility is useful for inferring a species response to climatic variables and for applying these relationships to novel climates to project the potential distribution and relative abundance of invasive organisms. In contrast to most habitat models, CLIMEX is process-oriented. This gives it an ability to project species ranges in novel climates with more confidence than regression based models like Bioclim or CLIMATE, which have a tendency to introduce range contractions under novel climates that are modelling artefacts that are inconsistent with observations or theoretical expectations. Many CLIMEX models have been developed for invasive insects, and many of these models have been well validated in terms of the range limiting factors. The performance of these models when projected into novel climates and compared with independent data in the exotic ranges gives us some confidence that the models will be robust under future climate scenarios. Thus, CLIMEX is fairly well adapted to projecting species ranges under future climate scenarios. However, a significant problem for all habitat models (including CLIMEX) that rely upon the known distribution of a species to infer its' habitat preferences is the decoupling of species ranges from the contemporaneous climate that gave rise to the distribution data. Species ranges are changing in relation to changes in climate. Lags in these range contractions and expansions in relation to a trending climate will inevitably give rise to projection errors.

Landscape structure and arthropod-mediated ecosystem services

Douglas A. Landis, Mary M. Gardiner, Anna K. Fiedler, J. Megan Woltz

Michigan State University, East Lansing, MI, United States

Introduction: Modern agricultural landscapes have been shaped by production systems aimed at maximizing crop yield and profitability and differ markedly in their ability to supply important Arthropod-Mediated Ecosystem Services (AMES) such as biological control and pollination. Highly simplified landscapes may lack critical infrastructure needed for some species and thus limit populations and diversity of beneficial arthropod communities. This in turn may limit the level of ecosystem services that can be garnered from such landscapes.

Methods: In a series of studies we have examined the impact of landscape structure on biological control of soybean aphid, *Aphis glycines* Matsumura, the role of native vegetation in promoting natural enemies and pollinators, and explored how directed versus unplanned landscape change may alter AMES. Using data from 23 sites across four states and two years, we calculated a biological control services index (BSI) based on relative suppression of soybean aphid populations relating it to landscape complexity and composition at multiple spatial scales.

Results: Landscape diversity and crop composition at a scale of 1.5 km surrounding the focal field explained the greatest proportion of the variation in BSI and predator abundance. We also identified 26 native plant species that show particular promise for use in habitat management to enhance AMES.

Conclusions: Our studies suggest that directed management of landscapes has the potential to stabilize or increase biocontrol services. In contrast, unplanned landscape changes driven by increasing demands for grain-based biofuel production have the potential to dramatically reduce biocontrol services in agricultural landscapes.

Phylogeny and evolution of Cynipoids

Matthew Buffington

Systematic Entomology Lab, USDA/ARS c/o NMNH, Smithsonian Institution, Washington DC, United States

The Cynipoidea (oak gall wasps and their allies) are a moderately speciose group of microhymenoptera that can be found world-wide. Of the five extant families, nearly all the species level diversity can be found within the Cynipidae and Figitidae. While the cynipids are fairly well known for their gall making abilities on plants such as the oaks and roses, the phylogenetics and taxonomy of the group are only now beginning to show some resolution. This, however, is confounded by the fact that molecular and morphological evidence are currently in disagreement over a few critical placements, even bringing into question the monophyly of the family as a whole. Relationships within the lesser-known Figitidae are also beginning to show signs of resolution. This group, largely endoparasites of cyclorrhaphous Diptera, plesiomorphically attack gall inducing Hymenoptera. This presentation highlights our current hypotheses of relationships and divergence estimates within Cynipoidea, providing novel insight into the evolution of the group.

The Encyclopedia of Life: A global, communal approach to arthropod systematics

David P. Shorthouse[1], David J. Patterson[1], Sarah Falwetter[2], Alexey Shipunov[1]

[1]Marine Biological Laboratory, Woods Hole, Massachusetts, United States, [2]Institute of Marine Biology and Genetics, Hellenic Centre for Marine Research, Heraklion, Crete, Greece

The Encyclopedia of Life (EOL) provides a vehicle for biodiversity information. EOL is committed to the Semantic Web. With the Global Biodiversity Information Facility (GBIF), EOL is exploring a Global Names Architecture that will assist machine to machine dialog about species. EOL is a member of CrossRef and will assign Digital Object Identifiers (DOIs) to its on-line species pages. Participation by experts will lead to a variety of new taxonomically intelligent and technically innovative tools and services to enhance appreciation for global biodiversity. EOL will also draw together distributed data from many partners inclusive of the millions of pages available through the Biodiversity Heritage Library and scholarly journals. We are developing new participatory tools that include on-line interfaces to help develop consensus taxonomies.

Gustatory and pheromone perception in *Drosophila*

Tetsuya Miyamoto, Jesse Slone, Hubert Amrein

Duke University Medical Center, Department of Molecular Genetics and Microbiology, Durham, North Carolina, USA

Introduction: In Drosophila, non-volatile chemicals are detected by a large number of 7 transmembrane receptors expressed in sensory neurons of taste sensilla located mainly in the labellum and the legs. Here, we investigate the role of several of these Gustatory receptors (GRs) necessary in the detection of food and pheromone compounds (sugars and long chain hydrocarbons, respectively), and we describe the behavioral phenotypes of flies lacking specific receptors.

Methods: Expression of individual Gr genes was performed using the Gal4/UAS expression system. Mutations in Gr genes were generated by homologous recombination or by PiggyBac/FRT mediated recombination. Behavioral analyses to measure the effects of *Gr* mutation included proboscis extension reflex, 2 –choice feeding assays and quantitative courtship analyses.

Results: Behavioral analyses of Gr64a-f mutant flies revealed that these six *Gr* genes are receptors for almost all sugars, including sucrose, glucose, trehalose and arabinose. Interestingly, the significant reduction of a behavioral response to trehalose is indicative of flies mutant for another Gr gene, Gr5a, and suggest multiple receptors may function as dimers or multimers for the detection of a single chemical. We also carried out a molecular genetic analysis of Gr32a, the closest homolog of the male-specifically expressed pheromone receptor Gr68a. Interestingly, Gr32a is not required for courtship of males towards females, but necessary to repress courtship among males.

Conclusions: The molecular-genetic characterization of several Gr genes and the behavioral analyses of mutant flies show that Gr genes have diverse functions in the perception of food chemicals and pheromones.

Impacts of CO_2 pollution on plant-insect interactions: A transcriptional and biochemical analysis of soybean defense signaling

Clare L. Casteel, Jorge A. Zavala, May R. Berenbaum, Evan H. DeLucia

Universtiy of Illinois - Urbana/Champaign, Urbana, IL, United States

Rising carbon dioxide (CO_2) levels are predicted to increase the productivity of ecosystems, however, growth in elevated CO_2 generally reduces the nutritional quality of plants for protein limited insects. Insects may increase food intake to compensate for reduced leaf nitrogen content, although this is not always the case. Incomplete understanding of the mechanisms governing plant-insect interactions under elevated CO_2 makes it difficult to predict how elevated CO_2 will influence ecosystems in the future. Based on previous studies examining global transcriptional profiles in soybean (*Glycine max*), elevated CO_2 exposure is hypothesized to modulate plant resistance through alterations in hormone signaling and defenses against herbivorous pests. To determine the impact of elevated CO_2 exposure on plant-insect interactions in soybean, magnitude and timing of three major hormone signaling pathways (jasmonic acid [JA], salicylic acid [SA], and ethylene [ET]) and related defenses were examined after Japanese beetle (JB; *Popillia japonica*) attack in controlled and open field environments under elevated CO_2. Elevated CO_2 exposure down-regulated the expression of transcripts related to JA and ET production and decreased accumulation of related metabolites (JA and protease inhibitors; PIs) in undamaged leaves. JB attack increased both transcripts and metabolite accumulation in ambient grown soybean leaves initially, but to a lesser extent over time or not at all in elevated CO_2. The modulation of JA and ET signaling transcripts and metabolites lowered plant chemical defense and can explain increases in damage observed in previous soybean studies that were not explained by changes in plant nutrition.

Neurochemicals in the mosquito chemosensory systems

KP Siju[1], Jan Bert Gramsbergen[2], Joachim Schachtner[3], Bill Hansson[4], Ignell Rickard[1]

[1]Swedish Agricultural University, Alnarp, Sweden, [2]University of Southern Denmark, Odense, Denmark, [3]Philipps University, Marburg, Germany, [4]Max Planck Institute for Chemical Ecology, Jena, Germany

Blood feeding insects, such as mosquitoes, primarily depend on their chemosensory systems to locate and identify blood hosts. In these insects, the need to fine tune the chemosensory systems, in order to adapt to complex environmental and behavioral conditions, is of paramount importance for their survival. Several putative neurochemicals present in the chemosensory system are believed to facilitate this modulation.

With the help of immunocytochemical and biochemical techniques we have studied the presence of neuromodulators, including biogenic amines and neuropeptides, in the chemosensory systems of disease vector mosquitoes. Immunocytochemical localization of the biogenic amine, serotonin, reveals the presence of a single serotonin-immunoreactive centrifugal neuron in the primary olfactory center or the antennal lobe (AL) that provide extensive serotonergic investment in the peripheral chemosensory organs, i.e. the antenna and the maxillary palp. In addition we find serotonergic neurons projecting into the labium. Titre analysis of all biogenic amines in the central nervous system using HPLC-ECD indicates a link between the titre of biogenic amines and the physiological state of the mosquitoes. To extend our analysis we also, for the first time, provide a detailed immunocytochemical map of neuropeptides such as FMRFamide, tachykinin, allatostatin and allatotropin in the AL of mosquitoes. Several of these neuropeptides are present in local interneurons as well as centrifugal neurons innervating the AL. The morphological data suggests a possible role of these neuropeptides in olfactory information processing. By using MALDI-TOF-MS analysis we are, furthermore, expanding our analysis to include all neuropeptides expressed in the AL of these mosquitoes.

Phylogeny and diversification of ants (Formicidae)

Sean Brady[1], Ted Schultz[1], Brian Fisher[2], Phil Ward[3]

[1]Smithsonian Institution, Washington, D.C., United States, [2]California Academy of Sciences, San Francisco, California, United States, [3]University of California, Davis, California, United States

Introduction: Resolving the phylogeny and timeline of major ant lineages is necessary to better understand the ecological dominance of ants and their coevolutionary relationships with other organisms.

Methods: We generated data from up to 10 nuclear genes from representatives of all extant ant subfamilies to address outstanding problems in ant phylogeny. Phylogenetic analyses were conducted using parsimony, likelihood, and Bayesian methods, including partitioned codon-model analyses. Divergence dating utilized penalized likelihood and Bayesian methods using evidence from the entire aculeate hymenopteran fossil record.

Results: Many relationships among major lineages were resolved robustly, but alternative hypotheses for early ant diversification could not be rejected. Estimates of the age of crown group ants ranged from ~115-135 million years ago. We explored the impact of these results on recently proposed ideas concerning codiversification between ants and angiosperms. Our sources of molecular data were also useful in resolving relationships at lower taxonomic levels. For example, we analyzed data from 26 of the 28 extant genera from the cosmopolitan subfamily Dolichoderinae. Our analyses revealed that the major Australian clade of dolichoderines is apparently of Neotropical origin and that this Australian radiation postdated the achievement of dolichoderine dominance in the northern hemisphere as judged by the fossil record.

Conclusions: Our molecular data robustly resolves many relationships at several taxonomic levels, but resolving early ant relationships with confidence will require additional data and taxon sampling. Robust phylogenies hold great potential for increasing our understanding of ant behavioral evolution, biogeography, and codiversification with other organisms.

Impact of green tree retention on boreal moths

Esther Kamunya[1], John Spence[1], Jan Volney[2]

[1]University of Alberta, Edmonton, Canada, [2]Canadian Forest Service, Edmonton, Canada

Introduction: Green tree retention (GTR) is a modification of traditional clear-cut harvesting whereby a proportion of a forest stand is left standing and alive at harvest to provide legacy elements. It is assumed that this promotes continuity and re-colonization of disturbed patches, thus mimicking natural processes of disturbance. However this assumption needs to be empirically tested. We used moth assemblages to monitor effects of GTR on biodiversity in experimentally harvested boreal forest stands at EMEND (Ecosystem Management Emulating Natural Disturbance) in NW Alberta, Canada. Forest lepidopterans play important ecological and environmental roles as primary insect herbivores and have potential to predict overall diversity of other taxa.

Methods: Using UV lights we trapped moths from two cover types (deciduous (ADOM) and coniferous (CDOM) both comprising two GTR treatments (20% and 50%) and unharvested controls. Moths were identified to species and their relative abundance was recorded. We estimated species richness by rarefaction and compared moth communities using multivariate techniques, including Non-Metric MultiDimentional Scaling (NMDS).

Results: Moth responses to harvesting varied with pre-harvest forest cover type. Species richness was higher in ADOM than CDOM stands. GTR decreased richness in ADOM stands, but retaining 50% forest structure maintained moth diversity close to that in undisturbed controls. In contrast, 80% reduction in forest cover increased diversity in coniferous stands which in turn grouped their lepidopteran assemblages together with those of ADOM stands, suggesting that forest moth assemblages were homogenized after harvesting. Most importantly, particular species-specific responses deviated from overall community response.

Conclusion: Maintaining a mosaic of habitat with varying disturbance intensity in each cover-type will better conserve moth assemblages of managed boreal forest ecosystems.

Long-distance gene flow among European corn borer populations in North America

Kyung-Seok Kim, Thomas Sappington

USDA-ARS, CICGRU, Ames, IA, United States

The European corn borer (ECB), *Ostrinia nubilalis,* is the main target of transgenic Bt corn expressing the Cry1Ab toxin. There is concern that strong selection pressure will lead to the evolution of resistance in ECB to Bt corn. Effective insect resistance management depends on knowledge of gene flow. We began a project in 2005 using 8 microsatellite DNA markers to measure gene flow spatially along two 450-mile transects through the central Corn Belt, and between years at a subset of locations. The results from both spatial and temporal population genetic analyses indicate that long-distance dispersal is very common in this insect. There is random mating within and between populations in the central Corn Belt, with no apparent barriers to gene flow, and per-generation dispersal is common out to 100s of km. This outcome was unexpected, based on circumstantial evidence suggesting maximum ECB movement of only about 80 km. However, this conclusion is consistent with recent field and laboratory behavior experiments in the U.S. and Europe that suggest long-distance dispersal is part of this insect's normal behavior. High gene flow over hundreds of km in the Corn Belt implies 1) that resistance to *Bt* corn will be slow to develop, but 2) if it does develop, it will spread geographically so quickly that local mitigation strategies likely will be ineffective. Thus, widely spaced sites, or pooling samples over widely spaced sites, for Bt-resistance monitoring is justified, at least for the common bivoltine Z-pheromone race in the Corn Belt.

Elucidation of the phylogenetic relationships and host-specificity of an oligophagous flea beetle (Coleoptera: Chrysomelidae: Galerucinae)

Tyler Eaton, S. Kristine Braman, Tracie Jenkins

University of Georgia, Griffin, Georgia, United States

Altica litigata is an economically important oligophagous flea beetle that is a pest on certain ornamental plants. Adult beetles are known to be aggregate feeders on the leaves of primroses of the genus *Oenothera* (Onagraceae) and opportunistic feeders on crape myrtles of the genus *Lagerstroemia* (Lythraceae). Gravid females oviposit on the leaves of *Oenothera* where the larvae feed until they pupate. *Altica litigata* is difficult to distinguish morphologically from other genera of *Altica*. Consequently, research into the species can lead to uncertainty. The purpose of this study was to illuminate the gene flow, genetic diversity, and population structure of *Altica litigata*.

Saproxylic insects in old hollow deciduous urban trees

Elina Peuhu[1], Meeri Mäki[2], Juha Siitonen[3], Kari Heliövaara[1]

[1]Department of Forest Ecology, Faculty of Agriculture and Forestry, University of Helsinki, Helsinki, Finland, [2]Department of Biological and Environmental Sciences, Faculty of Biosciences, University of Helsinki, Helsinki, Finland, [3]Finnish Forest Research Institute, Vantaa Research Unit, Vantaa, Finland

Introduction: Several rare and threatened saproxylic species occur in urban areas. Many of these species are specialized on temperate tree species, warm conditions and long-lasting habitats, which are found in old hollow trees. In Finland, saproxylic insects in urban areas have not been widely investigated. This study is a part of a larger project focusing on saproxylic insects living in old, hollow deciduous urban trees. The aim is to find out which species occur in urban parks and what kind of habitat characteristics they require.

Methods: We initiated a study on the occurrence of saproxylic Coleoptera, Hymenoptera and Diptera living in hollow deciduous trees in urban parks. The data were collected from linden, maple and elm trees in 2007. The trees were felled in April in a park located in southern part of Helsinki city. We took samples from wood mould and branches that seemed potential habitats for saproxylic insects. The samples were stored in a greenhouse for four months and then checked for saproxylic insects.

Preliminary results: *Stenostola dubia* (Cerambycidae) was abundant on linden branches. Predator species may have consumed some of the species before they were ever discovered. Tree species, and the specific part of the tree the sample was taken from, had an effect on the observed species assemblage. It seems that existence of a hole in a tree trunk affects species assemblage living inside the hollow in wood mould.

Pheromones and biodiversity - monitoring change in a changing world

Mattias Larsson[1], Glenn Svensson[2], Nils Ryrholm[3]

[1]Swedish University of Agricultural Sciences, Alnarp, Sweden, [2]Lund University, Lund, Sweden, [3]University of Gävle, Gävle, Sweden

Insect sex pheromones have been used extensively in integrated pest management but not yet for monitoring of rare and threatened insects, despite the growing concern for biodiversity and conservation. The legendary attractiveness of sex pheromones makes them an ideal tool for studying many insect species occurring at very low population densities, including newly established invasive species. We present two model systems that are likely the first to exploit pheromones in the context of conservation and biodiversity:

1) The sex pheromone-kairomone system of the threatened saproxylic scarab beetle *Osmoderma eremita* and its predator, the click beetle *Elater ferrugineus*, which breed in hollow trees in fragmented oak stands in pastoral landscapes.

2) Monitoring a whole range of tineid and clearwing moths in fragmented forest landscapes, using only a few single compounds from their phylogenetically restricted pheromone systems. Tineid moths breed in dead wood and/or associated fungi, making them potentially valuable indicators of mature forest with high levels of biodiversity.

Our investigations illustrate the versatility of pheromones for precise monitoring in space and time and include estimates of absolute population size by capture-recapture studies; estimates of presence/absence and population density on landscape and regional scales; monitoring of population fluctuations over several years, and studies of dispersal frequency and dispersal distance. We have shown that previous recapture models of *O. eremita* likely lead to severe underestimations of population size, and that patterns of disappearance for tineid moths appear to be very different from those of saproxylic beetles, which are studied more frequently.

In vivo models for exploring the molecular basis of tick feeding and pathogenesis

Deborah Jaworski[1], C. Jerry Bowen[1], Glen Needham[2]

[1]Oklahoma State University, Stillwater, OK, United States, [2]The Ohio State University, Columbus, OH, United States

Using in vivo models to study the molecular and physiological basis tick feeding and pathogenesis has become very tractable with immunological and RNAi technologies. Ticks are somewhat unique among blood feeding arthropods, because we can immunize hosts and subject them to tick feeding challenge. Through RNAi, we are able silence specific genes by injecting ticks with double-stranded RNA (RNAi) and feeding them on hosts. Some silenced genes lead to lowered fecundity, ablation of feeding or decreased pathogen transmission. For immunizations, we essentially produce hosts that are “immunological knockouts” of the tick protein. We discuss immunological- and RNAi-based tick-host models for tick feeding and pathogenesis; and their advantages and disadvantages for evaluating the function of a protein during tick feeding.

Variation in caterpillar chemical defense: Effects on predators versus parasitoids

Deane Bowers

University of Colorado, Boulder, Colorado, United States

The ability of insects to sequester defense compounds from host plants has evolved in many different groups of insects and involves a variety of different classes of chemical compounds. Most insect species that have this ability are specialists, but some are generalists and members of the Lepidoptera have been particularly well studied in this regard. Variation in the amounts and kinds of compounds sequestered by insects can be important for both predators and parasitoids of those insects. Using lepidopteran caterpillars as a model group, this talk will compare and contrast the effects of different groups of sequestered compounds on predators and parasitoids.

Whitefly Transmission of Sweet Potato Leaf Curl Virus

Alvin Simmons, Kai-Shu Ling, Howard Harrison, D. Michael Jackson

USDA, ARS, U. S. Vegetable Laboratory, Charleston, South Carolina, United States

Introduction: The sweetpotato whitefly, *Bemisia tabaci* (Gennadius) is highly adaptive and polyphagous on taxonomically diverse species of plants on a global scale. This whitefly transmits numerous plant viruses, including Begomoviruses (Geminiviridae). We recently found the *Sweet Potato Leaf Curl Virus* (SPLCV) in South Carolina and since conducted studies on the role of *B. tabaci* as a vector for this virus.

Methods: Laboratory, greenhouse, and field experiments were conducted on host range and on transmission, acquisition, and retention of SPLCV by *B. tabaci* on *Ipomoea setosa* and sweetpotato. Determination of SPLCV was made with symptom expression on indicator plants (*I. setosa*) and confirmed by Real-time PCR.

Results: Over 50 species of diverse taxa were identified as new hosts for *B. tabaci*, and over 40 species of *Ipomea* were identified as being susceptible to SPLCV. We did not detect SPLCV in over 70 species of other wild and cultivated plants. Data on transmission, acquisition, and retention will be presented.

Conclusions: Although individual *B. tabaci* appears to be moderately efficient in acquiring and transmitting SPLCV, the presence of the virus and an increasing population of the insect vector pose serious threat to sweetpotato production worldwide. These findings will help in the epidemiology of SPLCV in the sweetpotato field, and the resistant *Ipomea* may be useful in sweetpotato breeding programs.

Social life below ground: Colony breeding structure and inbreeding variation in subterranean termites

Edward Vargo

North Carolina State University, Raleigh, NC, United States

Introduction: Breeding systems of subterranean termites (Rhinotermitidae) are complex and poorly characterized. Colonies are founded by monogamous pairs of primary reproductives. Subsequently, colonies can be secondarily polygamous through production of neotenic reproductives that inbreed within the colony. To obtain a better understanding of colony breeding structure and how it varies among and within subterranean termite species, we conducted a comparative study of three species of *Reticulitermes* that are sympatric over much of the eastern U.S.: *R. flavipes*, *R. virginicus*, and *R. hageni*.

Methods: We used microsatellite markers to determine colony breeding structure and levels of inbreeding in several populations.

Results: We found important similarities and differences in breeding structures of these species. Most colonies of all species were simple families headed by monogamous pairs of reproductives. Nearly all of the remaining colonies contained low numbers of neotenic reproductives descended from simple families. In *R. flavipes*, a small number of colonies were mixed families, showing evidence of multiple unrelated same sex reproductives, probably arising from colony fusion. In general, inbreeding levels in all three species were low. In *R. flavipes*, for which we have the most extensive range samples, we found strong latitudinal variation in colony breeding structure with higher proportions of simple families in the south and progressively lower in the north.

Conclusions: Our results indicate that colonies of these subterranean termites are not as inbred as has been generally assumed, and that breeding structure is responsive to environmental factors that vary gradually across a latitudinal gradient.

Managing insect invasions: Lessons from biological control of weeds

Peter McEvoy, Eric Coombs, Fritzi Grevstad, Shon Schooler

[1]Oregon State University, Corvallis, Oregon, United States, [2]Oregon Department of Agriculture, Salem, Oregon, United States, [3]Olympic Natural Resources Center, Long Beach, Washington, United States, [4]CSIRO Entomology, Indooroopilly, Queensland, Australia

Introduction: Biological control introductions can provide more relevant information on the independent and dependent variables in the invasion processes of insects than is typical of most invasions. The introduction of two chrysomelid beetles, *Galerucella calmariensis* and *G. pusilla*, to North America for biological control of purple loosestrife (*Lythrum salicaria*) presented us with an opportunity to measure and model their rates of spread into new areas.

Methods: We compared spatial spread rates estimated by different methods; autonomous spread of different geographic populations; and autonomous and anthropogenic spread. We start with a basic reaction-diffusion model simplifying demography and movement.

Results: We compare observed spread with that predicted by the basic model; and we conclude that linear spread predicted by the basic model best describes autonomous spread by *Galerucella*. We evaluated the autonomous spread model based on both assumptions and predictions. Field observations closely matched model predictions: the radial distance increased linearly through time. However, field observations contradicted model assumptions by revealing that population growth is subject to Allee effects and stochastic variation and movement distances are leptokurtic.

Conclusions: Paradoxically, the data match the predictions of the basic model, but not the assumptions. A possible resolution to the paradox is that effects may be equal and offsetting: Allee and stochastic effects tend to slow the speed of an invasion, while leptokurtic dispersal tends to increase it.

Managing insect invasions: Lessons from biological control of weeds

Peter McEvoy, Eric Coombs, Fritzi Grevstad, Shon Schooler

[1]Oregon State University, Corvallis, Oregon, United States, [2]Oregon Department of Agriculture, Salem, Oregon, United States, [3]Olympic Natural Resources Center, Long Beach, Washington, United States, [4]CSIRO Entomology, Indooroopilly, Queensland, Australia

Introduction: Biological control introductions can provide more relevant information on the independent and dependent variables in the invasion processes of insects than is typical of most invasions. The introduction of two chrysomelid beetles, Galerucella calmariensis and G. pusilla, to North America for biological control of purple loosestrife (Lythrum salicaria) presented us with an opportunity to measure and model their rates of spread into new areas.

Methods: We compared spatial spread rates estimated by different methods; autonomous spread of different geographic populations; and autonomous and anthropogenic spread. We start with a basic reaction-diffusion model simplifying demography and movement.

Results: We compare observed spread with that predicted by the basic model; and we conclude that linear spread predicted by the basic model best describes autonomous spread by Galerucella. We evaluated the autonomous spread model based on both assumptions and predictions. Field observations closely matched model predictions: the radial distance increased linearly through time. However, field observations contradicted model assumptions by revealing that population growth is subject to Allee effects and stochastic variation and movement distances are leptokurtic.

Conclusions: Paradoxically, the data match the predictions of the basic model, but not the assumptions. A possible resolution to the paradox is that effects may be equal and offsetting: Allee and stochastic effects tend to slow the speed of an invasion, while leptokurtic dispersal tends to increase it.

Intraguild predation in predatory Heteroptera

Éric Lucas

Université du Québec à Montréal, Montréal, Québec, Canada

Intraguild predation is an ubiquist interaction within predatory insect guilds. Heteropteran species, as predators of the main crop pests (aphids, whiteflies, mites …) in annual and perennial systems, are involved in the interaction either as intraguild preys or intraguild predators. The impact of their biological formula (morphology, physiology, behaviour, development) on the direction, symmetry and intensity of the intraguild predation is discussed. Many heteropteran predators also are considered as zoophytophagous organisms, able to complete their life cycle on animal, or on plant food source. According to this omnivorous behaviour, predation on a phytophagous organism may be considered as intraguild predation. This unique link between heteropteran predators, non-heteropteran intraguild natural enemies, crop pests and plants can generate singular direct and indirect effects. Finally, intraguild predation may disrupt or not biological control of pest, according to the nature of the different interactions in the system.

Life history and population dynamics of temperate waterstriders: lessons from a 24-year bug count

John Spence

University of Alberta, Edmonton, Alberta, Canada

Introduction: Long-term studies of populations are scarce but required to fully understand the adaptive value of insect life-history strategies. Selective pressures associated with regulation of voltinism and dispersal behavior are better understood in a long-term context.

Methods: I have conducted, over a 24 year period, weekly censuses of the populations of five co-occurring species of gerrids on a small pond in central Alberta, Canada. All adult individuals were collected and marked each week. Experiments embedded in this work estimate predation and dispersal rates and variation in female fertility over time.

Results: There is significant long term variation in the success of these species, suggesting that annual variation shifts selective advantages among species. Few overwintered bugs that completed development on the pond actually reproduced there in the subsequent year and this average proportion varies between c. 10% and <0.5%, depending on species. Flight is a highly significant aspect of local population dynamics, explaining more local changes in population than does depredation in the two main species. I identify at least 4 sorts of dispersal flights, each associated with a different range of selective pressures. Some bugs begin leaving the pond for overwintering diapause as early as mid-July.

Conclusion: Pond-dwelling gerrid populations in central Canada exist as structured demes with much connection among units traversing juvenile development on particular ponds. Dispersal by flight is a central aspect of life-history strategy and, in most species, this co-exists temporally with reproduction with only very weak expression of the oogenesis-flight syndrome.

Extensile oviscapts: enigmas in early Lepidoptera evolution

Niels Peder Kristensen, Frank Hünefeld

[1]*Natural History Museum of Denmark, University of Copenhagen, Copenhagen, Denmark,* [2]*Institut für Spezielle Zoologie und Evolutionsbiologie, Friederich-Schiller Universität, Jena, Germany*

A telescope-like extensile female postabdomen ('oviscapt') with two pairs of long rod-like apodemes arising, respectively, from the anterior margins of segments VIII and IX, is a putative ground pattern autapomorphy of the superorder Amphiesmenoptera. The non-glossatan Agathiphagidae have an extra apophysis pair, since one pair arises from tergum VIII and one from the ventral plate of the same segment. Expectedly, the musculature of this three-apophysis-pairs postabdomen is exceptionally complex: as many as 24 muscle sets were identified in our recently completed examination, while we find no more than 11 sets in the basal glossatan family Eriocraniidae. Muscle configuration does not clearly indicate whether the single anterior apophysis in the typical lepidopteran complement is homologous with the dorsal or the ventral set in *Agathiphaga*, and it remains a possibility that it actually represents a fusion product of the two. That the three-apophysis oviscapt could even represent the amphiesmenopteran ground pattern condition is another issue which deserves particular scrutiny in the light of this configuration being discovered in 1996 in the intriguing basal caddisfly *Fansipangana*.

The occurrence of overall very similar piercing oviscapts with a terminal 'saw' in the glossatan families Eriocraniidae, Acanthopteroctetidae and Lophocoronidae is enigmatic, since according to present understanding these families do not form a monophylum, but arose in three successive splitting events during initial glossatan evolution. Parsimony would indicate this postabdominal configuration to be plesiomorphic in Glossata, but then a scenario with the more unspecialized abdominal apex in higher Lepidoptera being due to character reversal is required.

Asilidae from the Cretaceous and Tertiary (Diptera: Brachycera): phylogenetic placement, biogeography, and faunal comparison

Torsten Dikow[1], David Grimaldi[2]

[1]Biodiversity Synthesis Center, Field Museum of Natural History, Chicago, Illinois, United States, [2]Division of Invertebrate Zoology, American Museum of Natural History, New York, New York, United States

The study of extinct species has enormous potential for an examination of the early evolution of a taxon, its biogeography, and species diversity because fossilized specimens preserve *in situ* stages of the evolutionary history otherwise undetected. This presentation reviews the extinct Asilidae (robber flies, assassin flies) from the Cretaceous and Tertiary with particular reference to Dominican amber. The oldest fossils that can be unambiguously assigned to the Asilidae are Cretaceous in origin and can be placed on a comprehensive phylogenetic hypothesis providing not only a minimum age for Asilidae itself, but for a clade composed of Asilidae excluding Asilinae, Laphriinae, and Ommatiinae (110 Mya) as well as the Leptogastrinae (94 Mya). The comprehensive study of the 20 Mya specimens preserved in Dominican amber from Hispaniola Island offers an insight into the faunal composition of the Caribbean Asilidae fauna in the Miocene. For this analysis, 26 amber specimens are available and the extinct diversity can be compared to recently published reviews of the extant robber-fly fauna of Central America and the Caribbean. The extant diversity is well represented by the extinct amber species particularly within Asilinae, Ommatiinae, and Stenopogoninae. A number of presently distributed Laphriinae and Trigonomiminae genera on Hispaniola have not been found in amber. On the other hand, four Neotropical genera (Laphriinae: *Lampria*, *Smeryngolaphria*; Leptogastrinae: *Leptopteromyia*, *Schildia*) have been preserved in amber, but do not presently occur on Hispaniola. An exceptionally surprising finding is the presence of the Old World Leptogastrinae genus *Lobus* in Dominican amber.

Deep splitting events in the mecopterid endopterygotes: a diversity of diversification modes

Niels Peder Kristensen

Natural History Museum of Denmark, Copenhagen University, Copenhagen, Denmark

The clade Mecopterida ('Panorpoid orders' of Hinton's benchmark 1958 review, 'Panorpida' of Grimaldi & Engel) can be traced back to the Permian. Its subgroup Amphiesmenoptera (Trichoptera + Lepidoptera) constitutes the only truly robustly supported sister-group pair among extant insect 'orders', while relationships within the Antliophora (Nannomecoptera + Neomecoptera + Siphonaptera + Pistillifera [Mecoptera *s.str.*] + Diptera) remain debatable, and the suggested assignment of the Strepsiptera to the latter is particularly contentious.

The megadiverse' orders Lepidoptera and Diptera both instructively exemplify the 'additive typogenesis' concept but exhibit starkly contrasting diversification modes. The numerous apomorphies characterizing 'typical flies' (schizophoran Cyclorrhapha) were acquired over a long time span, and sizable radiations occurred in a number of successive evolutionary grades; remarkably, however, resolving the deepest splitting events within the Diptera has proved singularly difficult. In contrast, it seems possible to resolve in detail the sequence in which the first lepidopteran families arose, and hence the sequence in which individual elements of the 'apomorphy syndrome' characterizing 'typical Lepidoptera' (Ditrysia) were acquired. The non-ditrysian lineages, harbouring the bulk of the structural diversity within the Lepidoptera, account for only 1-2% of the species diversity in the order. Resolving the ditrysian radiation is as problematical as resolving basal dipteran diversification.

The deepest splitting events within Trichoptera are not definitely resolved, but most extant caddisflies evolved during radiations of the Annulipalpia and Integripalpia. The recently suggested monophyly of a (Nannomecoptera + (Neomecoptera + Siphonaptera))-clade offers an interesting scenario for flea origin/evolution, but support from ongoing morphological work is ambiguous

Heavy metals alter interactions in a grass-leaf miner system

Luc De Bruyn, Jan Scheirs

University of Antwerp, Antwerp, Belgium

We studied the effects of heavy metal exposure on host plant growth and survival and subsequent host choice and performance of the grass miner *Chromatomyia milii* (Diptera, Agromyzidae). Cadmium decreased plant growth in a dose-dependent way. *C. milii* preferred the control to the cadmium-exposed plants for feeding and oviposition. Moreover, preference for the control plants increased with increasing cadmium exposure of the alternative choice. Adult and offspring performance decreased with increasing plant cadmium exposure. This suggests that, at least under our laboratory conditions, host choice of *C. milii* is adaptive under pollution stress. Foliar cadmium concentration increased and the soluble sugar concentration decreased with increasing cadmium exposure. Regression analysis showed that both latter components might be responsible for the decrease in performance of *C. milii* on cadmium-exposed plants. The protein and amino acid concentration of the leaves, the amount of structural defences, and water concentration were not affected by the cadmium treatment.

Electronic agricultural atlas of insect pests and other harmful organisms of the Former Soviet Union

Andrei Frolov[1], Igor Grichanov[1], Mikhail Saulich[1], Elena Ovsyannikova[1], Genrikh Davidyan[1], Marina Berim[1], Julia Malysh[1], Alexander Afonin[2], Stephanie Greene[3]

[1]All-Russian Institute of Plant Protection, St. Petersburg, Russian Federation, [2]Saint-Petersburg State University, St. Petersburg, Russian Federation, [3]USDA, ARS National Temperate Forage Legume Germplasm Unit, Prosser, WA 99350, United States

Modern geographic information system (GIS) tools allow spatially explicit data on living beings to be assembled, digitized, georeferenced and placed into a framework that can be accessed by a wide audience. As a result of international cooperation, the *Ecological Atlas of Russia and Neighboring Countries: Economic Plants and their Diseases, Pests and Weeds* is now nearing completion. This project is the first attempt to construct a bilingual information and decision support system on the economic plants and the organisms that harm them, across the territories of the Former Soviet Union. Three Russian institutes and the USDA Agricultural Research Service are cooperating to develop the Atlas, which consists of species distribution maps, biological descriptions, (including photographs), climate and agroecological maps, along with easy to use GIS exploratory software. Of interest to entomologists, the Atlas presents 222 maps reflecting the distribution of harmful insects and mites. There are a total of 640 maps describing the distribution of organisms harmful to economically important plants. The maps are based on an extensive review of literature, as well as original surveys of various national collections. Pest, disease and weed distribution zones reflect levels of severity, usually high, moderate and low. Maps can be reviewed at http://www.agroatlas.ru/. Because many of these species have trans-continental and even cosmopolitan distribution, it is of interest world-wide. Researchers, teachers, agronomists and amateurs are now using the freely available published data, maps and pictures to support their own activities. The Atlas is supported by a grant from the USDA, ARS Former Soviet Union Cooperation Program, managed by the ARS Office of International Research Programs, U.S. State Department Non-Proliferation/Proliferation Threat Reduction, and the International Science and Technology Center.

Phylogeography as a tool to trace the origin of expanding populations of the pine processionary moth in the Mediterranean area

Carole Kerdelhué[2], Mauro Simonato[1], Andrea Battisti[1], Lorenzo Zane[1], Jerome Rousselet[3], Alain Roques[3]

[1]University of Padova, Legnaro PD, Italy, [2]INRA Bordeaux, Pierroton, France, [3]INRA Orléans, Olivet, France

Introduction: Although native to large areas of southern Europe, northern Africa, and Middle East, the pine processionary moth *Thaumetopoea pityocampa* is behaving as an invasive species in new parts of the range that become available because of climate change or human introduction. We want to understand the history of this group of species in the Mediterranean and to know how much diversity is present in the range macrorefugia, as starting points of routes to colonize upper elevation and latitude areas.

Methods: Exploring the phylogeographic structure of the pine processionary moths in their whole range (74 populations) by using sequence of mitochondrial DNA, thus concerning the female lineage that is the only relevant for the knowledge of the colonization routes in this species.

Results: A considerable amount of genetic diversity has been found at all major range macrorefugia, that can be identified with mountain ridges located in southern Europe, northern Africa, and Middle East. Major islands showing ancient occurrence of pines, such as Crete, Cyprus, and Corsica, are also centres of diversity whereas the populations on other islands (e.g. Sardinia) are of recent origin, either natural or anthropogenic.

Conclusions: Range expansion is occurring within each major clade with the same pattern, i.e. nearest neighbour origin. Selection of haplotypes particularly adapted to dispersal can be envisaged for at least one clade. Assessment of expansion rates are available for continental France from Battisti et al. (2005) and mean values are around 2.7 km/year, a much faster rate than that observed for trees (most 0.2, few up to 2 km/year, Huntley 2005) and putatively close to that of mobile beetles according to Holocene fossil evidence.

Molecular targets for bark beetle pest management

Claus Tittiger[1], Gary Blomquist[1], Christopher Keeling[2], Tidiane Aw[1], Sharon Young[1], Rubi Figueroa-Teran[1], Pamela Sandstrom[1], Andrew Gorzalski[1], Anna Gilg[1]

[1]University of Nevada, Reno, Reno, United States, [2]University of British Columbia, Vancouver, BC, Canada

Introduction: Mitigation of pine forest destruction by bark beetles is difficult due in part to the geographic scale of outbreaks and the physical inaccessibility of the insects beneath the bark of their host trees. In an effort to develop focused management strategies applicable to high-value, relatively small area forests, we are using functional genomics tools to identify species-specific genes/enzymes to serve as targets.

Methods: In a preliminary "proof-of-concept" experiment, a small EST database representing pheromone-biosynthetic male midguts from the pine engraver, *Ips pini* was constructed and used to fabricate custom cDNA microarrays. The arrays were used to identify genes implicated in the *I. pini* pheromone-biosynthetic pathway. Similarly, a more extensive EST database and oligonucleotide microarray representing *Dendroctonus ponderosae* midguts has been constructed and queried. The biochemical roles of candidate enzymes were further investigated through functional assays of recombinant proteins produced using a baculoviral system.

Results: Enzymes involved in terminal steps in the *de novo* synthesis of the pheromone component ipsdienol were first tentatively identified by clustering microarray expression data and quantitative RT-PCR. Subsequent biochemical assays confirmed the identities of most, if not all of the enzymes involved in the terminal steps of ipsdienol production: geranyldiphosphate/myrcene synthase, myrcene hydroxylase, and ipsdienol dehydrogenase/reductase. Similarly, monoterpene-metabolizing enzymes are being identified from transcriptomic analyses of *D. ponderosae* midguts and fat bodies. Both EST pools have examples of "unknown," apparently Scolytidae-specific genes.

Summary: Functional genomics techniques rapidly identified novel pheromone-biosynthetic, monoterpene metabolizing, and other unique enzymes that may be targeted for future control strategies.

An overview of the Heteroptera of the Afrotropical Region with special reference to the fauna of southern Africa and the Aradidae

Dawid H Jacobs

University of Pretoria, Pretoria, South Africa

Worldwide the Heteroptera comprise about 80 families divided into about 5 500 genera and 40 000 described species. The Afrotropical Region (including Madagascar) has a rich Heteropteran diversity with about 60 families comprising approximately 1 700 genera and 9 000 described species. Notwithstanding the high diversity, few families or subfamilies are endemic to the Region. Only the families Medocostidae and Paraphrynoveliidae and the subfamilies Ocelloveliinae (Veliidae), Stenocorixinae (Corixidae) and Afrocimicinae (Cimicidae) occur exclusively in the Region.

From southern Africa about 55 families with approximately 720 genera and 2 100 described species have been recorded. More than 5% of the genera are endemic to the region. The greatest endemisity appears to be concentrated in the Cape Fynbos and the more xeric areas like Namaqualand, the Cedarberg mountains and the Karoo. Evergreen forests also harbours some endemic genera but not the Savanna.

The Aradidae are discussed as an example of the problems and the taxonomic challenges that the Afrotropical fauna poses. For example: the Carventinae are presently represented by 16 genera and 40 described species. They are associated with evergreen forests and most genera and species are apterous with very low vagility limited distributions. A few genera and species are distributed widely and occur in forests that are separated by large stretches of grassland or Savanna. It is uncertain when and how these taxa have spread. A further curiosity is that some populations are morphological indistinguishable but have vastly different chromosome numbers.

Vapor activity of essential oils extracted from fruit peels of two *Citrus* species against adults of *Callosobruchus maculatus* (F.) (Coleoptera: Bruchidae)

Gholamhossein Moravvej, Mohammad Hassanzadeh-Khayyat, Salehe Abbar

[1]Department of Plant Protection, Faculty of Agriculture, Ferdowsi University of Mashhad, Mashhad; [2]Department of Pharmaceutical Chemistry, School of Pharmacy, Mashhad University of Medical Sciences, Mashhad; [3]Department of Plant Protection, Faculty of Agriculture, Ferdowsi University of Mashhad, Mashhad, Islamic Republic of Iran

Introduction: The mixing of plant oils is traditionally practiced against stored-product insects in Asia and Africa. Due to the problems encountered with the use of modern synthetic insecticides, recently interest in the use of biocides from plants has been revived. The present study investigated the effects of volatile fractions of *Citrus limon* and *C. reticulata* peel essential oils on the cowpea adult bruchid, *Callosobruchus maculatus* (F.).

Methods: The essential oils were extracted from fresh rind tissue (albedo and flavedo) of fruits by water steam distillation using a Clevenger apparatus. The 2-cm-diameter pieces of filter paper were impregnated with different oil concentrations. The filter paper was attached to the undersurface of the screw cap of a glass vial containing one- to 2-day old adults of *C. maculatus*. Mortality was recorded after 3, 6, 9, 12 and 24 h from the commencement of exposure. Mortality data at 24 h exposure time were analysed with the probit model using a Maximum Likelihood Program.

Results: The citrus oils had high fumigant activity against adult beetles. There were positive and linear significant relationships between percent mortality of adults and duration of exposure to the essential oil vapors within all concentration levels and both plant oils, although not significantly within the concentration of 110 µl L^{-1} of *C. reticulata*. Within each essential oil, the slopes of regressions of mortality rates on exposure times were smaller in low concentrations than those in high concentrations. The oil of *C. reticulata* was significantly more toxic than that of *C. limon* based on both 24 h LC_{50} (33 and 45 µl L^{-1}, respectively) and 24 h LC_{90} (75 and 99 µl L^{-1}, respectively) values.

Conclusions: The citrus peel oils can be used as potential control measure against cowpea seed beetles. More investigations are needed for evaluation of their effects on other developmental stages.

Regulation of bark beetle pheromone biosynthesis by JH III

Claus Tittiger[1], Gary Blomquist[1], Christopher Keeling[3], Jeremy Bearfield[1], Sharon Young[1], Matthew Ginzel[2]

[1]University of Nevada, Reno, Reno, NV, United States, [2]Purdue University, West Lafayette, IA, United States, [3]University of British Columbia, Vancouver, BC, Canada

Pine bark beetles rely on aggregation pheromones for successful tree colonization and reproduction. For *Ips* spp., pheromone production begins when pioneer males arrive at a new host tree and is stimulated in part by elevated JH III titres. The mechanism by which this happens is unknown, but likely involves a newly-discovered gene, *Ipi10G08*, that has homologs in other insects.

JH III apparently coordinates *I. pini* and *Dendroctonus jeffreyi* pheromone-biosynthetic enzymes in the male anterior midgut, leading to the suggestion that JH mediates pheromone biosynthesis in pine bark beetles. However, other factors including developmental and environmental cues also influence pheromone biosynthesis. Comparisons between *I. pini* and the closely-related *I. confusus* further indicate that, while JH appears sufficient to induce pheromone biosynthesis in *I. pini*, its activity in *I. confusus* appears limited to elevating pheromone-biosynthetic gene expression, with other factors required post-transcriptionally to activate the necessary enzyme activities. Thus, JH III plays an important, but not exclusive role in regulating bark beetle pheromone biosynthesis.

Flying after Linnaeus: Dipteran names since Systema Naturae (1758)

Neal Evenhuis[1], Thomas Pape[2], Adrian Pont[3], Chris Thompson[4]

[1]B.P. Bishop Museum, Honolulu, Hawaii, United States, [2]Natural History Museum of Denmark, Copenhagen, Denmark, [3]Oxford University Museum of Natural History, Oxford, United Kingdom, [4]Systematic Entomology Laboratory, USDA, ARS, Washington, DC, United States

Since the start of zoological nomenclature, new names for flies (Diptera) have been proposed at an average of more than eight hundred names per year.

Linnaeus (1758: *Systema Naturae*) and Fabricius (1805: *Systema Antliatorum*) provided the first and the last comprehensive summaries of contemporary knowledge of extant flies respectively. Today, version 10 of the *BioSystematic Database of World Diptera* (BDWD) contains nomenclatural data for 156,599 extant and extinct species in 154 families and 11,671 genera, which is about 10% of the described diversity of the world biota. The BDWD is a nomenclator, which allows for the retrieval of the single correct name for each dipteran, and by providing a framework for organizing and integrating current and future knowledge it is a comprehensive portal to knowledge about all flies.

Various statistics are presented to assess the growth in knowledge, from species accumulation curves and regional patterns of taxonomic output, to the number of workers, their productivity and error rates. With an estimated 98% of all Diptera names entered in the BDWD, the challenge now is to assure the highest quality through appropriate community participation, particularly by specialists and peers. At present, 15% of the entries have been verified and peer-reviewed.

We also present our visions for how to build and maintain large nomenclators, and how these can be used to alleviate the critical need to summarize and make available existing knowledge about our biota.

Education and training in insect rearing for biological control purposes in Brazil

José Roberto Parra

University of Sao Paulo, ESALQ, Piracicaba-SP, Brazil

Brazil's beginnings in entomology were significantly influenced by agrochemicals, differently from other countries in Latin America, which were under strong influence from American Universities, especially the University of California. The first parasitoid was introduced in this country in 1921, and few satisfactory results were obtained until the 1970's, except for sporadic cases such as the successful control of *Antonina graminis* with the introduced parasitoid *Neodusmetia sangwani*. In 1968, formal graduate courses were introduced in Brazil. Presently, about 2000 professionals have been trained in Entomology in our country, in addition to those that were trained abroad; from those trained domestically, 25% received training in Biological Control, thus creating a Biological Control Culture, so difficult to implement in a country deeply rooted in the use of agrochemicals. The scenario today has changed, and there are many examples in the country comparable to the best biological control programs in the world, with 2,000,000 ha of soybean being treated with *Baculovirus anticarsia* to control *Anticarsia gemmatalis*, 1,700,000 ha covered with inundative releases of *Cotesia flavipes* to control *Diatraea saccharalis*, 1,000,000 ha receiving *Metarhizium anisopliae* to control *Mahanarva* spp. in sugarcane, and 200,000 ha being treated with *Trichogramma* spp. to control pests in sugarcane, tomato, corn, etc. The research data generated in Brazil allowed the publication of many books, contributing toward the implementation of the above-mentioned Biological Control culture. Extension courses have allowed the formation of BC research groups in different parts of the country. As BC awareness increases, classical BC has returned to the scene, such as the recent case in which *Ageniaspis citricola* was introduced to control *Phyllocnistis citrella*. Education, awareness, and training were essential for the success cases just mentioned, and there is a tendency for a steady increase in the use of BC in Brazil.

Biological control of the sugarcane borer, *Diatraea saccharalis*, using *Cotesia flavipes* and *Trichogramma galloi*

José Roberto Parra[1], Paulo Botelho[2]

[1]University of Sao Paulo, ESALQ, Piracicaba-SP, Brazil, [2]Universidade Federal de São Carlos, Araras-SP, Brazil

The sugarcane borer, *Diatraea saccharalis*, causes huge damages, with significant sugar and alcohol losses in Brazil. Since the 1970's, Brazil uses *Cotesia flavipes*, an introduced parasitoid, to control the pest, whose losses in the 1980's reached 100 million dollars annually in the State of São Paulo, which responds for most of the Brazilian production. As the parasitoid became adapted, losses dropped to 20 million dollars annually, decreasing infestation intensity levels from 10% to 2% in that state. Currently, insects reared on *D. saccharalis* maintained on artificial diet for inundative releases in 1,700,000 ha are produced by about 30 laboratories located in sugarcane mills, in addition to some 15 private laboratories. *T.galloi*, the pest's most important egg parasitoid, is produced by 2 private companies and is also released inundatively in about 150,000 ha, with very interesting results, significantly reducing infestation intensity levels, especially when reared on the factitious host *Corcyra cephalonica*. As the area cultivated with sugarcane in Brazil is expected to double in the next few years, the potential to increase the area where *D. saccharalis* Biological Control is adopted becomes increasingly higher.

Local gradients in stoichiometry and trophic level of an omnivorous ant

Terrence McGlynn

California State University Dominguez Hills, Carson, CA, United States

While the relative abundance of resources are known to affect dietary choices in omnivorous animals, less is known about dietary shifts in response to resource quality. In this study, we sampled colonies of the generalist gypsy ant *Aphaenogaster araneoides* across a known stoichiometric gradient. This gradient drives the relative carbon:nutrient ratios of the base of the food chain. We conducted stable isotope analyses to calculate delta N15 as a measure of relative omnivory. We found that the trophic level of gypsy ants responds to the environmental stoichiometric gradient. We suggest that undocumented patterns in the distribution of nutrients in soils, plants and leaf litter may explain, in part, diet selection and competition among ants.

The exploitation of insects as attraction at leisure farms in Taiwan

Ying-Sheue Wei

Kainan University, Taoyuan County, Taiwan

Introduction: As the vigorous development of leisure agriculture, the insect theme leisure farms are prevailing during recent decades in Taiwan. These farms provide leisure experiences as well as educational value to visitors by insect exhibition, watching activity, and observation. But some theme insects are not native species but introduced spectacular species. And go to leisure farms for observing insects is more and more popular among pupils. The exploitation of insects at leisure farms was investigated.

Methods: The study was conducted a survey using the integrity of field observation data, the results of interviews of leisure farmers and literature reviews. The insect exploiting measures, insect species, and native or not was recorded. And the activities that leisure farms provided would also analysis.

Results: Butterflies, fireflies and honey bees were the most famous theme insects of leisure farms. Tremendous exotic beetles were gradually popular insect resources. The farms would usually grow exotic plants or flowers to mass rear particular species butterflies, and built artificial ponds for aquatic fireflies. Main activities at leisure farms were only to introduce what were the insects, where to find them, and how they look like. Little information about the ecological role of insects was mentioned. And those activities always provided as outdoor educational opportunities for pupils.

Conclusions: Although insects could be attraction at leisure farms, the exploitation manners were required to be improved. The cooperation of leisure farmers and entomologist would make conditions much better.

Evaluation of *Podisus maculiventris* (Hemiptera: Pentatomidae) for biological control of viburnum leaf beetle, *Pyrrhalta viburni* (Coleoptera: Chrysomelidae), an emerging landscape pest in North America

Gaylord Desurmont, Paul Weston

Cornell University, Ithaca, NY, United States

Introduction: *Pyrrhalta viburni*, an invasive chrysomelid native to Europe first detected in the USA in Maine in 1994, is becoming a major landscape pest in North America and poses a serious threat to a large portion of the U.S. and Southern Canada. Both larvae and adults feed on shrubs in the genus *Viburnum*, and can kill susceptible plants within a few years. Plants in both managed landscapes and natural areas are at risk. Among the few natural enemies of viburnum leaf beetle native to North America, the spined soldier bug, *Podisus maculiventris* (Hemiptera: Pentatomidae), shows the greatest promise for biological control.

Results: In laboratory assays, nymphs consumed in average 100.6 larvae or 16.9 adults during their development. In field settings on both caged and open-grown plants, *Podisus maculiventris* nymphs developed successfully preying on *P. viburni* larvae. Predation efficacy was correlated with size of shrubs and pest density: defoliation due to pest populations was significantly reduced when the predator:prey ratio was greater than 1:100, but no effect was seen otherwise. Other parameters, such as temperature, presence of refugia, presence of other predators, and nature of the host plant also influence predatory efficiency.

Conclusions: These results suggest that *P. maculiventris* has potential for augmentation biological control programs against viburnum leaf beetle subject to several constraints of environment and release conditions.

A Late Triassic radiation of herbivorous insects in the Karoo Basin of South Africa

Conrad Labandeira[1], John Anderson[2], Heidi Anderson[2]

[1]Smithsonian Institution, Washington, DC, United States, [2]South African National Bioidiversity Institute, Pretoria, Gauteng, South Africa

Introduction: Cited examples of ancient insect radiations involve expansion of insect herbivory on emerging Early Cretaceous angiosperms. An equally impressive radiation of insect herbivores occurred on a dominantly gymnospermous flora 90 m.y. earlier, indicating an earlier, unrecognized chapter in plant-insect associations.

Methods: Damage type (DT) data were gathered for 177,301 individual plant-organ specimens from 106, stratigraphically ordinated localities representing 7 habitat types from the Molteno Formation of South Africa. (A DT is a distinctive, diagnosable pattern of insect herbivore feeding.) 79 DTs were scored from the following herbivore functional feeding groups: external foliage feeding (30 DTs), piercing-and-sucking (8), oviposition (10), leaf mining (7), galling (15), seed predation (4), boring (2) and unknown feeding (2). Plant hosts included liverworts, horsetails, ferns, and gymnosperm seed plants such as pinopsids, especially voltzialean and podocarpaceous conifers; diverse ginkgoopsids such as peltasperms, ginkgoaleans and umkomasialeans; bennettitopsids; gnetopsids, and several unaffiliated taxa.

Results: A matrix of DTs versus locality versus habitat versus plant host reveals a complex pattern of insect herbivory involving differential palatability of plants, favorable physical environments, and insect herbivore colonization patterns. Targeting of plant hosts ranged from leaf-miner (DT141) monophagy on *Equisetites*, gall (DT122) oligophagy widely occurring on *Sphenobaiera* but also on *Dicroidium* and *Kannaskoppifolia*, and rampant polyphagy from cuspate margin feeding (DT12). The greatest diversities and highest abundances of DTs occurred in intermediate successional habitats, particularly *Sphenobaiera* Closed Woodland and Immature *Dicroidium* Riparian Forest.

Conclusion: The primary associations of phytophagous insects are on ancient gymnospermous seed plants, rather than relatively recent angiosperms.

Aggregative oviposition of viburnum leaf beetle, *Pyrrhalta viburni* (Paykull): Mechanisms and benefits of an unusual social behavior

Gaylord Desurmont, Paul Weston

Cornell University, Ithaca, NY, United States

Introduction: *Pyrrhalta viburni*, an invasive chrysomelid native to Europe, is an emerging landscape pest in North America. Larvae and adults feed on shrubs in the genus *Viburnum* in both managed landscapes and natural areas. *P. viburni* females lay eggs in small groups in cavities they excavate in the twigs then cover with a frass-like protective secretion. Infested twigs sometimes produce wound tissue in response to oviposition as a defensive reaction.

Methods: In laboratory trials, we conducted several choice-tests to determine oviposition stimuli. Analysis of egg mass densities on field-collected infested twigs and rearing of larvae in groups of different sizes were also conducted.

Results: We found that females prefer to oviposit on branches already infested by other females, and will lay their eggs in close proximity to egg masses already present. Both the egg mass cap and the cavity acted as positional stimuli, but not the eggs themselves, and presence of plant wound tissue made the twigs more attractive to females. *P. viburni* larvae showed reduced mortality and produced heavier adults when reared in groups rather than individually, suggesting benefit of larval group feeding. Analysis of egg mass densities on field-collected infested twigs revealed that production of plant wound tissue was negatively correlated with magnitude of infestation, suggesting that egg survivorship is higher on heavily infested twigs by overcoming plant defensive reaction.

Conclusions: Results of this research shed light on a rare case of subsociality for a chrysomelid, and add to our understanding of the ecology of this important pest.

Feasibility of acoustic technology for canegrub detection and management

Richard Mankin[1], Peter Samson[2], Keith Chandler[3]

[1]USDA-ARS-CMAVE, Gainesville, FL, United States, [2]BSES Limited, Mackay, Queensland, Australia, [3]BSES Limited, Bundaberg, Queensland, Australia

Introduction: Several scarabaeid and melolonthinid canegrubs are important root-feeding pests of Australian sugarcane. Control methods are applied optimally in advance of infestations, so growers are encouraged to judge future risk by monitoring current infestations, past trends, and proximity to other infestations. To reduce costs of digging up large quantities of sugarcane, alternative methods of detecting and estimating canegrub populations are being considered, including acoustic detection.

Methods: Acoustic recordings were obtained from 59 sites in sugarcane fields near Mackay and Bundaberg in Queensland using either or both a Bruel and Kjaer accelerometer system and an AED-2000 acoustic detection system with a TEAC digital recorder. Recordings were assessed by listeners as they were being collected, and afterwards by custom-written signal processing software, which considered the spectral and temporal patterns of the detected sounds. The root systems of the sugarcane stools were examined after recording.

Results: Almost all of the recording sites were acoustically assessed as potentially infested. When the root systems were examined, we confirmed that canegrubs or other sound-producing, subterranean insects were present. Because only greyback (*Dermolepida albohirtum*) and Childers (*Antitrogus parvulus*) canegrubs were considered economically important in the fields examined, we attempted to develop spectral and temporal pattern analyses to identify these canegrubs specifically. Many of the sites containing greyback canegrubs were easily identifiable due to characteristic scraping and chewing behavior.

Conclusions: Greyback canegrub populations were rapidly identified using acoustic detection technology. Further studies are needed to assess the feasibility of these systems for detection of other canegrub species.

Effects of farm and landscape vegetational diversity on attack on coffee plants by leafcutting ants

Sanford Eigenbrode[1], Edgar Varón[2], Luko Hilje[3], Nilsa Bosque-Pérez[1]

[1]University of Idaho, Moscow, Idaho, United States, [2]CORPOICA, Tolima, Colombia, [3]Centro Agronómico Tropical de Investigación y Enseñanza (CATIE), Turrialba, Costa Rica

Introduction: Coffee agroforestry systems often include shade trees, which potentially protect the coffee from insect pests. In addition, vegetational diversity at the landscape scale could influence insects within coffee plantations. These effects were examined in coffee farms in Costa Rica, focusing on leaf-cutting ants, *Atta cephalotes*.

Methods: *Atta cephalotes* feeding on coffee and alternative host plants, and the densities of ant colonies in 15 coffee plantations differing in vegetational structure were compared based on visual surveys. The effect of different land use coverages on colony density at different buffer radii was analyzed for the 24 farms, and the effect of forest edge on ant colony density was analyzed in three farms.

Results: *Atta cephalotes* workers removed much less coffee as a proportion of their total diet in diversified coffee systems than in monocultures. This is related to a preference by the ants for a dominant shade tree (coral tree, *Erythrina poeppigiana*) as compared with coffee. Total ant colony density was significantly higher in monocultures, compared to the other systems, which should confer additional benefits in reduced attack by *A. cephalotes* in these systems. Ant colony densities were greater near forest edges than other edges of coffee farms. Effects of land use at a landscape scale on *A. cephalotes* colonies were detected but were negligible.

Conclusions: At the farm scale increased vegetational diversity reduces risks of *A. cephalotes* injury to coffee. Landscape scale effects appear to be of lesser importance for management of this insect pest.

ZooBank: The Official Registry of Zoological Names

M. Alonso-Zarazaga, D.J. Brothers, N.G. Bogutskaya, P. Bouchet, D.G. Fautin, M.J. Grygier, R.B. Halliday, I.M. Kerzhner, M. Kottelat, F. Krell, S.O. Kullander, G. Lamas, S. Lim, E. Macpherson, S.F. Mawatari, A. Minelli, P.K.L. Ng, T. Pape, L. Papp, D.J. Patterson, R. Pyle, G. Rosenberg, P. Stys, J.V. Tol, Z-Q Zhang

International Commission on Zoological Nomenclature, London, United Kingdom

The current scale of global taxonomic studies poses considerable challenges to a registry developed in the age of printing press and card files. Some 15,000 to 20,000 new nominal species are proposed every year in zoology, and together with thousands of other Code-compliant nomenclatural acts these are scattered in a bewildering number of journals, monograph series, books, and CD-based publications.

The ICZN Secretariat and Commissioners in 2005 proposed "ZooBank" - a central, web-based registry of zoological names and nomenclatural acts - as a mechanism for making information about all names and their nomenclatural status more accessible. ZooBank was launched as a functional prototype web site on January 1st, 2008, coinciding with the 250th anniversary of the official start of Zoological Nomenclature. At its launch, the ZooBank registry included all 4,819 names established in the 10th edition of Linnaeus' *Systema Naturae*, as well as five new fish species names established in an article published concurrently with the launch of ZooBank.

The goal of ZooBank is not to replace existing nomenclatural catalog databases, and it will make no assessment or judgement of the taxonomic content of any piece of published work. ZooBank will function as an archived index of zoological names and nomenclatural acts that affect names, and ultimately contain information regarding the availability or non-availability of all names in zoology. The complete implementation details of the ZooBank registry are currently being discussed, developed, and tested, with involvement from ICZN Commissioners, GBIF, TDWG, catalog and database managers, and the taxonomic community at large.

The initial radiation and environmental context of leaf-miners: Late Triassic Karoo floras of South Africa

Conrad Labandeira[1], John Anderson[2], Heidi Anderson[2], Tsepang Makholela[2]

[1]Smithsonian Institution, Washington, DC, United States, [2]South African National Biodiversity Institute, Pretoria, Gauteng, South Africa

Introduction: Leaf-mining insects presently target plant hosts and exhibit distinctive distributions among habitats. Little is understood about these two aspects of leaf-miner ecology during the Late Triassic, when leaf-mining was launched 90 m.y. before the appearance of angiosperms.

Methods: Leaf mines were identified and scored on 177,301 plant organs from the Karoo Basin of South Africa, representing 30 of 106 localities, 25 of 212 potential plant hosts, and all 7 habitats ranging from wetland to mature forest biomes. Mines were divided into 7 distinctive morphotypes, using the Damage Type (DT) system.

Results: Most specimens reveal superb frass-trail geometry, including fecal pellets, sidewall reaction rims, terminal areas and occasional oviposition sites. The commonest mine (DT71) represented 97.8 % of occurrences, in 22/30 localities, and targeted the broadleaved, parallel-veined voltzialean conifer, *Heidiphyllum elongatum*, at a frequency of 94.2 %. This mesophyll mine avoided major veins and venules, resembling modern polyphagan beetle mines on palms. At Aasvoëlberg 311, 6.3 % of all *H. elongatum* leaves were attacked, often multiply, suggesting outbreak levels. DT71 frequencies track plant-host occurrence rather than specific habitats, occurring in *Heidiphyllum* Thicket, but also *Dicroidium* Open Woodland and Mature *Dicroidium* Riparian Forest where *H. elongatum* is abundant. Rare mine morphotypes, including the thin, tubular, frass-filled, lepidopteran-like DT41, DT45, DT104, and DT141 preferred ferns and sphenopsids, but also occasional seed-plant leaves, occurring in all habitats.

Conclusion: Leaf-mining originated in southern Gondwana on a gymnospermous flora, replete with elevated host specificities, distinctive mine morphologies, and resource partitioning within and between habitats.

The effect of alternative plant production practices on predator-herbivore dynamics in ornamental nurseries

Paula Shrewsbury[1], Rebeccah Waterworth[2], Ellery Vodraska[1]

[1]University of Maryland, College Park, MD, United States, [2]University of California, Riverside, CA, United States

Introduction: In the production of ornamental plants, many plant management practices disrupt natural enemy - herbivore dynamics resulting in more frequent pest outbreaks. This study examines the effect of alternative plant management practices on natural enemy taxa and abundance, and ultimately on herbivore suppression.

Methods: Two alternative plant management practices, wood chip mulch as a groundcover and pot-in-pot planting method, were compared to conventional practices, weed cloth ground cover and above ground planting method for their influence on predator taxa and abundance, temporal and spatial dynamics, and herbivore suppression. A factorial design with 2 ground cover types and 2 pot positions was used. Natural enemies and survival of sentinel cohorts of black cutworm, *Agrotis ipsilon*, were sampled from the foliage and ground layers of container grown ornamental plants. Cutworm survival was compared between the day and night.

Results: Predator abundance did not differ on the foliage regardless of ground cover type or pot position. However, at the ground level predator abundance was greater in pot-in-pot containers. This effect was enhanced in plots with wood mulch. Ground cover type had no effect on cutworm survival and survival was lower at the ground level compared to foliar. This effect was enhanced at night in the pot-in-pot method. Predator species varied temporally and spatially.

Conclusion: The pot-in-pot system should increase predator activity and reduce the likelihood of outbreaks of soil dwelling insects compared to the conventional above ground system. The addition of wood mulch over weed cloth may enhance these effects.

Predators on the plantscape

Sanford Eigenbrode[1], Claire Rutledge[2]

[1]University of Idaho, Moscow, Idaho, United States, [2]Connecticut Agricultural Experiment Station, New Haven, Connecticut, United States

Introduction: Not only caterpillars and other insect herbivores, but also their natural enemies, must negotiate plant surfaces that vary morphologically on different spatial scales. Crystalline surface waxes on plants impair attachment and locomotion by predators. As a result, variable crystalline waxes in combination with plant architecture, can influence predator foraging behavior, potential interpredator interactions, and impacts on prey.

Methods: To explore the implications of waxy bloom for predators, simulation models were developed and parameterized based on observations of foraging *Hippodamia convergens* larvae (Coccinellidae) on individual plants and arrays of plants differing in waxy bloom.

Results: The models reveal the effects of varying interpredator interactions on the functional response of the predator. The models also can be adjusted to create refugia consistent with observed differences in parts of plant surfaces exploited depending upon the presence of wax bloom. Models of *H. convergens* larvae moving in arrays of plants differing in wax blooms reveal some non-intuitive effects of waxy bloom on predator aggregation to prey in the canopy.

Conclusions: Observations and simulation models show that wax bloom can influence interpredator interactions and interplant movement by predaceous coccinellids.

The Paleozoic and Mesozoic insect and mite gall record

Conrad Labandeira

Smithsonian Institution, Washington, DC, United States

Introduction: Reviews of gall-inducing insects suggest that the preangiospermous fossil gall record is sparse or nonexistent. However, recent fossil discoveries of anomalous plant structures indicate a rich gall record involving major insect and mite lineages.

Methods: Anatomically preserved coal-balls were sawn, acetate peeled, and mounted on slides for examination of histological and cellular-level detail similar to modern embedded sectioned material. Compression fossils were studied as surface views and fractures revealing inner gall structure. Explicit criteria for gall assignment include organoid or histioid structure, anomalous inner tissue, internal chambers, host-plant and tissue-type specificity, and evidence for arthropod inhabitation.

Results: Many interesting occurrences define the pre-Cenozoic gall record. (1), Spindle cone galls on horsetail fructifications (Early Pennsylvanian, Euramerica). (2), Holometabolan gall on fern rhachises with tufts of nutritive tissue invading an inner cavity (Late Pennsylvanian, Euramerica). (3), Adelgid-like bud galls mimicking cone morphology of a walchian conifer (Early Permian, Euramerica). (4), Swollen stem galls on an herbaceous voltzialean conifer (Middle Triassic, Laurasia). (5), Eriophyoid-like compound galls with submillimeter sized chambers on corystosperm pinnules (Late Triassic, Gondwana). (6), Small, spheroidal, clustered galls on bennettitalean leaves (Middle Jurassic, Europe). (7), Ellipsoidal, primary-vein galls on palmate sycamore leaves (Early Cretaceous, North America). (8), Varied galls assignable to modern galler clades (latest Cretaceous, North America).

Conclusion: Major lineages of galling insects currently correspond to highly stereotyped and recognizable external and internal features of galls, a condition that now extends to the late Paleozoic. Varied plant hosts, tissue types and habitats were colonized by early galling insects.

Fast acting insecticides: Novel utilization in vector control

Kamlesh Chauhan, Thanh Le, Ulrich Bernier, John Grieco

[1]USHUS, Bethesda, United States, [2]Walter Reed, Silver Spring, United States

Introduction: Fast acting pyrethroid insecticides like transfluthrin and metofluthrin are used in household and hygiene products, mainly for the control of flying insects such as mosquitoes and flies. While metofluthrin has only recently been registered, a related compound, transfluthrin, has been approved for use in about 50 countries worldwide. The main formulation types available are mosquito coils and aerosols. A high vapor pressure is the main physiochemical property of these and related fast acting pyrethroids.

Methods: In our study we designed and evaluated molecular properties of such pyrethroids for efficacy, commercial viability, as well as adaptation to new long lasting formulations. All newly designed fast acting pyrethroids were evaluated using K&D module to determine knockdown and feeding attributes of female mosquitoes.

Results: An interesting feature revealed for these candidate pyrethroids was their continued effect on several resistance strains of mosquitoes. Mosquitoes came in vicinity of vapor of most of these compounds were neither able to blood feed nor do they survive during test period of three minutes.

Conclusions and Future Work: We believe that these compounds induce desirable toxic effect to vectors in minutes with high vapor pressure.

Insecticide defenses in the salt marsh mosquito *Aedes sollicitans*

L. B. Brattsten, Debin Sun, Shaoming Huang

Rutgers University, Department of Entomology, New Brunswick, NJ, United States

Larval salt marsh mosquitoes are controlled in New Jersey by treatment with BTI, temephos, and methoprene. Data from about eight years showing LC50s of temephos indicate that despite sometimes heavy treatments for many years, the larvae are sensitive to the compounds and even become increasingly sensitive if the compound is discontinued for a year or two. The toxicity of BTI is variable between larval instars. Treatment with both methoprene and temephos can increase the toxicity of temephos in lab experiments. In vivo experiments with synergists indicate that the larvae use mainly esterases to detoxify temephos and methoprene but can detoxify synthetic pyrethroids with both enzyme systems. They have high esterase activities and medium to high microsomal monooxygenase activities. They have several P450 genes including CYP6P10 and CYP6BB1 each in at least five variants. The P450-NADPH-reductase gene from Aedes sollicitans most closely resembles that of the Asian Anopheles minimus.

Molecular phylogeny of the Platygastroidea: The big leap to a robust classification

Andy Austin[1], Norman Johnson[2], Hans Klompen[2], Andrew Polaszek[3], Alejandro Valerio[1], Matt Yoder[2]

[1]University of Adelaide, Adelaide, South Australia, Australia, [2]Ohio State University, Columbus, United States, [3]The Natural History Museum, London, United Kingdom

Introduction: The Platygastroidea and the two families it includes, the Scelionidae and Platygastridae, are a diverse assemblage of mostly small parasitic wasps comprising 4,500+ described species. All scelionids and some platygastrids are endoparasitoids of insect and spider eggs, while other platygastrids attack sessile Homoptera and gall-flies (Cecidomyiidae). Although the superfamily undoubtedly is monophyletic, recent phylogenetic studies strongly indicate that 1) the family Scelionidae is not a natural group unless Platygastridae is contained within it, and 2) several tribes of the largest subfamily, Scelioninae, and both subfamilies of Platygastridae seem not to be monophyletic.

Results and Discussion: Here we present our latest results toward a phylogeny of the Platygastroidea, based on a multi-gene analysis (using mitochondrial and nuclear coding genes) of an extensive taxon sampling representing most of the currently recognised tribes. The phylogeny is discussed in relation to the evolution of host associations, the role that morphological studies might play in future studies, and whether or not a more natural classification can yet be proposed.

Signaling interactions between axons and glial cells regulating olfactory receptor axon sorting and targeting in the developing moth olfactory pathway

Nicholas Gibson, Mark Higgina, Leslie Tolbert, Alan Nighorn, Lynne Oland

University of Arizona, Tucson, United States

Introduction: The olfactory pathway of the moth *Manduca sexta* presents an opportunity to study developmentally critical neuron-glia interactions involved in axon sorting and targeting. Axons of olfactory receptor neurons (ORNs) extending toward the olfactory lobe in the brain induce the formation of a glia-rich "sorting zone" (SZ). Later arriving ORN axons encountering SZ glia separate from their neighbors, dramatically change directions, and fasciculate according to their target glomerulus. These changes are dependent on the presence of SZ glial cells. Growth-cone interaction with SZ glia alters the shape and rate of movement of the growth cones (Tucker and Tolbert, 2003). In the SZ, fibroblast growth factor (FGFRs) receptors are activated on glia, epidermal growth factor receptors (EGFRs) are activated on ORN axons, and the cell adhesion molecule neuroglian (an L1 homolog) becomes tightly anchored in axonal membranes.

Methods and Results: We are using pharmacological approaches and RNAi to disrupt growth factor receptor (GFR) activation and expression of neuroglian *in vivo* and *in vitro*. The results of disruption include abnormal fasciculation, disrupted axon extension, and downstream effects on axon targeting and glomerulus formation, consistent with downstream effects of GFR activation in the SZ that include anchoring of neuroglian in the membrane, thus stabilizing fasciculation between axons, and possibly glial proliferation and migration.

Conclusions: Our data support a model of signaling interactions in which SZ glia alter axonal behavior by regulating interactions between IgCAMs. Homophilic binding between CAMs then activates the GFRs, and stabilizes CAM attachment to the cytoskeleton. Funded by NIH DC008597.

Arthropod decomposer communities in native forests in northern New Zealand

Anne Tomlinson[1], Robert Hoare[2], Jacqueline Beggs[1]

[1]University of Auckland, Auckland, New Zealand, [2]Landcare Research, Auckland, New Zealand

Introduction: Insects and other invertebrates play an important role in the decomposition of plant litter and numerous studies have highlighted their effect on decomposition rates. New Zealand has a rich and diverse litter fauna, but there is little understanding of the ecology of decomposer communities in different forest habitats. Litter fauna were studied in mixed conifer-angiosperm forests in northern New Zealand to determine whether: (1) community composition varied between different species of tree litter, and (2) invertebrate decomposers increased decomposition rates.

Methods: Pitfall trapping was undertaken beneath one conifer species, kauri (*Agathis australis*) and two angiosperm species, kanuka (*Kunzea ericoides*) and puriri (*Vitex lucens*). A complementary laboratory rearing study using litter samples from the same three tree species allowed accurate identification of Lepidoptera, Coleoptera and Diptera on maturity. Litterbags were used to study the effect of invertebrate decomposers on decomposition rates.

Results: Insect assemblages differed between the three litter types. A notable finding was the dominance of the introduced moth *Opogona omoscopa* (Lepidoptera: Tineidae) in puriri litter. Decomposition rates were significantly faster in litterbags accessible to invertebrates and, in the case of puriri litter, there was a correlation between invertebrate abundance and the rate of decomposition.

Conclusions: The finding that insect assemblages varied in different litter species has implications for conservation because it suggests a relationship between plant diversity and insect diversity. The abundance of introduced species in puriri litter suggests that further research is required to assess the impact of non-native species on nutrient cycling in New Zealand forests and their effects on endemic litter fauna.

.

Fine-scale pine scale intraspecific phylogeography across North America (Hemiptera: Diaspididae)

Rodger Gwiazdowski, Benjamin Normark

University of Massachusetts, Amherst, Amherst, Massachusetts, United States

Broad biogeographic sampling yields the best opportunity for identifying patterns of diversification and speciation within a taxon. *Chionaspis pinifoliae*, (Hexapoda: Hemiptera: Diaspididae), the pine needle scale insect, native to North America, appears to be omnipresent and morphologically similar on almost every species of *Pinus* in North America. Sampling from localities spanning southern Mexico to Canada reveal morphologically similar individuals with highly divergent mtDNA haplolotypes, potentially representing cryptic species, which show striking patterns of variation that accord with both geography and host use. We will explore plyolgeographic patterns of molecular variation in light of current Pinus biogeography.

Scale Insects are economically important pests and methods are currently being developed for molecular identification of pest species by non-specialists. We will explore the utility of current molecular methods of species identification given a dense sampling of this species throughout its native range.

A contrary perspective on native bee declines: The Oregon experience

Sujaya Rao, William Stephen

Oregon State University, Corvallis, United States

Worldwide, there are reports of declining populations of bumble bees and other native bee species. Habitat destruction and pesticide use are two agriculture-related factors that have been reported having negatively impacted bee diversity and abundance. However, cropping systems benefit bees by the abundance of foraging resources that they provide. In particular, agroecosystems adjacent to native habitats, that offer nesting sites for both solitary and social bee species, facilitate build-up of native bee pollinator populations. In 2004 we stumbled upon a new sampling device that caught an extraordinary number of bees. Census studies conducted with this trap have revealed remarkable diversity and abundance of native bees in both native and agricultural landscapes in Oregon on the west coast of the United States. In addition, we detected 6 specimens of the bumble bee, *Bombus occidentalis,* which was considered to be near extinction on the west coast. We believe that we are experiencing an increase in the numbers of native bees in Oregon, especially in western regions. Here, the increase in agricultural production is providing an abundance of food resources within flight distance of an abundance of nesting resources in adjacent native ecosystems. Consistency in sequential availability of foraging resources is likely to have been a key factor for conservation and build-up of native bees in western Oregon.

Pyrethroid resistance in *Culex pipiens* sensu lato: bridging the gap between bench-work and the field.

Anthony Cornel[1], Lisa Reimer[1], Adama Sacko[2], Rory McAbee[1], Etienne Fondjo[3], Gregory Lanzaro[1]

[1]UC Davis, Davis, California, United States, [2]Malaria Research Training Center, Bamako, Mali, [3]Ministry of Health, Yaounde, Cameroon

Introduction: Operationally meaningful interpretations of laboratory based assays used to detect insecticide resistance and to determine the mechanisms of resistance in mosquitoes remains a challenge.

Results: Comparisons between bottle bio-assay and cage field-trial mortality on *Culex pipiens* s.l. revealed that the bottle bio-assays underestimated the extent of expected operational failures for pyrethroid resistant mosquitoes when exposed to various ULV formulations of registered pyrethrum and permethrin. WHO test kit insecticide susceptibility assays were shown to perform well in predicting resistance to DDT in Cameroon populations of east and west African *kdr*-type *Anopheles gambiae* s.s genotypes. The assay, however, showed weak associations between resistance to type II pyrethroids and both *kdr* genotypes. Similar insignificant correlations between knock down times and recovery after three hours of pyrethroid exposure in a bottle bio-assay were found in both Mali *An. gambiae* s.s. and California *Cx. pipiens* s.l. *kdr* S/S, R/S and R/R genotypes.

Conclusion: For the most part, the interpretations and sensitivity of laboratory based susceptibility assays and role of *kdr* and other resistance mechanisms fall short of understanding the complexities of toxicological and irritancy/repellency responses particularly to pyrethroids . This in turn limits our ability to draw conclusions about expected mosquito survival in the field and impacts on disease transmission in areas where pyrethroid and other chemical vector control programs are applied.

Oxygen-water tradeoffs in eggs of *Manduca sexta*

H. Arthur Woods

University of Montana, Missoula, MT, United States

For terrestrial insect eggs, deciding what eggshell permeability to have constitutes a key physiological problem. High permeability supports high internal levels of oxygen while simultaneously allowing high rates of water loss. By contrast, low permeability conserves water while potentially depressing internal oxygen to low levels. Balancing this tradeoff is complicated because eggs experience changing environmental conditions and developmental demand for oxygen. I have shown that eggs of the sphingid moth *Manduca sexta* exert fine control over the tradeoff. During development, rates of metabolism and water loss are tightly correlated, suggesting that permeability is progressively increased to support higher metabolic rates. This effect can be induced experimentally by external hypoxia. External manipulation of relative humidity (RH) also alters eggshell permeability—high RH results in high-permeability eggshells and low RH in low-permeability eggshells. This pattern suggests that eggs do not simply attempt always to conserve water. Rather, they appear to increase permeability to dump water in humid conditions. Recent experiments in my lab have shown that water loss is a prerequisite for normal air filling of the pharate 1st instar tracheal system. Water loss deforms the eggshell, thereby spring-loading it, and the tension exerted by the spring is used to drive expansion of nucleated air bubbles in the developing tracheae. Together these experiments indicate that the oxygen-tradeoff is real and pressing for eggs of *M. sexta*, that eggs exert control over the tradeoff, and that control over eggshell permeability has functional consequences for multiple aspects of egg developmental biology.

Floral odour patterns and pollinator guilds in a New Zealand alpine plant community

Mascha L Bischoff[1], Andreas Juergens[3], Janice M Lord[1], Alastair W Robertson[2]

[1]Otago University, Dunedin, New Zealand, [2]Massey University, Palmerston North, New Zealand, [3]University of KwaZulu-Natal, Pietermaritzburg, South Africa

The New Zealand alpine flora is thought to be of relatively recent origin and appears to have evolved rapidly under highly changeable conditions. Much of the alpine habitat in New Zealand arose 2-3 million years ago and all of it has been repeatedly altered by extensive glaciation in the Pleistocene. These challenging environmental conditions seem to have provided unusual opportunities for plant evolution in response to a novel, isolated, and always changing environment. The story of New Zealand alpine plants is a story of success due to processes of adaptive radiation, interspecific hybridisation and recombination, and despecialisation of pollination systems. Historically it has been assumed that pollinator services in alpine New Zealand are imprecise, that plants are therefore often self-pollinating, and there is little pollinator specialisation amongst the pollinator-dependent species. However, the pollinator dependence of the alpine flora and the patterns of insect visitation are largely unknown and so the assumptions remain untested.

In general, the New Zealand alpine flower colours are rather uniform and the morphology simple and unspecialised so the plants appear to offer little in the way of visual cues to allow pollinator discrimination. However, many of the plants emit a noticeable scent. We surveyed floral odours for a total of 18 plant species using GC/MS and observed flower visitor spectra for each plant species. Here we present patterns of connectance between flowers and their insect visitors and test the idea that these might be created by patterns of floral odour advertisement acting at a community level.

The pollinator crisis: native bees in native habitats and agricultural landscapes

Sujaya Rao

Oregon State University, Corvallis, United States

Globally, biodiversity in native bee pollinators is threatened. Losses have been ascribed to several human-related activities such as habitat destruction and fragmentation, improper pesticide use, diseases, and competition with introduced species. In this symposium, we address the situation covering a range of species from bumble bees to stingless bees, and present case histories that address both new concerns and conservation practices for arresting further declines.

Morphogenesis in insect extraembryonic development

Kristen Panfilio

Department of Zoology, University of Cambridge, Cambridge, United Kingdom

Introduction: Almost all hemimetabolous insects undergo katatrepsis, a repositioning of the embryo in the egg by extraembryonic membranes. The *zen* gene has been implicated in effecting katatrepsis in the milkweed bug *Oncopeltus fasciatus*. However, the precise morphogenetic defect resulting from *zen* transcript depletion has been uncertain in this and in other species.

Methods: The dynamics of katatrepsis in wild type and *zen*-depleted (pRNAi) *Oncopeltus* embryos were analyzed from time-lapse movie data, supplemented by analysis of fixed samples.

Results: In *zen*-depleted embryos, preparatory tissue reorganization occurs but katatrepsis does not ensue. There is an increase in egg activity prior to the katatrepsis stage. Wild type activity is a quasi-periodic 'bouncing' movement that leads directly to extraembryonic membrane rupture, which is the initiation of katatrepsis. A similar phenomenon occurs in *zen*-depleted embryos, but it is delayed, reduced in amplitude, and ultimately subsides without membrane rupture.

Conclusions: These investigations identify a single point of failure in katatrepsis after depletion of *Oncopeltus zen*. The delay in activity suggests that there is a window of opportunity for membrane rupture. The reduced amplitude of activity corroborates a role for *zen* in membrane contraction. The lack of epithelial rupture supports a role for *zen* in alteration of intercellular structural integrity. Overall, *Oncopeltus zen* seems to have a highly specific role in morphogenesis at mid embryogenesis. Functional studies in other insect species suggest that this may reflect the ancestral role of *zen*, which implies that Zen function has changed in the holometabolous insect lineage.

Estimation of insect migration trajectories with flight parameters measured by Insect Monitoring Radar

Haikou Wang[1], V Alistair Drake[2]

[1]Australian Plague Locust Commission, Australian Government Department of Agriculture, Fisheries and Forestry, GPO Box 858, Canberra, ACT 2601, Australia, [2]School of Physical, Environmental and Mathematical Sciences, UNSW@ADFA, Australian Defence Force Academy, Canberra, ACT 2600, Australia

Introduction: Meteorological trajectory models have been widely used to simulate migration pathways of windborne insects, based on the assumption that migrating insects flow like air particles in the wind field. However, radar observations have revealed that migrating insects flap their wings actively during flight and many macro-insects demonstrate a capacity for orientation. Automated insect monitoring radars (IMRs), which can measure the ground speed, displacement direction and body alignment of insects flying through their vertically-pointing beam, have revealed mutual orientation by Australian plague locusts, *Chortoicetes terminifera* (Walker), during nocturnal migration. Therefore, to estimate insect migration pathways more accurately, the flight behaviours of the migrants must be taken into account.

Methods: Trajectories are calculated by three methods. First, simulated upper winds are linearly interpolated from the 6-hourly analysis grid output of the Australian Bureau of Meteorology's Limited Area Prediction System (LAPS). Second, the flight parameters of *C. terminifera* measured by the IMR are used alone to calculate trajectories for the nights when collective orientation is observed, on the assumption that migrating locusts some distance away made the same course changes, at the same time, as those flying over the IMR. Third, the simulated winds are used to estimate the airspeed and cross-wind angle of plague locusts passing over the IMR, and these are then combined vectorially with simulated winds to calculate modified wind trajectories. Python script language is used to program trajectory models and ArcGIS is used to plot the results.

Results: The plague locusts usually migrate under the influence of tropical troughs in eastern Australia. They migrate northwards with right-shifted headings but southwards with left-shifted headings. The comparison study shows that trajectories estimated using these three methods are significantly different in both direction and distance.

Conclusions: Insect flight behaviours affect the migration pathway significantly. To locate the source and destination of migrant insects, the orientation behaviour must be included along with the wind in the trajectory model.

Non-target impact of the use of fruit fly (Tephritidae) male lures and Biolure

Luc Leblanc[1], Daniel Rubinoff[1], Roger Vargas[2]

[1]University of Hawaii, Department of Plant and Environmental Protection Sciences, Honolulu, Hawaii, United States, [2]United States Department of Agriculture - Pacific Basin Agricultural Research Center, Hilo, Hawaii, United States

Introduction: Male lures and female attractants are widely used for fruit fly monitoring and more recently for their control as environmentally-friendly alternatives to insecticide cover sprays. Their potential non-target attraction impact should however also be minimal.

Methods: Traps baited with *Bactrocera* male lures (Cue-lure, methyl eugenol) and the Mediterannean fly attractant Biolure were maintained and emptied weekly in native and non-native forest and in orchards on the Hawaiian Islands. All non-target insects were counted and identified to species. Attraction to lure or to decaying fruit flies accumulating in traps was assessed by comparing lure trap catches with catches of unbaited control traps and traps artificially baited with decaying fruit flies.

Results: Cue-lure did not attract non-targets and methyl eugenol attracted limited numbers of non-native flower-associated insects and native plant bugs. Large numbers of saprophagous non-targets were however attracted whenever dead trapped fruit flies accumulated inside traps. These same non-target species were also attracted in traps baited with Biolure and with decaying fruit flies. Beneficial predatory or parasitoid insects were not attracted to lures or decaying flies. Numerous native species, especially Drosophilidae, were captured in traps set up in native forest, but not in orchards.

Conclusions: Most published past records of male lure attraction was actually attraction to decaying fruit flies caught by the lure. Non-target impact is minimal if traps are distant from native forest.

Effects of clearfell harvest area on beetle biodiversity

Stephen Pawson[1], Raphael Didham[2], Eckehard Brockerhoff[1]

[1]Scion, Christchurch, New Zealand, [2]University of Canterbury, Christchurch, New Zealand

Clearfelling remains the predominant forest harvesting model in most countries despite criticism of it environmental and aesthetic impacts. Comprehensive studies have previously compared the relative impacts of clearfelling and alternative harvesting systems, however, the impacts of clearfell harvest area remain largely unstudied. In this trial, the first large scale experimental trial, of different harvest areas (0.01 ha to 500 ha), we sampled all Coleoptera by pitfalling in transects between recent clearfells and adjacent mature *Pinus radiata* plantation stands.

Multivariate analyses of the 350 species sampled indicate that beetle assemblages were most strongly defined by the clearfell – mature-forest interface. Species composition was independent of clearfell size, once harvest area exceeded 0.05 ha, and there was no indication of a clearfell harvest area threshold response in beetle biodiversity. However, an edge mediated threshold response occurred in the community structure of non-harvested stands adjacent to clearfells. Beetle community composition at 125 m into forest stands changed significantly when neighbouring harvest areas exceeded a threshold area between 0.5 and 5 ha.

The changes in beetle composition we observed, in a temperate exotic monoculture plantation, would question the merit of prescriptive size restrictions for clearfelling; as minimum economically viable harvest areas have the same impact on beetle communities as larger harvest areas. Instead, harvesting strategies should focus on landscape-scale planning to ensure areas of core forest habitat and forest dispersal pathways are maintained whilst avoiding potential edge effects from regenerating clearfells.

Evaluation of a pheromone: Lure trap for monitoring distribution of the red palm weevil population in Egypt

Sadek Salem, Atef Abdel-Razek, Hussein Salama

National Research Centre, Cairo, Egypt

Introduction: The red palm weevil (RPM), *Rhynchophorus ferrugineus* (Olivier) is known as the most destructive insect pest of palm trees in the Middle East. As an internal tissue borer, detecting infested palms become extremely difficult in the early stage of attack.

Methods: A specially designed 5 liter plastic bucket with lid was used and 10 to 12 round holes (2–3 cm diameter) were made in each bucket at 10 cm height from its base for weevils entrance. Lures included general attractants for red palm weevil such as slices of sugarcane, slices of palm trunk, yeast, shredded date palm and Lannate (0.1%). The lid of the bucket has two holes: the first used to hang two bottles each containing 20 cm^3 of ethyl acetate. The second used to hang the pheromone capsule.

Results: The traps used in this study showed significant increase in weevils captured during the first year compared with that for the second year. Also, our investigations of captured weevils showed that the ratio of females to males captured was 1.07: 1.00 and the ratio of gravid females to non gravid ones was 2.24: 1.00 with maximum increase during May 2003. This indicating that they have been already mated before entering the traps. The synergistic effects of temperature and humidity with pheromone traps in capturing the red palm weevils were also recorded with more significant effects for the temperature regimes than the humidity.

Conclusions: The results recommended the use of trapping of red palm weevils in IPM strategies for control of red palm weevil, because of their benefit in reducing the population build up of red palm weevil in the field.

Understanding the factors that influence the geographical expansion of *Cactoblastis cactorum* in non-native habitats

Stephanie Bloem[1], Kenneth Bloem[2], Stephen Hight[3], James Carpenter[4], Silvia Dorn[5], Mark Sarvary[5], Helmuth Zimmermann[6], Joel Floyd[7]

[1]USDA-APHIS-PPQ-CPHST-Plant Epidemiology and Risk Analysis Laboratory, Raleigh, NC, United States, [2]USDA-APHIS-PPQ-CPHST, Raleigh, NC, United States, [3]USDA-ARS, Center for Medical, Agricultural, and Veterinary Entomology, Tallahassee, FL, United States, [4]USDA-ARS, Crop Protection Management and Research Unit, Tifton, GA, United States, [5]Institute of Plant Sciences, Applied Entomology, ETH Zurich, Switzerland, [6]HZ and Associates, Pretoria, South Africa, [7]USDA-APHIS-PPQ-EDP, Riverdale, MD, United States

Introduction: *Cactoblastis cactorum* is renowned for its role as a highly successful biological control agent for weedy Opuntia cactus, but more recently it is notorious as an invasive pest in North America. Interestingly, historical accounts of the geographical expansion of *C. cactorum* when deployed as a biological control agent suggest that dispersal ability is rather limited compared to the more robust dispersal documented for *C. cactorum* as a pest in the southeastern States of the USA and some offshore islands near Yucatan, Mexico.

Methods: Laboratory bioassays using a flight mill were used to examine the influence of age, gender, mating status, body size and seasonal generation on diel flight pattern and flight performance of adults. Direct evidence of dispersal was studied using release/recapture techniques.

Results: Both laboratory bioassays from ETH Zurich and field release/recapture trials in the USA and Mexico detected heterogeneity in the population with respect to dispersal behavior and ability, and measured differences associated with various parameters.

Conclusions: The factors that influence the geographical expansion of *C. cactorum* in non-native habitats are numerous and provide opportunity for complex interactions. Laboratory bioassays and field trials have provided some insights into this complicated area of study and have demonstrated the value of *C. cactorum* as a model system for future studies. This information is then used to design better control and management methods towards the insects' eradication and delimitation that would prevent its further invasion to sensitive cactus areas in the USA and Mexico.

Biology and conservation ecology of selected saproxylic beetles in Tasmania's southern forests

Belinda Yaxley[1], Simon Grove[2], Richardson Alastair[1], Simon Wotherspoon[1]

[1]University of Tasmania, Hobart, Tasmania, Australia, [2]Forestry Tasmania, Hobart, Tasmania, Australia

Studies worldwide have demonstrated that dead wood is a key habitat for forest insects. In Europe, many saproxylic species are red-listed, due to long-term changes in dead wood availability brought about by intensive forest management. Once species become this scarce, it is difficult to find practical and affordable ways to manage production forests that still allow for their recovery. In hindsight, it would have been preferable to have conducted forestry in a way that didn't threaten them in the first place. The philosophy behind the present study is that in Tasmania's commercially important lowland wet eucalypt forests, forestry is still at an early stage of intensification, presenting an opportunity to use a scientific approach to developing management regimes that not only generate forest products but also cater for biodiversity. The study involves developing an understanding of the ecology of several key saproxylic beetle species, and of their relationships with dead wood and with forest management. Multiple study sites have been selected to cover the range of forest ages and types present. In each study site, a suite of dead wood attributes has been measured. These are being compared with site-level and log-level data on populations and microhabitat associations of these beetle species. Findings show that particular species have very narrow habitat preferences, which will make them vulnerable to forestry in the absence of mitigation measures. The intention is to use these findings to help derive forest management approaches that will meet the twin needs of commercial forestry and conservation.

Will climate change alter the relationship between predator biodiversity and herbivore suppression?

William Snyder

Washington State University, Pullman, WA, United States

The dominant trend across terrestrial communities is for herbivore suppression to strengthen with greater predator biodiversity. However, widespread ecological disruption is likely to be triggered by global climate change, with complex implications for biodiversity-biocontrol relationships. In the state of Washington (USA), it is predicted that warming temperatures will foster invasion of agroecosystems by new, exotic arthropod and pathogen species. These new arrivals would change the species composition of natural enemy communities. We can use the extensive literature documenting the ecological impacts of previous predator invasions to predict likely effects of new invaders. Often, invasive predators displace similar native predator species, achieving far higher densities than natives and thus exerting far stronger impacts on prey. Thus, following successful invasion we would predict that species identity (sampling) effects will replace complementarity as the dominant factor underlying predator biodiversity effects. Because invaders are often dominant intraguild predators, negative predator-predator interactions may further dampen any benefits of predator diversity for herbivore suppression. Unlike predators, in the biodiversity-ecosystem functioning literature pathogens have rarely been considered as a component of natural enemy diversity. This relative dearth of information makes it difficult to predict the outcome(s) of invasion by new insect pathogens. However, because of clear ecological differences between predators and pathogens, these two natural enemy guilds might be particularly likely to complement one another. In summary, changing distributions of predator and pathogen species may form a key impact of global climate change, altering the relationship between biodiversity and biological control in many agroecosystems.

Evolution of the gustatory receptor (Gr) family in mosquitoes

Hugh Robertson, Lauren Kent

University of Illinois, Urbana, Illinois, United States

Introduction: Olfaction and gustation in insects is mediated by the insect chemoreceptor superfamily of proteins. The gustatory receptor or Gr family comprises most of the diversity of this superfamily, containing both gustatory and olfactory receptors. Mosquitoes are major vectors of diseases worldwide and are known to employ chemical cues in host-seeking behavior and might employ them in other behaviors.

Methods: We manually constructed gene models for the Grs in *Anopheles gambiae*, *Aedes aegypti*, and *Culex pipiens*, using the publicly available genome sequences, and analyzed their phylogenetic relationships using corrected distance methods.

Results: *An. gambiae* has 60 Gr genes encoding 89 Grs, through alternative splicing of the first long exon in four genes. *Ae. aegypti* has 79 Gr genes potentially encoding 114 Grs, however 19 of these are pseudogenic, so the Gr repertoire of this species is around 95 proteins. *C. pipiens* has 77 Gr genes potentially encoding 136 proteins, but 13 are pseudogenic, leaving 123 functional proteins. Phylogenetic analysis reveals the expected orthologous conservation of the three carbon dioxide receptors. Mosquitoes have nine sugar receptor lineages, with differential loss and duplication in each genus. There are several other simple conserved orthologs, some orthologs have been lost from one or more genus, and many gene lineages have duplicated in one or more genus. The alternatively-spliced loci show particular expansion in Aedes and Culex.

Conclusion: Although the expansion of the Gr family in culicines is enigmatic, these results provide the groundwork for functional work on the mosquito Grs, and expression studies are underway in *Anopheles gambiae.*

Biodiversity and host relationships of *Caenocholax fenyesi* sensu lato

Alexander Hayward, Dino McMahon, Jeyaraney Kathirithamby

University of Oxford, Oxford, United Kingdom

Male and female members of the strepsipteran species *Caenocholax fenyesi* have separate host preferences, with males parasitic in ants (Formicidae) and females parasitic in sword-tail crickets (Trigonidiinae). The species is Neotropical in distribution, with a large range extending from the southern USA to northern Argentina. Fossil specimens found in Baltic and Dominican amber suggest that the species has undergone little morphological change over the last 30-40 million years. In this study we investigated the molecular diversity and host range of the species using specimens gathered from across its range. Analysis of mitochondrial COI and nuclear 18S sequences revealed a high degree of variation indicative of a set of cryptic species, and molecular clock estimates suggest a relatively ancient date of divergence for the lineages. Male *C. fenyesi* was sampled from three different subfamilies of ant, with the same lineage sometimes found to parasitize different subfamilies at the same site.

Metamorphosis to the postgenomic era: RNA interference of neuropeptidergic systems in the red flour beetle *Tribolium castaneum*

Yoonseong Park, Richard Beeman

[1]Kansas State University, Manhattan, Kansas, United States, [2]USDA-ARS-GMPRC, Manhattan, Kansas, United States

The study of insect neuropeptides has experienced an immense change in the last decade with the development of whole-genome DNA sequencing technology. During the current postgenomics phase of red flour beetle research, our efforts are directed mainly towards the assignment of functions of neuropeptides and towards an understanding of evolutionary trends. RNA interference (RNAi) in *Tribolium* has become a versatile tool to investigate the functions of neuropeptidergic systems. The injection of dsRNA into the body cavity of postembryonic stages elicits systemic RNAi affecting tissues throughout the entire body, including target genes expressed in the central nervous system, such as neuropeptide and their receptors. We have been interested in the functions of neuropeptidergic systems involved in the control of water and ion regulation, and in insect ecdysis behavior. For example, RNAi of ecdysis triggering hormone and one of its receptor variants resulted in lethal deficiency in pre-ecdysis and ecdysis behavior. Postembryonic RNAi of ion transport peptide, which is known to be involved in water resorption in the hindgut of locust, resulted in mummification and death. We find that analysis of hypomorphic or amorphic phenotypes following injections of double stranded RNA provides critical information needed to understand the role(s) of particular neuropeptidergic signals in the biology of the organism.

Genetic differentiation and outbreak species in agroecosystems

Raul Medina

Texas A&M University, College Station, United States

Empirical evidence shows that morphologically cryptic genetic differentiation is more frequent than previously thought in plant feeding and parasitic insects. However, although genetic differentiation has been demonstrated in feral herbivorous insects, we still ignore under which conditions we can predict this differentiation to occur. If this phenomenon is as common in ago-ecosystems as it seems to be in feral habitats, then we need to consider it when designing IPM strategies. It has been postulated that morphologically cryptic genetic differentiation in predators and parasitoids may be crucial in determining the success or failure of biocontrol programs. For example, parasitoid populations that oviposit on the same herbivorous host species may differ genetically when their hosts are attacked on different plant species. Thus, introduced parasitoid populations associated with the same insect host but on different plant species might be ecologically and reproductively isolated. Similarly, in a transgenic crop scenario, if individuals from the same pest species are reproductively isolated when in association with crops or with adjacent feral vegetation, uncultivated plants cannot be considered as refuges to dilute resistance genes to transgenic plants. The purpose of this presentation is to motivate future researchers to gather information on HAD on their study systems so we can accumulate enough case studies to further our understanding of the relevance of evolutionary forces in agro-ecosystems.

The honey bee *Apis mellifera* genome: genes shared by bees and humans, but lost from Drosophila

Hugh Robertson

University of Illinois, Urbana, Illinois, United States

Introduction: An EST project on the honey bee brain was published in 2002, and a high-quality draft sequence of the honey bee genome in 2006. One interesting aspect of these two sequence resources is the presence of hundreds of genes that bees have that are highly conserved throughout most of animal evolution, including in our own genome, but are missing from Drosophila.

Methods: Examination of the honey bee brain ESTs revealed ~100 genes/proteins with strong matches to human proteins, but not Drosophila. These genes were examined in the draft genome assembly to provide full-length proteins for phylogenetic analysis. All available arthropod genomes were examined for these genes, and a few have been worked up extensively.

Results: Among these 100 genes are several known to be missing from Drosophila, such as telomerase and DNA methylase 1 and 3. Others include pteropsin and one of the cryptochromes. Examination of the pattern of loss on the phylogenetic tree of arthropods indicates that gene loss is mostly a background process at a reasonably steady rate, although there might be an acceleration in the Diptera.

Conclusion: Major aspects of insect and indeed general animal biology have been lost from the central insect molecular genetic model *Drosophila melanogaster*. In many cases these have been replaced or compensated for in some way in Drosophila flies, but others might underly significant differences between Drosophila and other insects.

Social evolution in paper wasps: natural history, genomics, and beyond

James H. Hunt

North Carolina State University, Raleigh, North Carolina, United States

Sociality in insects cannot be understood by a narrow focus on the origin and behavior of workers. For a clear understanding of the social evolutionary process, one must also know the origin and behavior of gynes. In paper wasps (*Polistes*), workers and gynes as sibling offspring are differentiated during larval development. One developmental pathway leads to hopeful reproductives trapped in a worker role through a combination of colony context and their own physiology. Another developmental pathway leads to future reproductives in a physiological state of diapause who, through their behavior, lead to the colony demise. Selection acts at the level of the colony to favor traits that engender this pattern. Recent genomics-based research provides gene expression data that constitute one of multiple lines of evidence that now are converging in strong support of the developmental components of this pattern. Those genomics data are presented and placed in evolutionary context. The evolution of sociality in paper wasps now can be clearly seen, and it points the way to understanding insect social evolution generally.

STEPP: spatio-temporal population probability models for delimiting pest incursions and monitoring eradication success, and a demonstration using painted apple moth

John M. Kean

AgResearch, Lincoln, New Zealand

Introduction: Successful incursion response relies on accurately delimiting the pest population, application of effective eradication treatments, and determining when the likelihood of continued pest presence becomes acceptably small. Here, I propose that spatio-temporal population probability (STEPP) models, which combine conventional population models with statistical probability approaches across space and time, can inform delimitation and eradication monitoring. A STEPP approach is demonstrated using painted apple moth (*Teia anartoides*) in Auckland, New Zealand.

Methods: A population model for daily temperature-determined male production was used in conjunction with spatially-explicit pheromone trap locations and attraction radii to determine the daily probability of detecting a wild population at a particular location. Over time, these probabilities multiply up to decrease the likelihood of presence given ongoing lack of detection. The model was parameterised for painted apple moth using data collected during the Auckland incursion response, allowing spatio-temporal risk maps to be produced.

Results: The model suggested that trapping in winter yields relatively little useful information on painted apple moth presence. Eradication was likely to have been successful in the main infestation areas by mid 2005, with subsequent catches likely to represent further small incursions, as corroborated by molecular evidence. It was plausible that a wild population was present in the Otahuhu area in 2005 but very unlikely that it remained by the end of 2006.

Conclusions: STEPP models can assist decision-making during incursion response, but depend on quantification of sampling efficacy and good data management. They show particular potential for use with future automated trapping systems.

Bombyx neuropeptide GPCR transcriptome reveals authentic neuroendocrine network

Naoki Yamanaka[1], Dusan Zitnan[2], Yu Kaneko[3], Kiyoshi Hiruma[3], Yoshiaki Tanaka[4], Tetsuro Shinoda[4], Hiroshi Kataoka[1]

[1]The University of Tokyo, Chiba, Japan, [2]Slovak Academy of Sciences, Bratislava, Slovakia, [3]Hirosaki University, Aomori, Japan, [4]National Institute of Agrobiological Sciences, Ibaraki, Japan

Background: Neuropeptides are among the most important class of molecules involved in diverse aspects of life history in metazoans. Insects have been one of the ideal model systems to investigate neuropeptide circuitry, but the systematic analysis of their signaling has been hampered by the small size of the best-studied model insect, *Drosophila melanogaster*.

Results: In this study, G protein-coupled receptors (GPCRs) for neuropeptides were comprehensively cloned and systematic expression analyses were performed in the large lepidopteran insect, *Bombyx mori*. In order to unequivocally demonstrate the effectiveness of this approach, we chose regulatory pathways of the juvenile hormone (JH) biosynthesis as a target of our detailed analysis, and characterized the long-sought allatotropin (AT) receptor. JH plays the pivotal role in many physiological events in insects, and AT is thought to stimulate JH biosynthesis in the corpora allata (CA). Surprisingly, however, the AT receptor was predominantly expressed not in the CA but in the corpora cardiaca (CC), an organ closely located to the CA. Indeed, by using reverse-physiological approach, we purified and characterized novel allatoregulatory peptides produced in the AT receptor-expressing CC cells, which may mediate indirect AT activity on the CA.

Conclusions: To our knowledge, this is the first report of the comprehensive cloning of neuropeptide GPCRs conducted in any organism. All of the above findings confirm the effectiveness of our systematic analyses, providing a solid framework for the combinational bioinformatic, molecular, biochemical and physiological approaches to tackle unsolved problems in neuropeptide research.

This work was supported by PROBRAIN.

The insect chemoreceptor superfamily

Hugh Robertson

University of Illinois, Urbana, Illinois, United States

Introduction: The insect chemoreceptor superfamily mediates the olfactory and gustatory senses of insects. It has now been described from several insects representing diverse orders. The evolutionary origins of these chemoreceptors remain unclear.

Methods: We manually annotated the superfamily from the available diverse insect genomes, as well as the crustacean *Daphnia pulex* and the tick *Ixodes scapularis*. Extensive searches for distant relatives in the Caenorhabditis nematode genomes reveals related receptors, known as GURs and SRRs. Membrane topology analysis support the assertion of the Vosshall laboratory that these are not GPCRs.

Results: The odorant receptor or Or family is a relatively recent expansion of one gene lineage within the superfamily. The remainder of the superfamily constitutes the so-called gustatory receptors or Grs, although some of these are olfactory in function, e.g. the carbon dioxide receptors. Amongst the Grs, the carbon dioxide receptors are the most conserved, however all available genomes below Tribolium on the phylogenetic tree do not have this gene lineage. The sugar receptors also show considerable conservation, but differential expansion in various insects. Most other Grs are species-specific lineages.

Conclusion: With a few exceptions, the insect chemoreceptor superfamily shows primarily lineage-specific expansions expected of ecologically-relevant genes when compared across orders of insects and classes of arthropods. Nevertheless, distant relatives are recognizable in nematodes, indicating that this novel superfamily of environmental sensors predates the Ecdysozoa.

Twelve years after the adoption of Bt maize in the U. S.: Impacts of landscape level suppression of European corn borer in several midwestern states

William Hutchison[1], Roger Moon[1], Tim Leslie[2], Shelby Fleischer[2], Mark Abrahamson[3], Krista Hamilton[4], Kevin Steffey[5], Mike Gray[5], Von Kaster[6], Rick Hellmich[7], Robert Wright[8], Thomas Hunt[8], Paul Mitchell[9]

[1]University of Minnesota, St. Paul, MN, United States, [2]Pennsylvania State Univ., State College, PA, United States, [3]Minn. Dept. of Agric., St. Paul, MN, United States, [4]Wisconsin Dept. of Agric., Madison, WI, United States, [5]University of Illinois, Urbana, IL, United States, [6]Syngenta Corp., Slater, IA, United States, [7]USDA-ARS, Ames, IA, United States, [8]University of Nebraska, Lincoln, NE, United States, [9]University of Wisconsin, Madison, WI, United States

Transgenic maize, transformed to express various Cry toxins from the bacterium, *Bacillus thuringiensis*, has been widely adopted by U.S. growers, particularly in the Midwestern states. Statewide adoption rates now exceed 55% in several states. Since commercialization in 1996, populations of the European corn borer (ECB), (*Ostrinia nubilalis*), have gradually declined. Although ECB has a broad host range, we hypothesized that the species could be affected by the vast area of Bt maize in the Midwest landscape (e.g., 7 million ha in 4 major states). We present evidence from autumn larval surveys (1943-2007) and moth flight data (light traps; since the 1980s), to examine the hypothesis of a regional suppression effect due to Bt maize over the past 12 years. Larval survey data for Minnesota, Illinois and Wisconsin indicated a 6-7 year cycle (periodicity) in ECB dynamics. We therefore examined the relationship between a 7-year moving average of fall larval density as a function of the annual and cumulative increase in proportional Bt maize use in each state, from 1996 to 2007. For Illinois and Wisconsin a significant linear reduction in larval populations was observed, relative to Bt maize use, with R^2 = 0.69 and 0.83, respectively. For Minnesota, with a higher cumulative Bt maize use rate, we found a non-linear significant reduction (R^2 = 0.83). Similar reductions were observed for annual moth flights in relation to Bt maize use. The impact of the landscape level suppression of ECB is discussed within the context of cyclical population dynamics and IPM implications.

Peptidergic and monoaminergic mechanisms regulating circadian rhythms in insects

Makio Takeda, Susumu Hiragaki, Qi-Miao Shao, Le Thi Dieu Trang, Hana Sehadova

Kobe University, Kobe, Hyogo, Japan

Recently, the molecular mechanism underlying circadian rhythm has been investigated in some model insects such as *Drosophila melanogaster,* cockroaches, and silkmoths. About a dozen of genes have been found in *D. melanogaster* .They form interlocked negative feedback loops. Homologous genes have been found in other insects but with some unique features to each species. The output pathways to regulate peripheral rhythms seem to vary. Unlike central cog mechanisms, the output pathway has not been worked out even in *D. melanogaster.* A convincing factor regulating this pathway is PDF, pigment dispersing factor in *D. melanogaster.* Since PDF-ir resides in the putative circadian pacemaker cells that express most of the clock gene products and that using mutants causing different degrees of optic lobe deformation, the number of PDF-expressing neurons and the strength of rhythmicity have a strong correlation. Also, a *pdf* mutant lost the rhythmicity. However, it is not likely that all output pathways are PDF-regulated, since *lark* mutant produces abnormal eclosion rhythms but locomotor activity rhythm is intact and pdf receptor is not expressed in neurosecretory cells.

Although surgical operations point to the accessory medulla region of the cockroach as the most critical locus to keep normal circadian rhythms, the IHCinvestigations have demonstrated that clock proteins-like antigens are not restricted to a particular part of the brain. We will show data indicating not only PDF but other factors are involved in circadian regulation. The classical scheme that the circadian pacemaker of the orthopteroid insects is located at the accessory medulla using PDF as an output messenger will be reappraised by focussing other factors, since this site expresses several other peptide-like immunochemical reactivities, such as BPP/NPF, glicentin, PHI, gastrin/CCK in *P. americana*, while some peptides like ATH, ASH and GABA caused phase shifts in *Leucopheae*. Melatonin and 5HT also are important in regulating circadian system in cockroaches and moths. There are several NAT genes but some have E-box in the regulatory region, and this is the access point of clock core mechanism to output pathway. I will show the neuroanatomical structure of peptides and indolamine mechanisms regulating circadian system and give its functional implications.

Building Sanitary/Phytosanitary (SPS) capacity in East Africa

Karl Suiter[1], Lloyd Garcia[2], Ronald Stinner[1]

[1]North Carolina State University, Raleigh, NC, United States, [2]USAID East Africa, Nairobi, Kenya

The East African Phytosanitary Information Committee (EAPIC) is a regional effort between Kenya, Tanzania, Uganda and Zambia to develop official country-specific and regional pest reporting tools in support of phytosanitary activities in East Africa. Through the efforts of EAPIC, a regional pest list encompassing species of concern found throughout all East African member countries has been developed. Additionally, the four EAPIC countries have deployed the Pest Information Management System (PIMS), an internet-based plant pest reporting database that supports SPS and pest reporting activities.

The PIMS software provides a mechanism for countries to create official country-specific pest lists, document pest status, generate distribution maps and archive related documents. This system will facilitate trade and permit trading partners the ability to harmonize border inspection protocols across the region. The outcome of these activities will in turn promote an increased flow of agricultural commodities across member borders and serve to guide future SPS activities and infrastructure building within the region.

The ability to share information relating to pest status among trading partners in the region will serve to satisfy international reporting obligations of contracting parties to the Food and Agriculture Organization's International Plant Protection Convention. Plans are underway to automate reporting of pest status to the IPP portal from the PIMS software through the creation of a dynamic data sharing link between these two systems.

Appropriate floral resources enhance biocontrol and obviate insecticide use against a major vineyard pest.

Marco Jacometti, Samantha Scarratt, Steve Wratten

Lincoln University, Canterbury, New Zealand

Introduction: Leafrollers (Lepidoptera: Tortricidae) are a major pest in New Zealand vineyards. They damage grapes directly and facilitate botrytis bunch rot, one of the world's most important vineyard diseases. Leafrollers are usually managed with insecticides, but these can become sub-optimal as pesticide resistance increases and international markets demand wine with low or no residues. Alternative methods for managing leafrollers are being sought, including conservation biological control techniques.

Methods: In this research, buckwheat (*Fagopyrum esculentum*) was sown in the inter-vine row space in two commercial vineyards in New Zealand.

Results: The nectar provided increased the efficacy of *Dolichogenidea tasmanica*, a parasitoid of leafroller caterpillars and parasitism rates increased to five times those in the control at harvest. As a result, the percentage of bunches infested with leafroller caterpillars reduced from 7% to 2%, the latter being below the economic threshold of 5% of bunches infested.

Conclusions: This research demonstrates how deploying appropriate floral resources in vineyards can obviate pesticide use, reduce variable costs and provide marketing advantages. The latter have been demonstrated through contingent valuation and other economics techniques, leading to the marketing of eco-tourism in working vineyard landscapes. This research is currently being adopted by commercial vineyards throughout New Zealand.

The role of the matrix in shaping ground-dwelling arthropod diversity and community composition of native remnants embedded within a pastoral and blue gum (*Eucalyptus globulus* Labill) plantation landscape

Chela Powell, Peter Ades, Nick Collett, Charlma Phillips

[1]*The University of Melbourne, Victoria, Australia,* [2]*Department of Primary Industries and Resources of South Australia, South Australia, Australia*

Introduction: Detailed information regarding the effects of monoculture plantation establishment on native plants and animals is limited and has usually concentrated on exotic soft wood plantations and higher level vertebrates such as marsupials and birds. The principal aim of this study was to investigate the role of the matrix in shaping epigeal arthropod diversity and community composition of native vegetation remnants embedded within a pastoral and blue gum (*Eucalyptus globulus.* Labill) plantation landscape. This study focuses on how the relatively recent change in the land use (from pasture to blue gum plantation) in the matrix surrounding native vegetation remnants affects local remnant arthropod communities.

Methods: Arthropods were sampled using both pitfall and flight intercept traps established within remnants surrounded by blue gum plantation (planted in 2000-2002), pasture and within continuous native forest in the Green Triangle region of south-east South Australia, and south-west Victoria. Pitfall sampling was carried out twice each season for 7 days over a 12 month period, while flight intercept trap sampling was conducted twice (summer and winter) during the study. All invertebrates were identified to ordinal level, while Coleopterans were identified to family level, and the 3 most abundant coleopteran families were identified to species level.

Results: Sampling results will presented and analysed using multiple regression through the statistical package SAS ©. The outcomes of this study will be used to aid in the development of management strategies aimed at maintaining and enhancing arthropod biodiversity in the Green Triangle region. Remnants of varying sizes and vegetation quality will be compared for their ability to support arthropod communities similar to that of regional contiguous native woodland, with the specific aim of identifying those remnants that should be targeted for conservation management by plantation owners.

The irresistible allure of an ant-eating assassin

Matthew Bulbert[1], Marie Herberstein[1], Gerasimos Cassis[2]

[1]Macquarie University, Sydney, NSW, Australia, [2]University of NSW, Sydney, NSW, Australia

Introduction: Members of the subfamily Holoptilinae (Insecta: Hemiptera: Reduviidae) are reputed to be obligate myrmecophages. Early accounts of two species suggest the bug uses an elaborate predatory tactic to deceive ants. The tactic culminates in ants compelled to interact with an extraordinary morphological adaptation known as the trichome. Recent characterisation of this structure revealed a complex arrangement of specialised hairs, unicellular glands and exaggerated cuticular modifications. My study aims to investigate the nature of this ant-true bug interaction using an Australian species of Holoptiline known as *Ptilocnemus lemur*.

Methods: The predatory behaviour of *P.lemur* was observed in the field and the laboratory. Chemical attractiveness of *P.lemur* towards foraging ants was experimentally tested using a Y-maze olfactometer; and the characterisation of chemicals, emitted at various behavioural states, was attempted using GC-MS and solid phase microextraction.

Results: *P.lemur* adults were regularly observed taking *Myrmecia pilosula;* an aggressive solitary forager. As expected, *P.lemur* presented the trichome to visiting ants by rising up on their hind legs. Ant-trichome interaction resulted in predatory success. However, unlike other species of Holoptilinae, it appears *P.lemur* initially attracts the ants' attention by waving its elaborately adorned tibia. Y-maze experiments, where visual signals were omitted, showed that foraging *M.pilosula* were attracted to adult *P.lemur* irrespective of sex; but only when *P.lemur* had entered its 'attacking' state. The chemical profile of the bug also varied accordingly.

Conclusions: *P.lemur* can be added to an incredibly small list of animals that lure and ultimately deceive prey through a multimodal signalling system.

Finishing the sequence of the *Bombyx mori* genome

Qingyou Xia[1], Kazuei Mita[2]

[1]Southwest University, Chongqing, China, [2]National Institute of Agrobiological Sciences, Tsukuba, Japan

We present a complete silkworm genome sequence obtained by the integration of data from two WGS projects performed independently in 2004. In the new assembly, sequence coverage of the merged WGS reads, together with a newly generated fosmid- and BAC-end data, reached 8.48x. The new assembly has the best continuity (> 3.7 Mb in N50 scaffold size, and 15.5 Kb in N50 contig, respectively) among the sequenced insect genomes. Using a high-density SNP linkage map consisting of 1,577 markers, about 87.4% of the scaffold sequences were anchored to all the 28 chromosomes. Comparison between the linkage map and the assembly indicated that both the assembly and the genetic map were reliable for subsequent analyses. The coverage of repeats in the *Bombyx* genome, 44%, is substantially higher than those in other insects, contributing larger genome size of *Bombyx*. *De novo* gene prediction was performed using gene finder BGF by pre-filtering classifiable TEs. It gave a gene count of 16,329. In conclusion, the new genome assembly made available a more precise annotation of the structure and function of the *B. mori* genome. The data presented and analyzed herein can facilitate us to explore evolutionary patterns of insect genomes and will serve as a useful tool for gleaning new insight into genetic, developmental and regulatory events.

BugWise, a programme providing opportunities for the community to work with invertebrates in a meaningful way

Matthew Bulbert, John Gollan, Helen Smith

Australian Museum, Sydney, NSW, Australia

Introduction: Invertebrates are generally undervalued by society and regularly overlooked in biodiversity surveys. *BugWise* was created to address the negative perceptions and the constraints that prevent the wider community from working with invertebrates in a meaningful way. In the process, *BugWise* aimed to involve community in the development of cost-effective and user-friendly reporting tools for interventions such as restoration.

Methods: Workshops were designed to show the link between invertebrates and the lifestyles of humans and to address common misconceptions. Reporting tools and associated resources were created and tested with the direct involvement of the community through both workshop and field activities. The foundations of the tools require the user to identify invertebrate signs or directly measure invertebrate processes.

Results: Volunteers provided feedback that significantly improved usability and accuracy of the resources. Field testing showed applicability of the methods to a wide variety of habitat types. The simplicity of the methods allowed rapid assessment of data quality and training needs. Volunteers gained value from the interaction with museum scientists and a sense of ownership in the products they helped refine. Moreover, participants gained greater appreciation of invertebrate diversity and the importance of the conservation of invertebrates. Appreciation has persisted beyond the workshops through the distribution of the *BugWise* methods through a dedicated website.

Conclusion: The *BugWise* model proved to be successful in developing practical applications through an interdisciplinary partnership of industry stakeholders, community volunteers, ecologists and taxonomists. The tools resulting from the programme alleviate the need for expensive laboratory processing.

Molecular cloning and characterization of *Tret1*-orthologs facilitating trehalose transport in insects

Takahiro Kikawada, Yasushi Kanamori, Ayako Saito, Yuichi Nakahara, Ken-ichi Iwata, Daisuke Tanaka, Kanako Mitsumasu, Masahiko Watanabe, Takashi Okuda

National Institute of Agrobiological Sciences, Tsukuba, Ibaraki, Japan

Introduction: Trehalose is the main hemolymph sugar in insects. Nevertheless, mechanisms of trehalose transport across cellular membrane in insects were unknown. Recently, we cloned a facilitated trehalose transporter, *Tret1*, from the sleeping chironomid, *Polypedilum vanderplanki*. We examined whether *Tret1*-orthologs from which deduced protein possess activity for trehalose transport exist in other insects.

Methods: *Tret1* orthologs were searched on public DNA databases such as FlyBase, AnoBase, BeeBase and SilkBase. Trehalose uptake activity of proteins translated from the obtained orthologs was investigated using *Xenopus* oocyte expression system. Subcellular localization of the deduced proteins was evaluated using the expression of a fusion protein with GFP in the oocyte. Tissue-specific expression pattern of *Tret1*-ortholog in *B. mori* was examined by quantitative RT-PCR (Q-PCR).

Results: *In silico*, candidates for *Tret1*-orthlogs were cloned from *Drosophila melanogaster, Anopheles gambiae, Apis mellifera* and *Bombyx mori*, and designated as *DmTret1, AgTret1, AmTret1* and *BmTret1*, respectively. Interestingly, *D. melanogaster* possesses another paralog for *DmTret1*, so further designated as *DmTret1-1* and *DmTret1-2*. All proteins deduced from these orthologs were localized in the cellular membrane. *Xenopus* oocyte expression system showed that all the orthologous proteins except DmTRET1-2 have activity for trehalose transport across the cellular membrane, indicating that *DmTret1-2* is a pseudogene of *Tret1*. Q-PCR revealed that *BmTret1* is mainly expressed in the fat body, which is consistent with the tissue-distribution of *Tret1* gene expression in *P. vanderplanki*. This result suggests that TRET1 would be involved in discharging trehalose from the fat body into hemolymph in many insect species.

Conclusion: Several dipteran, hymenopteran and lepidopteran species had TRET1 showing trehalose transport activity for across the cellular membrane in the fat body, indicating TRET1 is widespread among insects for blood sugar regulation.

Invasions and origins of *Quadrastichus erythrinae* (Hymenoptera: Eulophidae), and devastation of Pacific *Erythrina* species

Mark Wright, Daniel Rubinoff, Russell Messing

University of Hawaii at Manoa, Honolulu, Hawaii, United States

Introduction: In 2004, *Q. erythrinae* was described from Singapore, where is was causing severe damage to ornamental *Erythrina* (coral) trees. By 2005, it had further progressed to Taiwan, Japan, China, the Phillipines, and Hawaii. In Hawaii *Q. erythrinae* attacks endemic *Eyrthrina* in addition to ornamental species. Many trees are killed by these gall insects. This project aimed to seek biological control agents of this insect, and to elucidate its origin.

Methods: Wasps were collected from *Erythrina* spp. in South Africa, Mozambique, Tanzania and West Africa. Parasitoids were reared in quarantine, and gall wasps were kept for DNA extraction. A phylogeographic analysis of the samples was done to seek the origin of the invasive species. At least eight species of gall forming wasps were extracted from the sampled material.

Results: Numerous parasitoids were reared from the samples. Three species are currently being evaluated for biological control releases. Phylogeographic analysis based on mitochondrial and nuclear genes suggest a south-east African origin, but no match has yet been found that pinpoints the origin.

Discussion: The exact origin and route of escape that *Q. erythrinae* followed are not yet completely known. This species has demonstrated unprecedented invasive characteristics for an insect, and will have impacts on a broad geographical scale. The phylogeographic analysis revealed a complex of Eulophidae associated with *Erythrina* in Africa, which begs the question ‘why have no others become aggressively invasive’?

Alteration of social interactions with an immune-challenged nestmate in honeybees.

Freddie-Jeanne Richard[1], Arnaud Aubert[2], Christina Grozinger[1]

[1]North Carolina State University, Raleigh, NC, United States, [2]Université François Rabelais, Tours, France

Immune response pathways have been relatively well-conserved across animal species, with similar systems in both mammals and invertebrates. Social insects, such as honeybees and ants, provide ideal grounds for pathogens' dissemination, with controlled environmental conditions in the hive, high population densities, and frequent interactions. Interestingly, despite this theoretical vulnerability, honeybees have substantially reduced numbers of genes associated with immune function compared to solitary insect species. This suggests that honeybees may have developed complementary mechanisms - such as behavioural modifications - to deal with disease. Here, we demonstrate that activation of the immune system in honeybees (using a non-replicative bacterial coat protein: lipopolysaccharides, LPS), alters the responses of healthy nestmates toward the treated individuals. Furthermore, these altered behavioral responses of healthy bees match significant changes in the overall cuticular hydrocarbon profiles of immune-challenged bees. Since cuticular hydrocarbons play a critical role in nestmate recognition and other social interactions in a wide variety of insect species, modulation of such chemical profiles by the activation of the immune system could play a crucial role in the social regulation of pathogen dissemination within the colony.

DNA analysis to determine the origin of winter moth in North America and hybridization with its congener Bruce spanworm

Joseph Elkinton, George Boettner, Marinko Sremac, Rodger Gwiazdowski, Roy Hunkins, Adam Porter, Susan Schuefele

University of Massachusetts, Amherst, MA, United States

Introduction: The northeastern United States has experienced a novel outbreak of winter moth, *Operophtera brumata*, an invasive defoliator from Europe. We wished to map the extent of the infestation and to determine where the moths came from.

Methods: To map the infestation we deployed a grid of pheromone-baited traps. The traps also captured Bruce spanworm, *Operophtera bruceata,* a North American congener of winter moth. The adult males of these two species are difficult to distinguish based on wing characters. We dissected genitalia and sequenced the CO1 gene to distinguish the species. To detect hybrids between them, we looked for intermediate genitalia and we sequenced the nuclear gene G6PD.

Results: We found winter moth in coastal New England from Long Island to Maine. Further north and west we recovered only Bruce spanworm. Although many moths in the zone where the two species overlapped had intermediate genitalia, the G6PD sequences showed that hybrids occur but are rare. DNA analyses show that all winter moths from North America (Nova Scotia, British Columbia and New England) have an identical CO1 haplotype. In contrast populations of winter moth in Europe and Bruce spanworm in North America both show considerable sequence variation.

Conclusion: These facts may indicate a founder effect and a single introduction of winter moth to North America, However, the same haplotype that is ubiquitous in North America is also both dominant and widespread in Europe. Thus, at present, we cannot rule out multiple introductions of this haplotype to North America

The role of habitat structure on disease-infected insects invading Australia

Kylie Anderson[1], Mohamed Sallam[2], Bradley Congdon[1]

[1]James Cook University, Cairns, Queensland, Australia, [2]BSES Ltd, Gordonvale, Queensland, Australia

Introduction: Ramu Stunt disease of sugarcane and its vector, *Eumetopina flavipes*, are present in Papua New Guinea (PNG). Disease-free *E. flavipes* populations occur on the Torres Strait Islands (TSI) and northern peninsula area (NPA) of mainland Australia. Infected *E. flavipes* could disperse from PNG through the TSI and introduce Ramu Stunt into commercial Australian sugarcane. No data exists on *E. flavipes* habitat use when it colonises new regions. The effect of habitat structure (abundance and spatial distribution of hosts) on *E. flavipes* abundance was used to assess the likelihood of its successful establishment and population growth, and so determine likely TSI entry-points for Ramu Stunt infected *E. flavipes*.

Methods: The distribution of *Saccharum* host species, their occupancy by and abundance of *E. flavipes* if present was assessed at key locations in PNG, TSI and NPA.

Results: *E. flavipes* was always present in PNG, but not the TSI and NPA. When present, *E. flavipes* population size was extremely variable. In PNG, the abundance of *E. flavipes* varied considerably among four *Saccharum* host species. Of the PNG *Saccharum* species, two were present in the TSI and NPA. In contrast to PNG, *E. flavipes* abundance did not vary between them.

Conclusion: Habitat structure may affect the persistence of *E. flavipes* at some TSI and NPA sites. In PNG, hosts may provide a continuous habitat that is available for re-colonisation by *E. flavipes*. All PNG and particularly persistent TSI populations may be sources from which dispersal of Ramu Stunt disease infected *E. flavipes* could occur.

Field host range of *Melanagromyza eupatoriella* in Jamaica: implications for biological control of *Chromolaena odorata*

Marsha Robinson[1], Costas Zachariades[2], Dwight Robinson[1], Jane Cohen[1]

[1]University of the West Indies (Mona), Kingston 7, Jamaica, [2]ARC- Plant Protection Research Institute, Private Bag X6006, Hilton 3245, South Africa

Introduction: The neotropical shrub *Chromolaena odorata* (Asteraceae, has become one of the worst invasive alien weed species in the tropical and subtropical regions of Asia, Africa and Oceania. Biological control is critical in developing a successful management programme to control the spread of the weed. Previous studies in the neotropics highlighted the stem-tip killing fly, *Melanagromyza eupatoriella* (Agromyzidae), as a candidate for biological control of *C. odorata*.

Methods: Surveys were conducted in Jamaica to determine the field host range of the insect. Data was also collected on the prevalence of *M. eupatoriella* in relation to environmental parameters. Sites were selected based on the presence of *C. odorata* with shoot tips damaged by *M. eupatoriella* larvae, along with other species of Asteraceae.

Results: Damage by *M. eupatoriella* on *C. odorata* was observed at most sites, with over thirty species of Asteraceae being surveyed. To date, damage similar to that caused by *M. eupatoriella* larvae has been observed infrequently on four other Asteraceae, found growing alongside *C. odorata*, viz. *Bidens alba*, *Bidens reptans*, *Mikania micrantha* and *Calea jamaicensis*. Adult Agromyzidae were obtained only from *B. alba*. Taxonomic studies will determine if the damage is caused by *M. eupatoriella* or another species. Further research will establish the specificity of the insect in a controlled environment.

Conclusion: Although the presence of *M. eupatoriella*-like damage on other Asteraceae is a concern, it occurred at low levels and mines were often incomplete. This damaging fly thus still shows potential for biological control of *C. odorata.*

Development of a field-deployable chigger surveillance trap

Kriangkrai Lerdthusnee, James W. Jones, Jittawadee R. Murphy, Jason H. Richardson

Armed Forces Research Institute of Medical Sciences, Bangkok, Thailand

Introduction: Methods to assess relative risk in space and time are prerequisites for effective vector–borne disease control programs. However, there are no tools or methods specifically designed for conducting a rapid survey for ectoparasites such as chigger-mites, the vector for scrub typhus.

Methods: Several chigger trap models were designed (based on behavior and propensity of chiggers to climb upwards), made (by black-plastic sheet, paper or cloth), into several shapes, and tested against the black-plate, as the control trap. Traps were placed in the middle or spread-out in the testing platform area of 1x1 m^2. Ten to 40 live-chiggers (depending on number of traps tested) were randomly released into the platform. Numbers of chiggers approaching trap(s) were recorded through time, with 10 replications for each test. Evaluations on the difference between “Plastic-model” vs “Paper-model” were compared. Field trials of selected models were also conducted.

Results: Trap models with plastic base wrapped up with black cloth appeared to be more effective. Chiggers preferred the plastic model over the paper model. Preliminary field trials of the down-selected chigger trap model were initiated in order to evaluate their performance in the natural chigger-mite habitats.

Conclusions: Trap model with black cloth base captured more number of chiggers than the ones made from plastic or paper alone. Further evaluations are being conducted to improve trap attractiveness using attractants (CO_2, animal’s excreta, and commercially produced attractants).

Traversing a treacherous landscape: An overview

Myron Zalucki

University of Queensland, Brisbane, Queensland, Australia

Foraging behaviour of external feeding caterpillars; where they feed, “rest” and how often and where they move; will be influenced by many factors, both proximal and evolutionary. The former will pertain to internal and external ambient conditions. Internal factors comprise stage, age, nutritional balance, moisture and thermal balance. External factors include microclimate, surface waxes as well as plant and leaf “toughness”, trichomes and their constituents and internal plant attributes, such as, various constitutive allelochemicals, plant nutrients, plant exudates and changes in these as a result of feeding damage, so called induced defences. In addition, interaction with conspecifics and contact with natural enemies (predators and parasitoids) often causes drop off and other changes in behaviour, apart from mortality. The interactions among these factors at various spatial scales will likely result in complex movement patterns and distribution of damage to plants and plant parts. Obtaining nutrients whilst avoiding toxins in plants is not as simple as selecting a plant part and staying there. The plant part changes as a result of feeding and natural enemies are likely attracted to such damage. Moving is also likely to be hazardous as caterpillars may encounter both searching and sit-and-wait predators. The relative importance of these factors to the evolution of foraging strategies and what we might expect to be the distribution of damage and effects on survival are difficult to estimate but can be addressed experimentally within a modelling framework.

Progress in the development of a semiochemical-based system for managing *Lygus* spp. in an Arizona landscape

Jacquelyn Blackmer[1], Lynn Forlow Jech[1], David Hall[2], Jerry Hall[3], Michelle Fountain[3]

[1]US ALARC-ARS-USDA, Maricopa, Arizona, United States, [2]Natural Resources Institute, University of Greenwich, Chatham Maritime, Kent, United Kingdom, [3]East Malling Research, East Malling, Kent, United Kingdom

Introduction: Chemical attractants and repellents produced by insects and plants can be used to manipulate insect populations; however, a sound understanding of the mechanisms involved is needed to ensure effectiveness in the field. Trap design, placement, and insect activity levels must be taken into consideration.

Methods and Results: Through a combination of olfactometer bioassays and field-based experiments we have examined many of these factors for the *Lygus* species *L. lineolaris* and *L. hesperus* and found that in the laboratory females are more likely to respond to plant volatiles, especially in the presence of a green visual cue; however, in the field, males are more likely to be trapped. This difference is likely due to differences in flight activity relative to gender, as field populations, based on sweep samples, are usually at parity. Trap catches were enhanced by manipulating trap color, shape, height, orientation, and position in the field, but plant volatiles in combination with our traps have not been effective in trapping a higher number of *Lygus* spp. to date. Putatitve *Lygus* pheromones have also been examined, in combination with our most effective traps, and significantly higher numbers of male *L. lineolaris* were trapped with a binary combination. This response was short lived, but is the first report of significant attraction in the field by *L. lineolaris* to putative *Lygus* pheromones.

Conclusions: Ongoing studies are focusing on testing additional plant volatiles, confirmation of the response of *L. lineolaris* and other *Lygus* spp. to putative pheromone components in different cropping systems, and further refinement of our traps.

Why the browntail moth went extinct in much of its invasive range in North America

Joseph Elkinton[1], Dylan Parry[2], George Boettner[1]

[1]University of Massachusetts, Amherst, MA, United States, [2]State University of New York, Syracuse, NY, United States

Introduction: The browntail moth *Euproctis chrysorrhoea,* was introduced to North America near Boston from Europe in 1897. It became an important defoliator of many tree species throughout New England and was also a human health hazard due to severe skin rashes caused by urticating hairs from the larvae. Beginning around 1915, however, browntail populations receded gradually to coastal enclaves at the tip of Cape Cod, Massachusetts and on islands in Casco Bay in Maine, where high densities have persisted ever since. Until now no studies have explained why it declined and why it persists in coastal enclaves.

Methods: We analyzed historical data from the 1920s on levels of parasitism of browntail moth in New England and we created experimental populations of browntail moth at inland and coastal locations on Cape Cod.

Results: We present evidence that a major cause of the decline was the generalist tachinid parasitoid *Compsilura concinnata,* which was introduced to North America in 1906 to control gypsy moths. Analysis of historical data revealed high levels of parasitism of browntail moth by this species at inland sites, but low levels in coastal areas. We confirm this pattern in the experimentally created browntail populations at both inland and coastal locations on Cape Cod.

Conclusion: We conclude that *Compsilura concinnata,* was responsible for extirpation of browntail moth from most of its former range in North America.

Why the browntail moth went extinct in much of its invasive range in North America

Joseph Elkinton[1], Dylan Parry[2], George Boettner[1]

[1]Universtiy of Massachusetts, Amherst, MA, United States, [2]State University of New York, Syracuse, NY, United States

Introduction: The browntail moth *Euproctis chrysorrhoea,* was introduced to North America near Boston from Europe in 1897. It became an important defoliator of many tree species throughout New England and was also a human health hazard due to severe skin rashes caused by urticating hairs from the larvae. Beginning around 1915, however, browntail populations receded gradually to coastal enclaves at the tip of Cape Cod, Massachusetts and on islands in Casco Bay in Maine, where high densities have persisted ever since. Until now no studies have explained why it declined and why it persists in coastal enclaves.

Methods: We analyzed historical data from the 1920s on levels of parasitism of browntail moth in New England and we created experimental populations of browntail moth at inland and coastal locations on Cape Cod.

Results: We present evidence that a major cause of the decline was the generalist tachinid parasitoid *Compsilura concinnata,* which was introduced to North America in 1906 to control gypsy moths. Analysis of historical data revealed high levels of parasitism of browntail moth by this species at inland sites, but low levels in coastal areas. We confirm this pattern in the experimentally created browntail populations at both inland and coastal locations on Cape Cod.

Conclusion: We conclude that *Compsilura concinnata,* was responsible for extirpation of browntail moth from most of its former range in North America.

Tropical forests are both evolutionary cradles and museums of leaf beetle diversity

Duane McKenna

Harvard University Department of Organismic & Evolutionary Biology, Cambridge, MA, United States

Introduction: The extraordinary species richness of tropical forests is usually portrayed as a relatively recent and rapid development or as a result of the gradual accumulation or preservation of species over time. These explanations have led to alternative views of tropical forests as evolutionary 'cradles' or 'museums' of diversity. Biogeographic and fossil evidence implies that the history of diversification among tropical insects may be expected to exhibit features characteristic of both 'cradle' and 'museum' models. However, this possibility has not been explored in detail for any group of insects.

Methods: Using molecular phylogenetic and other data I reconstructed relationships and timing and patterns of taxonomic diversification in herbivorous Neotropical leaf beetles in the genus Cephaloleia (aka "rolled leaf hispine beetles").

Results: I present evidence for (i) comparatively ancient Paleocene–Eocene diversification associated with global warming and Cenozoic maximum global temperatures, (ii) moderately ancient lineage-specific diversification coincident with the Oligocene adaptive radiation of Cephaloleia host plants in the genus Heliconia, and (iii) relatively recent Miocene-Pliocene diversification coincident with the collision of the Panama island arc with South America and subsequent bridging of the Isthmus of Panama.

Conclusions: Taken together, these results demonstrate that for Cephaloleia and perhaps other groups of insects, tropical forests are at the same time both evolutionary cradles and museums of species diversity.

Colonizastion process of the threatened damselfly, *Mortonagrion hirosei*, inhabiting the artificially established reed community

Yuko Teramoto, Mamoru Watanabe

University of Tsukuba, Tsukuba, Ibaraki, Japan

Introduction: A new reed community was artificially established by transplanting reed rhizomes adjacent to the natural habitat of the threatened damselfly, *Mortonagrion hirosei*. The goal for the mitigation project was that the damselfly had immigrated and colonized the newly established habitat. The adult population size was considered to be one of the indicators for assessing the mitigation project.

Materials and Methods: During the flying season, from late May to early August, a weekly line census method was carried out. There was a good relationship between the daily number of adults detected per 10m along the transect line and the estimated daily number of adults per square mater calculated by the Manly & Parr method based on mark-and-recapture samplings.

Result and Discussion: In the original habitat, the estimated population size was stable at 15,000-18,000 for 4 years, that is about 20 adults per square meter. In the established habitat, a few adults was found daily in 2003 that is the 1st year of the establishment of the reed community. Adults seemed to be restricted near the original habitat because they have low flight activity throughout the life span. Then the population increased with year after year, but the growth rate decreased. Then, in 2007, the estimated population size was 79,000, 39 adults per square meter, probably due to result of the density dependent process. Although, the established reed community has not been fully grown up yet, the mitigation project for conservation of *M. hirosei* is now successful.

The mechanisms enabling movement of caterpillars on plants at the macro scale

Lynda Perkins, Bronwen Cribb, Jim Hanan, Ezekiel Glaze, Myron Zalucki

University of Queensland, Brisbane, Australia

Introduction: In order to model movement of an herbivorous insect on a plant we have divided interactions between plant and insect into two scales: macro and micro. At the macro scale, we have determined the affect of plant architecture and developmental stage using 1st instar *Helicoverpa armigera* on garden pea as our model.

Methods: Observations followed by targeted bioassays were used to determine how the architectural attributes of peas affected the movement of larvae. The results were used to create a set of 'rules' for the movement our model caterpillar. The simulated movement of the model caterpillar was compared to the movement of real caterpillars in glasshouse trials.

Results: Our modelling suggests that phototaxis and geotaxis as determined by the angle of plant structures are important mechanisms directing the movement of caterpillars. Plant attributes such as enclosed spaces, structural complexity, and the presence of flowers influence movement but not in a directional manner. The developmental stage of the larva affects its behavioural response to movement cues.

Conclusions: Phototaxis and geotaxis are mechanisms responsible for gross movement of early instar *H. armigera*, but these behaviours may be modified by plant attributes.

Plant-pollinator interactions in changing landscapes

Neal Williams[1], Elizabeth Crone[2], Rachael Winfree[3], Ramiro Aguilar[4], T'ai Roulston[5], Laurence Packer[6], Simon Potts[7], Robert Minckley[8]

[1]Bryn Mawr College, Bryn Mawr, PA, United States, [2]University of Montana, Missoula, MT, United States, [3]Princeton University, Princeton, NJ, United States, [4]UNAM, Morelia, Mexico, [5]University of Virginia, Boyce, VA, United States, [6]York University, Toronto, ON, Canada, [7]University of Reading, Reading, United Kingdom, [8]University of Rochester, Rochester, NY, United States

The loss and degradation of habitat resulting from human activities are among the greatest threats to biological diversity and to the ecological interactions and functions that depend on this diversity. Pollination is one such function that is a critical to plant and animal persistence, and which increases with the diversity and abundance of pollinators in the community. The tendency has been to consider natural habitats as good for pollinators and human-altered habitats as uniformly bad; however, recent studies call this generalization into question. We used a formal meta-analysis and hierarchical modelling to test the responses of native bee communities to different landscape changes and other anthropogenic disturbances. The meta-analysis revealed that habitat loss and fragmentation negatively affect abundance and diversity. Response to other disturbance types was variable, in part due to limited samples. The more detailed hierarchical model allows us to explore whether functional-traits help explain responses of bees within and among disturbance types. Here we define functional-trait groups as species with similar life histories (social vs. social), nesting strategies, body sizes, or trophic specialization. Preliminary results from different studies show that general nesting habit (e.g., ground-nesting vs. twig-nesting) and sociality can determine sensitivity to different land use changes. Less is known about the role of other functional traits.

Ecologically sustainable chemical recommendations for agricultural pest control?

Linda Thomson, Ary Hoffmann

University of Melbourne, Victoria, Australia

Introduction: Moves towards sustainability require a reduction in chemical toxicity loadings and conservation of natural enemies to maintain pest control. There is a lot of information based on laboratory and semi-field tests, such as that provided by the IOBC, on responses of natural enemies to chemicals but very few translations of these effects into field impacts particularly under commercial conditions.

Methods: We assessed the cumulative impact of chemical inputs across an entire season on the communities of natural enemies in vineyards. We calculated a chemical toxicity score for 19 commercial vineyards based on IOBC toxicity ratings and application number, and compared this to extensive field collections to determine if natural enemy populations can be related to predicted toxicity loadings. Invertebrates were sampled four times during the growing season using canopy sticky traps and ground level pitfall traps and abundance of natural enemies related to the toxicity score using ordination techniques. Further, we compared the metric used in this study to different approaches for assessing the impact of chemicals on agricultural ecosystems.

Results: Ordination analyses using non-metric multidimensional scaling indicated community structure in vineyards correlated to site chemical use. One ordination axis from canopy data and two axes from ground level data correlated to overall IOBC ratings for the vineyards and principal components analyses identified the taxa involved.

Conclusions: Our metric based IOBC toxicity ratings correlated with chemical effects on field populations of natural enemies in commercial vineyards where complexes of pesticides were applied. We proposed how effectiveness of metrics could be extended to include persistence and habitat features.

Factors in the establishment of boneseed leaf roller in New Zealand

Shaun Forgie[1], Darren Ward[1], Margaret Stanley[2]

[1]Landcare Research, Auckland, New Zealand, [2]University of Auckland, Auckland, New Zealand

Introduction: South African boneseed, *Chrysanthemoides monilifera monilifera,* naturalised in New Zealand in 1870. Boneseed threatens native biodiversity in coastal areas by shading out and preventing native seedling recruitment. Biocontrol of boneseed with the leaf roller *Tortrix s.l.* sp. *chrysanthemoides* began nationwide in 2007. This talk describes experiments to quantify the effect of generalist predators (especially Argentine ants, *Linepithema humile*) and parasitoids on invertebrate communities on boneseed, and their potential impact on establishment of the boneseed leaf roller.

Methods: We investigated boneseed plants with (control) and without (treatment) infestations of Argentine ants. Invertebrate assemblages on boneseed were determined by weekly foliage beating; placement/tethering observations and counts of defoliation, herbivory and sooty mould, all based on varying rates of ant traffic. To examine *Tortrix* establishment, 20 larvae on ten plants were monitored weekly for survivorship over several months.

Results: An increase in the proportion of Argentine ants visiting plants showed decreases in defoliation, herbivory and presence of predators; and increases in the proportion of sooty mould accumulation on stems and leaves. Ants removed significantly more invertebrates from leaves containing honeydew-providing homopterans than from leaves without homopterans. Significantly more *Tortrix* larvae were found developing on treatment plants than control plants. All but two larvae were subsequently killed with 14% per cent parasitism recorded.

Conclusions: Generalist predators (Argentine ants) and parasitoids (braconids and tachinids) play a significant role in shaping invertebrate community assemblages on boneseed, and combine to significantly effect successful establishment by biological control agents.

Operation Full Stop - 10 years of area-wide termite management

Claudia Riegel[1], Frank Guillot[2], Edgar Bordes[1]

[1]City of New Orleans Mosquito and Termite Control Board, New Orleans, LA, United States, [2]USDA/ARS, New Orleans, LA, United States

The French Quarter in New Orleans has had a long history of severe termite pressure from the Formosan subterranean termite (FST), *Coptotermes formosanus.* FST was accidentally introduced into New Orleans in the mid 1940's and its identity was first confirmed in 1966. Operation Full Stop began in 1998. It is the first project to apply area-wide management of subterranean termites in an expansive urban area with the aid of pest control professionals. The goal of the project was to reduce the termite pressure in the French Quarter. Therefore, they were required to utilize technologies such as termite baiting systems and non-repellent termiticides which are expected to eliminate termite colonies. This termite caused costly, reoccurring, structural damages to many buildings and trees including many of historic significance. Without intervention, the French Quarter was destined for destruction by FST. Green space such as parks with infested trees, railroad lines, and Mississippi river levee in the French Quarter were also included in the program. In-ground termite activity was evaluated monthly using independent monitoring stations and alate density was measured each April to July. A 15 city block section of the French Quarter (an area) was added to the program every two years. Since inception of the program, alate density across the French Quarter has been reduced from 44% to 75%. A 98% reduction in FST has been observed along the railroad and levee. An effort has been made to inspect every property in the program. Operation FullStop was a pioneer program that has reduced the overall termite activity in the French Quarter. Effort has been placed on identifying and treating above-ground infestations and infested trees. This project has also utilized improved termite detection tools and more thorough treatments to continue the effort to further reduce the subterranean termite population in the French Quarter.

Developing a systems approach for false codling moth on 'Hass' avocado

Tertia Grové, Marinda De Beer

ARC-Institute for Tropical and Subtropical Crops, Nelspruit, South Africa

Introduction: False codling moth, *Thaumatotibia leucotreta* Meyrick (Lepidoptera: Tortricidae) is a quarantine pest on avocado which prevent exportation of 'Hass' to new markets. A quarantine treatment needs to be developed before new markets can be exploited. A systems approach relies on knowledge of the pre- and postharvest biological factors that influence pest survivorship. The objective of the research is to obtain biological data that can be used in a systems approach.

Methods: The time frame for the development of visible lesions was determined. Fruits were artificially infested with eggs on the tree to determine if the larvae could develop. Male moths were monitored in 'Hass' orchards. The number of fruit with lesions was also determined. Fruit firmness was measured by using a densimeter and the correlation between firmness and the instars present in the fruit was determined. Insecticides and granulovirusses were evaluated for the control of *T. leucotreta*. Bagging of fruit to prevent infestation was also evaluated. Fruit infested with eggs in the orchard were picked 2, 4 and 6 weeks after infestation and the survival rate was determined. A survey was conducted to determine infestation levels in the field. A systems approach was evaluated during 2004, 2005 and 2006.

Results: Lesions were visible from two weeks after infestation of the larvae and therefore fruit with lesions can be sorted prior to entering the packhouse and again in the packline. Experiments done indicated that larvae could develop further than 1st instar. It also seemed that 'Hass' was partially resistant to the development of larvae when attached to the tree. As soon as the fruit were harvested, larvae started developing further. Field studies indicated that infestation usually started during January. Fifth instar larvae were only present in soft fruit. Fenpropathrin and the granulovirusses were effective in reducing the infestation rate of fruit. Bagging reduced the number of larvae present in the fruit but was a labour intensive method. Survival rate of larvae in fruit on the tree which were left to develop further after harvest, varied between 4.05% and 0.90% and depended on the time of infestation prior to harvest. Fruit that become infested shortly before harvest would be of higher risk. The survey conducted in the different production areas indicated that infestation levels in commercial orchards were usually <1%. Lower risk areas can be selected for export. No survival of larvae occurred in the systems approach tested.

Conclusion: A systems approach for *T. leucotreta* seemed to be a viable option to reach quarantine security on 'Hass' avocado.

Molecular phylogenetics and phylogeographic analysis of the Australian termite genus *Coptotermes*

Haidi Badawi

Melbourne University and Flinders University SA, Australia

This study will focus on the genus *Coptotermes* phylogeny, especially from Australian regions, by using 4 different genes which are 16S, COII, COI and H3 (the histone3 gene will be used for first time within *Coptotermes* phylogenies). The study will use different analyses of this combined data set of 3000 bp, to give a better phylogenetic model of Australian *Coptotermes* within the global *Coptotermes* view, moreover the study will focus on the phylogeographic status of *Coptotermes* by discussing the dispersal of haplotypes among the geographical localities by using NCPA nested Clade phylogeographic analysis.

Use of sequence data can provide some enormous advantages over other data types, including the ability to rapidly generate very large character suites and ease of analysis.

A simple approach to integrating insecticides into cotton IPM

Lewis Wilson, Simone Heimoana

CSIRO Plant Industry, Narrabri, New South Wales, Australia

Introduction: Insecticides are an important component of IPM systems. Establishing their ideal use in IPM systems requires information on efficacy against target pests, effects on beneficial populations and potential to induce secondary pest outbreaks. We developed a simple method which incorporates these variables and tested it by using it to compare several control options for the green mirid (*Creontiades dilutus*), a key pest in Australian Bt-cotton.

Methods: Field plots of irrigated cotton were either untreated or treated with petroleum spray oil (PSO), salt (NaCl), low rate fipronil alone or with salt, high rate fipronil, low rate indoxacarb alone or with salt or PSO and high rate indoxacarb. Insecticides were applied 4 times at 10 d intervals and plots sampled pre-spray and twice weekly thereafter. Key pests and a wide range of beneficials were recorded. Data were analysed for treatment effects, which were ranked according to the reduction in beneficial abundance compared with the untreated control; VL (very low), less than 10%; L (low), 10-20%; M (moderate), 20-40%; H (high), 40-60%; VH (very high), > 60% and risk of pest resurgence.

Results: All rates of fipronil provided effective control of green mirids. Reduced rates of fipronil were more selective than the full rate but all rates increased abundance of mites, *Helicoverpa* spp. and aphids. Indoxacarb was effective against mirids at the full rate but not at the lower rate unless salt or PSO were added. Indoxacarb at the full rate was as selective as low rate fipronil and at the low rate was even more selective. Indoxacarb did not induce mite outbreaks but had higher aphid numbers.

Conclusions: This approach has been used to evaluate the IPM fit of a wide range of insecticides. Meta-analysis of commercial crops managed with more selective insecticides had higher beneficial populations, confirming the value of rankings generated using this method.

Clock and photoreceptor in the photoperiodic regulation of diapause in the flesh fly *Sarcophaga similis*

Shin G. Goto

Osaka City University, Osaka, Japan

Introduction: Physiological processes underlying photoperiodism comprises 3 components, i.e., photoreceptor(s), photoperiodic clock(s) and hormonal effecter(s). Although our knowledge on the endocrinological details in the expression of photoperiodism has advanced, information on functional photoreceptor(s) and photoperiodic clock(s) are still limited. Here I approached the mechanisms of the photoperiodic clock and photoreception in the flesh fly *Sarcophaga similis*.

Results and Discussion: *Sarcophaga similis* enters pupal diapause in response to short days. Destination to diapause or nondiapause could be altered by a few long- or short-day cycles. Larvae discriminate photoperiods qualitatively and count the number of the photoperiodic cycles. Nanda-Hamner protocol revealed that the circadian oscillator is involved in the photoperiodic response. Experiments on 24h asymmetric skeleton photoperiods revealed that two phases (early and late) in the scotophase are sensitive to light for averting diapause. Experiments on non-24h asymmetric skeleton photoperiods revealed that the response at the early phase is reversible, but that at late phase is irreversible. Based on the external coincidence model which is verified in another *Sarcophaga* species, I suggest that the late phase is the photoinducible phase (Φ_i). Only light of short-wavelength (blue and UV) was effective in the early phase, whereas light of broad wavelength as well as that of short-wavelength successfully averted diapause in the late phase. From these results, I suggest that different photoreceptors are involved in the expression of photoperiodism in these phases.

Molecular phylogeny of the horse flies: a framework for renewing tabanid taxonomy

Shelah I. Morita[2], Keith M. Bayless[1], Brian M. Wiegmann[1]

[1]Department of Entomology, North Carolina State University, CB 7613, Raleigh, North Carolina, 27695-7613, United States, [2]Department of Botany and Zoology, University of Stellenbosch, Private Bag X1, Matieland, 7602, South Africa

Introduction: Horse flies (Diptera: Tabanidae) are an economically, medically, and ecologically important group containing bloodfeeding pests and long-proboscid pollinators. This group, with over 4,300 described species, has experienced a severe loss of taxonomic expertise. The TabanidPEET project will fill this gap by training at least four postgraduates. As a framework for student taxonomic revisions, we present here a new higher-level molecular phylogeny of the horse flies. This work will guide morphological character choice and focus student projects on evolutionary units. We also ask the following questions: 1) Are the three current subfamilies monophyletic? 2) Is pollinator morphology ancestral in Tabanidae? 3) When did the major tabanid clades diverge and radiate? 4) What are the morphological and life history features supporting tabanid clades?

Methods: Using exemplars from 10 of 11 tribes, we sampled two nuclear (CAD, AATS), and one mitochondrial (COI) gene. Phylogenetic inference was performed using Parsimony and Maximum Likelihood in Paup*, and using Bayesian Inference in Beast. Character reconstruction was optimized using BayesTraits and MacClade.

Results: Our phylogenetic hypothesis for Tabanidae is largely concordant with previous hypotheses, but also indicates several newly recognized groupings that will form the basis for focused taxonomic revisions. Divergence time estimates based on nucleotide data and fossil evidence reveal rapid radiations in the early history of horse fly diversification.

Conclusions: The current taxonomy of Tabanidae at the subfamily and tribal level needs to be revised based on new molecular evidence. Additionally, long-proboscides appear to be ancestral, suggesting that tabanids are ancient pollinators.

Elucidating cotton genotypes resistant to whitefly, *Bemisia tabaci* (Gennadius) (Homoptera: Aleyrodidae) by population build up studies under no choice conditions

Vikas Jindal, G.S. Dhaliwal

[1]Punjab Agricultural University, Regional Station, Faridkot/ Punjab, India, [2]Insect Biopesticide Research Centre, Jalandhar/Punjab, India

Introduction: Plant resistance has become an important component of cotton integrated pest management (IPM) for management of whitefly, *Bemisia tabaci,* an important pest of cotton in India. Therefore, cotton genotypes resistant/tolerant to whitefly were identified and evaluated.

Methods: Twelve cotton genotypes, *G hirsutum*(10) and *G. arboruem*(2), raised upto standardized (14-leaf) stage were released with five newly emerged pairs of whiteflies (F_1) under no choice conditions. After 25 days, eggs, immatures (nymphs+pupae) and adults were recorded to identify genotypes, not suitable for whitefly development. The experiment was repeated with F_2 and F_3 generation of whiteflies.

Results: In F_1 generation experiment, RS2098 recorded minimum eggs (2.17/6.5cm^2), immatures (12.00/6.5cm2) and adults (60.00/plant), however, F846 recorded maximum eggs (54.23/6.5cm^2), immatures (58.33/6.5cm^2) and adults (815.00/plant). In F_2 generation experiment, LD694, NHH44 and Supriya recorded minimum eggs (1.77/6.5cm^2), immatures (6.00/6.5cm^2) and adults (46.00/plant), respectively, while maximum eggs and immatures were found on F846. In F_3 generation experiment, RS2013 recorded lowest eggs (0.83/6.5cm^2) and LD694 recorded lowest immatures (0.83/6.5cm^2) and adults (22.67/plant). Genotypes IS-376/4/1/20/72, RS2098 and F846 recorded maximum eggs, immatures and adults, respectively.

Conclusions: LD694 was categorized as resistant; LK861, Supriya, RS2013, RS2098 and PA183 as moderately resistant; IS-376/4/1/20/72, NHH44, TxMaroon2-78, *Bt*6304, CNH911 as moderately susceptible and F846 as susceptible one. LD694 was found to be resistant in three consecutive generations of whitefly, hence, the chances of development of biotypes of whitefly are low for three generations, but detailed studies are further required.

Spatial analysis of the influence of adjacent vegetation on the abundance and distribution of natural enemies in a vineyard in south eastern Australia

Linda Thomson

University of Melbourne, Victoria, Australia

Introduction: Adjacent vegetation increases the relative abundance of natural invertebrate enemies on farmland and can assist in invertebrate pest control. The provision of vegetation either adjacent to the crop or within the crop can provide refuge from the effects of applied chemicals and sources of new populations.

Methods: We investigated the abundance and diversity of natural enemies in a range of vegetation types adjacent to vineyards in south eastern Australia. Invertebrates were sampled four times in 2 consecutive seasons at 10 sites, adjacent to either remnant native forests or shelterbelts, using canopy sticky traps and ground level pitfall traps. At one site we investigated the spatial distribution with 100 sampling points in a single vineyard and at 9, transects were set up from the vegetation into the vineyard. Distribution and abundance of natural enemies was mapped using spatial analysis by distance indices (SADIE) and ANOVAs. We also directly assessed impacts on predation and parasitism of eggs of an important vineyard lepidopteran pest.

Results: The abundance and distribution of vineyard natural enemies was influenced by adjacent vegetation, traps adjacent to vegetation with higher numbers of a range of natural enemies and sentinel eggs higher levels of parasitism. These results indicate that the abundance and distribution of vineyard natural enemies is influenced by adjacent vegetation and that there are direct beneficial effects on the control of a moth pest.

Conclusions: The conservation of remnant vegetation and planting of shelterbelts around vineyards may have direct economic benefits in terms of pest control which should promote the maintenance of vegetation by growers specifically for improving pest control.

Floral niche models best explain proboscis length evolution in long-tongued, bloodsucking pollinators (Diptera: Tabanidae)

Shelah I. Morita

[1]Population Biology Graduate Group, University of California, Davis, California 95616, United States, [2]Department of Botany and Zoology, University of Stellenbosch, Private Bag X1, Matieland, 7602, South Africa

Introduction: The relationship between plants and their pollinators has often been upheld as the best example of bioticaly mediated speciation, specialization, and co-divergence. Hypotheses regarding the mechanism of trait evolution in these relationships are focused on plants. They include two main hypotheses 1) plants and pollinators are in a coevolutionary race and 2) pollinators are relatively constant and plants evolve in response to pollinator shifts. Here I address the adaptive significance of pollinator morphology in species complex of long-tongued horse flies by asking: 1) Have long proboscides evolved multiple times? 2) Is their evolution consistent with a coevolutionary arms race (always increasing)? 3) Is pollinator morphology adapted to floral niches?

Methods: I sampled nuclear and mitochondrial genes from 9 of the 11 tabanid tribes with multiple geographic exemplars within the *Philoliche aethiopica* species complex. Twenty trees were randomly sampled from a Bayesian posterior distribution of 20 million generations, representing 13 unique topologies and branch lengths variation. For each tree, branch lengths in terms of time were estimated in r8s, character reconstruction was optimized using BayesTraits (Maximum Likelihood) and Mesquite (Max-Min Squared Changes Parsimony). Floral association models were tested using OUCH.

Results: Ancestral reconstruction supports multiple, independent evolutions of long proboscis morphology. Max-Min coding shows evolution of both longer and shorter proboscides. OUCH models strongly support the adaptive significance of Floristic Region and *Wastonia* floral morphology.

Conclusions: Proboscis length evolution seems labile and non-directional, incongruent with a coevolutionary arms race. However, proboscis length appears to evolve in response to floral niches.

Egg whites and whitegrubs - transgenic sugarcane for grub control

Kerry Nutt, Rachael Hassall, Peter Allsopp

BSES Limited, Brisbane, Australia

Major losses are inflicted on the Australian sugar industry by a complex of 19 species of whitegrubs (Scarabaeidae: Melolonthinae). The control of whitegrubs by insecticides is made difficult by their subterranean life style, but there are few alternatives for control and commercial sugarcane varieties lack natural resistance to whitegrub attack. Genetic modification of sugarcane cultivars to enhance resistance to whitegrubs has been investigated as an alternative method of control for whitegrubs. Artificial diet feeding trials conducted by Allsopp & McGhie (1996) found that avidin, a biotin binding protein from chicken egg white, could reduce larval growth and increase larval mortality of *Antitrogus parvulus* (Childers grub). A gene for vacuole-targeted avidin, under the control of the maize ubiquitin promoter, was introduced into sugarcane by microprojectile bombardment. Efficacy of avidin producing sugarcane was tested using cut leaf bioassays with late first instar (5d old) sugarcane armyworm (*Leucania* spp.). Larvae were fed transgenic sugarcane leaf sections from plants expressing avidin at average concentration ranging from 0.01-0.03 µM (µmoles/kg of fresh leaf tissue). Avidin expressed in sugarcane at this level had no significant effect on armyworm development or survival. Although avidin has conferred insect resistance to tobacco (Burgess et al. 2002), improvements in transgene expression in sugarcane need to be made if it is to become an effective whitegrub control method.

Analysing border interceptions and establishments of bark and ambrosia beetles: Can we identify traits of successful invaders?

Eckehard Brockerhoff[1], Jean-Claude Grégoire[2], Robert Haack[3], Milos Knizek[4], Andrew Liebhold[5], Robert Rabaglia[6]

[1]Scion / New Zealand Forest Research Institute, Christchurch, New Zealand, [2]Université libre de Bruxelles, Bruxelles, Belgium, [3]USDA-FS, East Lansing, Michigan, United States, [4]Forestry and Game Management Research Institute, Jiloviste, Czech Republic, [5]USDA-FS, Morgantown, West Virginia, United States, [6]USDA-FS, Arlington, Virginia, United States

Many bark and ambrosia beetles (Scolytinae) are highly destructive forest pests and they also include numerous successful invaders. Exports of logs and timber and the widespread use of wood packaging materials are recognised pathways for invasions of Scolytinae. We used information on border interceptions and records of establishments to improve our understanding of invasion pathways and the characteristics of successful invaders. By combining interceptions of true bark beetles in New Zealand and the United States we obtained data on species found in shipments from around the world. The probability of establishment somewhere in the world was positively correlated with interception rates of species, but interceptions alone can only partially explain the variation in this relationship. To identify other determinants of invasiveness of Scolytinae, we compiled a list of factors that could be correlated with invasiveness, such as body size, breeding behaviour, mating system, occurrence of outbreaks, etc. Results from a comparison of several prominent Scolytinae genera will be presented.

Phylogenetics of the *nasuta-albomicans* complex of *Drosophila*

H.A Ranganath

Bangalore University, Bangalore, Karnataka, India

Introduction: Inter-racial hybridizations between *Drosophila nasuta nasuta* and *D.n.albomicans* of the *nasuta* subgroup of *Drosophila* have resulted in the evolution of novel karyotypically stabilized hybrid lines.

Results: In each of the hybrid lines, called 'Cytorace', the chromosomes of parental races, namely, of *D. nasuta* and *D. albomicans* are differentially represented. These newly evolved hybrid cytoraces have gone through 600 generations under laboratory conditions. This assemblage of *D. nasuta*, *D. albomicans* and Cytoraces is named as '*nasuta-albomicans* complex'. The pattern and extent of anagenetic changes among these cytogenetically closely related members are evaluated and analyzed by adopting different sets of phenotypes, namely, karyotypes, mating behaviour, parameters of fitness, morpho-phenotypic components, Isozymes, Yolk Proteins, DNA markers etc.

Conclusion: Extent of genetic similarity and difference among members of this complex presents a complex profile and the implications of these studies will be discussed in relation to phylogenetic analysis of the group.

Microbial control of soil dwelling pests – progress and prospects

Trevor Jackson

AgResearch, Lincoln, New Zealand

Soil dwelling pests pose particular problems in insect control as they are protected by the soil and difficult to treat. The soil, however, acts as a reservoir for microorganisms, which can include insect pathogens. Insect disease usually occurs as a delayed-density-dependent response to pest build up and is often responsible for natural pest population collapses. Pathogenic microbes can be isolated from diseased insects, cultured, formulated and used as biopesticides for control of pest species. These include preparations of specific strains of bacteria, fungi and virus which have been used successfully for control of a range of soil dwelling pest problems. Most success has been achieved where the pathogens are able to persist within the host's environment. Use of pathogens in soil dwelling pest control has been limited by cost of production, application technology and specificity but, through efficient production processes and correct targeting of control, successful niche markets for microbial control products have been established. Current products provide models for analysis and future developments. The prospects for microbial control are improving with greater appreciation of soil ecosystems and the need to avoid disruptions with chemical pesticides.

Juvenile hormone and soldier-caste differentiation in the termite *Hodotermopsis sjostedti*

Richard Cornette[2], Shigeyuki Koshikawa[1], Hiroki Gotoh[1], Toru Miura[1]

[1]Hokkaido University, Sapporo, Hokkaido, Japan, [2]National Institute of Agrobiological Sciences, Tsukuba, Ibaraki, Japan

Termites present complex caste differentiation systems, leading to a wide array of polymorphism patterns, which are adapted to specific social tasks. As in most other social insects, the termite caste differentiation is mainly triggered by juvenile hormone (JH), but its mode of action is still poorly understood.

In the damp-wood termite *Hodotermopsis sjostedti*, soldier caste differentiation can be induced from the totipotent caste called “pseudergates” by treatment with the JH analogue pyriproxyfen (JHA).

Focusing on this induced soldier caste differentiation, we used histological, physiological and molecular approaches to investigate how JH regulates specific caste morphogenesis.

During the soldier caste differentiation, fat body growth occurred rapidly after JHA treatment, accompanied by storage of protein granules, which were mobilized for morphogenesis prior to the presoldier molt. JHA also induced conspicuous changes in the corpora allata, and particularly hypertrophy of the molt gland.

Moreover, intrinsic JH titer was quantified by the LC-MS method during artificially induced soldier differentiation and also in all natural castes. The obtained JH titer patterns validate the previous model of termite caste determination for most pathways, with the exception of pseudergate stationary molt, which occurs after a peak of JH, prior to the molt.

Specific gene expression induced by JHA treatment was also investigated by differential display and suppressive subtraction, leading to the identification of several JH-regulated genes, such as P450, hexamerins and a putative nuclear protein. Those genes are suggested to participate in the regulation of JH titer and in the mechanism of response to JH.

Multidiscipline approach for studying the climate and molecular phylogeographic analysis of termites

Haidi Badawi, Amgad Elmahdi

[1]Biological Sciences, Flinders University, Adelaide, Australia, [2]CSIRO land and water, Adelaide, Australia

Global warming issue and increasing vulnerability of biodiversity are the main issues facing the world and particularly Australia, Australia has a rich fauna of termites mainly in mainland areas. Termites are primarily tropical and subtropical insects, and play an important role as an 'ecosystem engineers' because of their ability to decompose wood material. They have major effects as nutrients recyclers, and in influencing energy flow. Since Australia is facing sever drying conditions and reduced rainfall and precipitation which in turn reduced soil moisture and changed soil physical characteristics. Therefore, recently there are few study attempted to identify and establish the link between termites' distribution (phylogeographgy), invasions to climate and how this distribution might change with global warming and changes in drought frequency.

Hence, this study attempts to study the link between termites phylogenography and climatic conditions by applying molecular DNA bar-coding analysis for termites species from different climatic zones and states to develop a multidisciplinary integrated distributional model approach for Australian termite fauna in consideration of several factors such as vegetation type, ecosystem nature, temperature average, average rainfall, evaporation rate and soil type. This study can give answers for the major questions about Australian termite's fauna biodiversity. Preliminary results show there is a clear tradeoff between climate conditions and termite's distribution and biodiversity, the most sensitive parameters are rainfall, soil moisture, precipitation and temperature.

Multidiscipline approach for studying the climate and molecular phylogeographic analysis of termites

Haidi Badawi, Amgad Elmahdi

[1]1Biological Sciences, Flinders University, Adelaide, Australia, [2]CSIRO land and water, Adelaide, Australia

Global warming issue and increasing vulnerability of biodiversity are the main issues facing the world and particularly Australia, Australia has a rich fauna of termites mainly in mainland areas. Termites are primarily tropical and subtropical insects, and play an important role as an 'ecosystem engineers' because of their ability to decompose wood material. They have major effects as nutrients recyclers, and in influencing energy flow. Since Australia is facing sever drying conditions and reduced rainfall and precipitation which in turn reduced soil moisture and changed soil physical characteristics. Therefore, recently there are few study attempted to identify and establish the link between termites' distribution (phylogeographgy), invasions to climate and how this distribution might change with global warming and changes in drought frequency.

Hence, this study attempts to study the link between termites phylogenography and climatic conditions by applying molecular DNA bar-coding analysis for termites species from different climatic zones and states to develop a multidisciplinary integrated distributional model approach for Australian termite fauna in consideration of several factors such as vegetation type, ecosystem nature, temperature average, average rainfall, evaporation rate and soil type. This study can give answers for the major questions about Australian termite's fauna biodiversity. Preliminary results show there is a clear tradeoff between climate conditions and termite's distribution and biodiversity, the most sensitive parameters are rainfall, soil moisture, precipitation and temperature.

Preliminary investigations into a potentially new ant invader in Kruger National Park, South Africa

Hendrik Sithole, Catherine Parr, Izak Smit

[1]South African National Parks, Mpumalanga, South Africa, [2]Environmental Change Institute, Oxford University Centre for the Environment, University of Oxford, England, United Kingdom

Introduction: A rapid increase in the abundance of *Lepisiota incisa* (Forel) in residential areas of Kruger National Park (KNP) raised concerns that it might be exotic and invade KNP's ecosystems. This prompted this study to (i) explore current distribution and abundance of *L. incisa* around main residential area, (ii) assess ant diversity at *L. incisa*-dominated and non-dominated habitats, (iii) investigate mechanisms responsible for its dominance, and (iv) determine aggression levels among its nests.

Methods: Spread of *L. incisa* from residential area was determined by bait transects from the gardens' edge into undisturbed natural areas. Ant diversity and composition was determined by pitfall trapping in five habitats varying in disturbance. Aggression levels were assessed by introducing individual ants from one nest to another, and noting behaviour on a four-level aggression scale.

Results: *Lepisiota incisa* decreased in abundance when moving further away from the residential area. It was most abundant in gardens. Species richness of other ants was significantly lower in gardens. Ant assemblage composition varied significantly between all habitats. *Lepisiota incisa* recruited to baits significantly faster in gardens, and mostly coexisted with other species. Aggression level was low among eight nests, but high between the ninth and other eight nests.

Conclusions: *Lepisiota incisa* could be exotic. It remains confined to settlement but it may spread because it sustained itself on sites that are far from the residential area. There is unicoloniality among most nests. Its ability to exploit anthropogenic conditions, mostly coexist with other ants and unicoloniality among nests, cause it to dominate residential area.

Fruit fly population and damage in SIT and non-SIT treated deciduous fruit growing areas of the Western Cape Province, South Africa

Aruna Manrakhan, Pia Addison

University of Stellenbosch, Matieland, Western Cape, South Africa

Introduction: Two fruit fly species (Diptera: Tephritidae) that hamper production of commercial fruits in the Western Cape Province, South Africa, are Mediterranean fruit fly (Medfly), *Ceratitis capitata* (Wiedemann) and Natal fruit fly, *Ceratitis rosa* Karsch. Since 1999, a Sterile Insect Technique (SIT) programme was implemented and is ongoing to control Medfly populations in some deciduous fruit growing areas. In areas where SIT is not implemented, growers use mainly poisoned protein bait sprays to control fruit flies. A study was conducted from 2006 to 2008 to determine and compare fruit fly population levels and damage in areas under these two management practices.

Methods: Five study areas were selected: 3 under SIT and 2 under non-SIT control. In each area, 3-5 orchards were selected and in each orchard 4 traps baited with a food attractant, Biolure- 3 component, were placed. Traps were monitored on a fortnightly basis. At harvest, mature ripe fruits were examined on trees for fruit fly damage. All infested fruits were brought to the laboratory and incubated to determine species composition and degree of infestation.

Results: Medfly was the dominant species in traps and in infested fruits. Patterns of fruit fly population were similar in all study areas with a peak occurring between February and April, coinciding with the end of the fruiting season. There was no distinct association of Medfly adult population levels with management practices. Stone fruits and table grapes were the most susceptible hosts. Very low levels of damage (<1%) were recorded on pome fruits.

Developing a process-based population model for *Paropsis atomaria* Olivier, an emergent pest in subtropical hardwood plantations in Australia

Simon Lawson[1], Helen Nahrung[1], Mark Schutze[2], Anthony Clarke[2], Michael Duffy[2], Elizabeth Dunlop[2]

[1]Department of Primary Industries & Fisheries, Indooroopilly, Qld, Australia, [2]Queensland University of Technology, Brisbane, Qld, Australia

Introduction: The eucalypt leaf beetle, *Paropsis atomaria*, is an emerging pest of eucalypt plantations in subtropical eastern Australia, and potentially overseas, due to its wide host range of more than 20 eucalypt species and broad geographical distribution.

Methods: Low temperature thresholds, temperature-induced mortality, and day-degree requirements for immature stages were obtained in the laboratory using beetles sourced from temperate and subtropical zones and combined with field mortality estimates of these stages to produce a process-based population model, ParopSys, using DYMEX™. To validate the model, phenological data were obtained every two weeks between October 2005 and April 2006 from a field population of the beetle.

Results: ParopSys accurately predicted timing, duration and relative abundance of life-stages in the field and number of generations in a spring-autumn (September to May) field season. Two generations were predicted in the Australian Capital Territory, and up to four in Queensland, closely matching field observations.

Conclusions: ParopSys provides a basic tool enabling forest managers to: 1) use the number of generations and seasonal fluctuations in abundance to estimate the pest risk of *P. atomaria* prior to plantation establishment, 2) predict the occurrence and duration of damaging lifestages in the field, and 3) assist in decision making with regard to selection and timing of controls. Additionally, by using local climatic data the pest potential of *P. atomaria* can be estimated to predict the risk of establishment if accidentally introduced overseas. Improvements to the capability and complexity of ParopSys will be made as more biological data become available.

Biomimicry of termite engineering as solution for water and soil conservation

Amgad Elmahdi, Haidi Badawi

[1]Csiro land and water, Adelaide, Australia, [2]Biological Sciences, Flinders University, Adelaide, Australia

Nature has so much to offer to the current challenges facing societies and world, but unfortunately, societies tend to ignore or resort nature's offer/solution as the last option. Nowadays, world/mankind is facing a huge number of environmental problems. However, if researchers pay more attention to studying and understanding nature and nature's positive laws, it should help them play a critical role in overcoming and healing most of these problems. The main focus of this study is to present humanity and termites as design partners in the creation of a new dimension of water and soil conservation understanding. This understanding is based upon the likelihood that termites, as truly symbiotic detrivores, have developed optimal architecture and design for water and soil conservation in ecosystems over millions of years.

In this biomimicry concept study the objective is to present and discuss termite design for better water and soil management by government, industry and the public. Termites create environments that regulate and maintain near-constant moisture and temperature (green energy technology). Termites also create self-regulating energy systems that need no mechanical power for cooling and/or heating. In tropical climates, termites improve soil structure and moisture holding capacity and conserve water irrespective of changing environmental conditions. Thus, the focus/emerge question is can water and soil stakeholders mimic termite management systems in their bid to manage and sustain natural water and soil systems?

Heat and odour of *Macrozamia* cycad cones offer mixed cues to their host specific thrips pollinators

Irene Terry, Gimme Walter, Robert Roemer, Chris Moore

[1]University of Utah, Salt Lake City, UT, United States, [2]University of Queensland, Brisbane, QLD, Australia

The cones of Australian *Macrozamia* cycads are pollinated by host specific *Cycadothrips* species. Cones have daily thermogenic bouts during their pollination phase when male cones dehisce pollen and female cones are receptive. During a thermogenic event, cone odor emissions greatly increase and thrips leave their male host cones en masse. Later in the day the thrips recolonise male cones and some thrips enter females and pollinate them. Male cones serve not only as the sole food source for *Cycadothrips* (pollen) but also as a site for mating, oviposition, shelter and a nursery for their developing young. Why, then, do thrips leave such a suitable environment when there is ample pollen remaining and why do some of them visit female cones that offer little to no reward. Results of behavioural assays demonstrate that cone odors act in a concentration-dependent, push-pull, manner that drives thrips from cones at high concentrations and attracts them at lower levels. Female cones attract thrips by emitting the same chemical volatiles as their conspecific males, but at lower concentrations. Even though odour alone is sufficient to drive thrips out of cones, cone temperature and light are important modulators of thrips behaviour. Results suggest that either cone volatiles or thermogenic temperature increases drive thrips from cones, and only cone fragrances attract them.

Fatal attraction or just attraction? Evaluating alternative hypotheses on the occurrence of sexual cannibalism in praying mantids

Michael R. Maxwell[2], Katherine L. Barry[1], Shekar Viswanathan[2]

[1]Macquarie University, NSW, Australia, [2]National University, La Jolla, California, United States

Introduction: Sexual cannibalism, the consumption of the male by the female during or after courtship or copulation, occurs in many mantids. Explanations of the occurrence of sexual cannibalism have typically centered on ultimate considerations (fitness consequences to the sexes). In the North American mantid *Stagmomantis limbata,* we examine various proximate explanations (mechanistic, physiological) that address the question: how does a male come to be with a cannibalistic female? Field and captive experiments examine mechanisms of mate attraction and nutritional influences on female behavior.

Methods: Presence of female pheromone was analyzed via behavioral assays in the field and gas chromatography. Females were maintained on food-abundant and food-limited diets to examine male responses in field.

Results: Females appear to release tetradecanal as part of long-range pheromones. Male attraction is dependent on the female's nutritional status.

Conclusions: This study argues against a purely "Visual search" conducted by males, as well as against the notion that food-limited females attract males as part of a "Foraging" tactic. Two hypotheses concerning the expression of sexual cannibalism remain viable. The first is "Fatal mate", which posits that relatively well-fed females emit pheromones, and then attack males at some stage in the sexual encounter. The second is "Poaching" by poorly-fed females that do not emit pheromones, but may intercept males that are attracted to the pheromones of conspecific females.

Determination of *Lantana camara* L. (Verbanaceae) biotypes and evaluation of its biological control agents in Swaziland

Cebisile N. Magagula

University of Swaziland, Kwaluseni, Swaziland

Introduction: The study sought to ascertain the various *Lantana* biotypes in the country based on morphological features of the *Lantana* plants. Additionally, the existence of biological control agents which are known to have been introduced and established in South Africa, was to be determined.

Methods: Insects collected from *Lantana camara* by beating and visual inspections in three sites within the country were assessed and compared with natural enemies that have been released in South Africa. The study sites were located in the highveld (Hhohho), middleveld (Nhlambeni) and lowveld (Tambuti).

Results: Based on flower colour, three lantana biotypes were observed during the survey and these had varying distribution within the regions assessed. Six out of the nine natural enemies released in South Africa were found during the survey. Three of these, i.e. *Orthezia insignis,* a sap sucking bug; *Telionemia scrupulosa*,also a sap sucking bug and *Octotoma scabripennis,* a leaf mining bug were found only in the highveld. *Hypena laceratalis,* a leaf chewing moth caterpillar; *Ophiomyia camarae*, a seed feeding fly and *Ophyiomia lantanae,* the herringbone leafminer, were found in all three regions. The highveld had the highest number of natural enemies and the highest level of damage compared to the middleveld and the lowveld.

Conclusions: Due to the varying climatic conditions, further investigation on a suite of these agents in the country is needed to ensure that any natural enemies used are able to cope and compensate for each other and with any limiting factors which would negatively impact their individual impact.

Modelling the potential distribution of the Asiatic citrus psyllid, *Diaphorina citri* Kuwayama (Hemiptera: Psyllidae), in Australia under increasing temperatures predicted by climate change

Kyla Finlay[1], Jean-Phillipe Aurambout[2], Joanne Luck[1]

[1]Biosciences Research Division, Department of Primary Industries, Victoria. 621 Burwood Highway, Knoxfield, VIC 3180, Melbourne, Victoria, Australia, [2]Future Farming Systems, Department of Primary Industries, Victoria. 32 Lincoln Square North, Parkville, VIC 3052, Melbourne, Victoria, Australia

Introduction: Effects of climate change on Australian agriculture via impact on agricultural pests and diseases are virtually unknown. This paper assesses the impact of increasing temperatures on the behaviour, distribution and breeding potential of the exotic Asiatic citrus psyllid, *Diaphorina citri* Kuwayama (Hemiptera: Psyllidae), vector of the bacterial disease huanglongbing (citrus greening) and a major threat to the Australian citrus industry.

Methods: A combined plant physiology and pest development spatial model was developed to understand the effect of increasing temperatures on the behaviour, distribution and breeding potential of *D. citri* in relation to its citrus hosts. The model was then applied to scenarios of changing climatic conditions at a continental scale.

Results: Detection of potential *D. citri* infestations should start earlier in the season due to temperature effects on timing of the first flush (new tissue growth). As warmer temperatures shorten the psyllid life cycle and period of flush availability, an overall decrease in psyllid numbers is predicted throughout Australia. However results will be spatially heterogeneous with increasing temperatures in southern Australia presenting an increased threat from *D. citri.* The model has the potential to include variables such as increased growth of host due to elevated CO_2, presence of alternate hosts and reduced water availability.

Conclusions: Overall *D. citri* presents a reduced threat to Australian citrus under increasing temperatures but southern Australia will become more suitable to establishment and infestation of *D. citri.* Pest-host integrated models provide a powerful tool to assist in prioritizing biosecurity threats.

Novel associations between insects, ophiostomatoid fungi and tree hosts following anthropogenic spread

Michael J. Wingfield, Bernard Slippers, Wilhelm de Beer, Jolanda Roux, Brenda D. Wingfield

Forestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, South Africa

The ophiostomatoid fungi including species of *Ophiostoma sensu lato* and *Ceratocystis sensu lato* are well known associates of insects. While there are interesting exceptions, most *Ophiostoma* spp. are vectored by bark beetles whereas the majority of *Ceratocystis* spp. are associated with casual vectors such as nitidulid beetles and flies. The acquisition of novel vectors of the *Ophiostoma* spp. following anthropogenic spread has been well-known since the onset of Dutch Elm Disease, early in the last Century. As the movement of people and products around the world has grown, there has been a concomitant increase of new introductions of Ophiostomatoid fungi in many parts of the world. Intriguing and worrying associations between these fungi and unexpected insect associates are emerging. To define and understand these associations is complicated by a confused and incomplete taxonomy of the fungi. This is particularly true in the case of *Ceratocystis* spp., which are taxonomically less well known than *Ophiostoma* spp. However, DNA-based techniques allowing phylogenetic inference and population genetic analyses have contributed substantially to our understanding of these important fungi and their insect associates. It is thus likely that many new discoveries relating to the Ophiostomatoid fungi and their vectors will emerge in coming years. These in turn will lead to new concepts in forest protection and they will elevate our capacity to deal with the emerging pest and disease problems associated with a relatively poorly understood group of pathogens that threaten world forests.

Anhydrobiosis in the sleeping chironomid, *Polypedilum vanderplanki*: unique tactics to survive drought

Takashi Okuda[1], Takahiro Kikawada[1], Minoru Sakurai[2], Takao Furuki[2], Ken-ichi Akao[3], Yuichi Nakahara[1], Oleg Gusev[1], Ayako Saito[1], Masahiko Watanabe[1], Yasushi Kanamori[1], Daisuke Tanaka[1], Ken-ichi Iwata[1], Mika Fujita[1], Kanako Mitsumasu[1], Richard Cornette[1]

[1]National Institute of Agrobiological Sciences, Tsukuba, Ibaraki, Japan, [2]Tokyo Institute of Technology, Yokohama, Kanagawa, Japan, [3]JASCO Corporation, Hachioji, Tokyo, Japan

Polypedilum vanderplanki is a temporal pool dweller in the semi-arid regions of Africa. The small and shallow pools are easily dried up during dry season and *P. vanderplanki* larvae are also desiccated completely. They are however able to revive within an hour after rehydration by the next rain as if without ill effects. This developmental arrest with zero-metabolism is so called “cryptobiosis” or “anhydrobiosis” Our interest is to know the mechanism how *P. vanderplanki* larvae can stand complete desiccation. Larvae accumulated a great amount of trehalose (20% of larval dry weight) as compatible solute replacing water upon dehydration. LEA (late embryogenesis abundant) proteins (initially isolated from plant seeds) also occurred in *P. vanderplanki*. Physico-chemical analysis revealed that the anhydrobiotic larvae enter a vitrified state which is certainly stabilizing molecules and cell membranes of the larvae under complete dehydrartion, and both hydrophilic molecules (trehalose and LEA proteins) were importantly contributing to the glass formation. Other protective factors such as heat-shock proteins (HSPs) and anti-oxidative enzymes were also expressed for self-protection. Nevertheless, to our surprise DNA was damaged during anhydrobiosis. The mending of the damage should take place after rehydration.

Recently we isolated a trehalose transporter, *tret1* from *P. vanderplanki.* This gene has a great potential for application such as anhydro- and cryo-technology.

The success of biopesticides in Australian broadacre crops

Caroline Hauxwell[1], Patrick Buerger[2], Dave Murray[1]

[1]Department of Primary Industries & Fisheries, Queensland, Australia, [2]Ag Biotech Australia Pty Ltd, Richmond, New South Wales, Australia

Broadacre crop production in Australia was in crisis in the late 1990s due to high pest pressure from *Helicoverpa* spp. and escalating cost of and resistance to chemical insecticides. An integrated management strategy that included the use of baculovirus insecticides was introduced to break the cycle of insecticide resistance and maintain beneficial insects while reducing pest damage.

Biopesticides based on Nucleopolyhedrovirus (NPVs) have efficacy against insecticide resistant *Helicoverpa* spp. and low impact on natural enemies. They can be used in the early season to control spring flights of *H. punctigera* and emerging *H. armigera* populations, which reduces early season selection for insecticide resistance and further pest outbreaks by maintaining beneficial insects.

Research and development by the Queensland Department of Primary Industries (DPI&F) has supported the registration and manufacture of four commercial NPV insecticides: 'Gemstar', imported from the USA, and three domestic products, 'Vivus', 'Vivus Gold' and 'Vivus Max'. High quality, availability and viable pricing created a successful market in a broad range of commercial crops including sorghum, cotton, sweetcorn and lettuce. Further research in targeting, timing and formulation by DPI&F led to improved field efficacy. In grain sorghum, 95% of the sprayed crop area is NPV treatment.

Surveys have shown that mainstream growers and agronomists give top priority to efficacy, resistance management, maintaining beneficial insects and reducing secondary pest outbreaks. The success of NPVs has increased grower confidence in biopesticides as part of an integrated strategy, and led to a demand for similar 'soft' options against emerging sucking pests.

Improved formulation of *Baculovirus* insecticides against *Helicoverpa armigera* in Australian broadacre crops

Caroline Hauxwell[1], Andrew Reeson[2]

[1]Department of Primary Industries and Fisheries, Queensland, Australia, [2]CSIRO Sustainable Ecosystems, Canberra, ACT, Australia

Biopesticides based on Nucleopolyhedrovirus (NPV) are established tools in pest control and insecticide resistance management against *Helicoverpa* sp. in Australian cotton, sorghum and horticultural crops.

A range of commercial additives and reducing sugars, including mannitol, were tested for improvement of NPV efficacy on cotton. While many additives enhanced performance to some degree, there was a significant increase in efficacy with increased relative sweetness. Mannitol, thought to increase efficacy through neutralizing free radicals generated in the cotton leaves, was found to have limited enhancement effects relative to significant increases in efficacy with high sweetness additives.

Emulsified spray oils increased NPV efficacy at 2%, but with reduced enhancement with increasing concentrations. However, a combination of emulsified oil with high sweetness sugars resulted in a dramatic increase in viral potency on cotton plants. Ultra Low Volume application of NPV in oil with low cost, high-fructose sugar additives was more effective at controlling *Helicoverpa* in field trials than conventional spray application in water. The results demonstrate the benefits of practical, low-cost additives to enhance NPV field efficacy.

The ovo-pupal parasitoid *Fopius arisanus*, a promising biocontrol agent for the peach fruit fly, *Bactrocera zonata*, in Reunion Island

Serge Quilici[1], Pascal Rousse[1], Christophe Simiand[1], Antoine Franck[1], Frédéric Gourdon[1], Thomas Mangine[2], Ernest Harris[2]

[1]CIRAD, La Réunion, France, [2]USDA, Hawaii, United States

Introduction: The peach fruit fly, *Bactrocera zonata*, is a polyphagous tephritid which established in Reunion Island in 2000 and became dominant in the lowland areas. The ovo-pupal parasitoid *Fopius arisanus* was introduced from Hawaii in 2003, in collaboration with USDA. Studies were conducted to determine its survival and specificity on the tephritid species of economic importance present in Reunion Island. Releases were then conducted in various sites in order to obtain the acclimatization of the parasitoid.

Methods: Laboratory studies were conducted to determine the pre-imaginal development of the parasitoid on its different tephritid hosts. The response of adult female to host habitat and host odors was determined using a release-capture method in field-cages.

Results: Laboratory studies showed that this parasitoid could develop on several tephritids of economic importance, though *B. zonata* was the preferred host. The females positively responded to odours of various plants and to a kairomone present on tephritid eggs. In 2006, surveys revealed the presence of the parasitoid in various areas, on different host-fruits. On Indian almond (*Terminalia catappa*), on which *B. zonata* is the dominant species, the level of parasitism, though very variable, could at times reach 70-80 %.

Conclusion: The successful acclimatization of this parasitoid aims at decreasing the populations of the peach fruit fly in “reservoir areas” where huge populations used to develop in the absence of an effective biocontrol agent. Future studies will focus on defining the impact of this promising parasitoid in different ecological conditions and on different host fruits.

Codling moth and CpGV interactions: Resistance versus virulence

Marie Berling[1], Miguel lopez-ferber[1], Benoît Sauphanor[2], Antoine Bonhomme[3]

[1]EMA, ALES, France, [2]INRA, Avignon, France, [3]NPP, PAU, France

Introduction: The *Cydia pomonella Granulovirus* (CpGV) is widely used in codling moth control. Since 2004, after fifteen years of application, some CpGV resistant populations were detected in organic orchards in France, Germany and Italy. The resistance ratio can reach 50,000–fold in the laboratory. Virus formulations commercialized in Europe all derive from the same Mexican isolate and the resistance seems to be directed against this isolate.

Results: In a first step, various viral isolates were used to challenge both the susceptible (Sv) and the resistant (Rgv) laboratory colonies of codling moth. Among them, the NPP-R1 isolate was the most promising. Its efficiency on Sv larvae was similar to that of the Mexican isolate. On the Rgv colony, it presented the highest activity with a LC_{50} and LC_{90} respectively 6- and 18-fold higher than on the Sv colony. The success of the pest control in field could be tampered by this difference of efficiency between resistant and susceptible larvae. The second step was thus to try to improve the efficiency of NPP-R1 by successive cycles on Rgv larvae. After only four cycles of selection, this process led to a 30 % reduction in the LC_{50} on the Rgv strain. An even higher improvement was observed for the LC_{90} on this strain which was divided by three. No significant variation on the efficiency was observed on Sv larvae

The ancient origins, phylogeography and conservation of Hawaii's aquatic moths

Daniel Rubinoff, Patrick Schmitz

The University of Hawaii, Honolulu, Hawaii, United States

Introduction: The Cosmopterigid moth genus *Hyposmocoma* may be the most diverse endemic Hawaiian genus with nearly 400 recognized species though little research has been conducted. Amongst this diversity are aquatic moths, capable of remaining submerged for days. The evolution of this globally rare lifestyle in Hawaii has implications for the patterns and constraints of insect evolution. Because *Hyposmocoma* has endemic species from 20 million year old Hawaiian atolls, direct examination of lineage age and time of colonization is possible. Additionally, patterns of *Hyposmocoma* diversity can guide prioritization of regions and habitats on which conservation attention should be focused.

Methods: Aquatic and terrestrial moths were reared from across the Hawaiian Islands, including Northwest atolls. Phylogenies, based on sequence from two nuclear and one mitochondrial gene, are constructed using maximum parsimony, maximum likelihood and Bayesian models.

Results: Multiple invasions and reversions of the aquatic ecology are strongly indicated despite it being a globally rare evolutionary pathway due to the constraints of an aquatic lifestyle. Biogeographic patterns are presented. *Hyposmocoma* may be one of the oldest extant lineages in the archipelago. Species appear to be universally single-island endemics, some with very restricted ranges.

Conclusion: Aquatic *Hyposmocoma* are extremely diversified, and have rapidly evolved in and out of the aquatic environment. Riparian degradation appears to have limited the range of many populations, and aquatic *Hyposmocoma* may serve as indicator species for assessments of riparian habitat or water quality. Aquatic Lepidoptera are a global evolutionary anomaly, making Hawaii's radiation especially worthy of examination and preservation.

Allee effects and high dispersive behaviour: Antagonist forces in potentially invasive bark beetles

Jean-Claude Grégoire[1], Marius Gilbert[2]

[1]Université Libre de Bruxelles, Bruxelles, Belgium, [2]Fonds National de la Recherche scientifique, Bruxelles, Belgium

Introduction: Among the numerous records of Scolytine beetles established in new areas after having crossed a geographic barrier, there is no mention of aggressive, tree-killing *Ips* or *Dendroctonus* species. The continental European species, *Ips typographus*, in particular, has been regularly intercepted in the UK, the US and Canada but there is no record of successful establishment of this species.

Methods: An "invasion" experiment was performed within the distribution area of the species but in an area (Champagne, France) devoid of spruce and hence devoid of *Ips typographus*. 35 m³ of infested timber was introduced from Belgium in a pine and oak stand and beetle dispersal was followed using pheromone traps. In parallel, the reservoir of beetles in the air was followed in a 180 km transect of pheromone traps starting in spruce area and ending deep in the spruce-free area.

Results: Out of the estimated 300,000 insects released, only 5,000 were caught, mostly in the near vicinity of the infested timber. The catches along the transect steeply declined with the distance to the spruce area.

Conclusions: It is hypothetised that the conditions for success of highly dispersive species such as *Ips typographus* lie in the presence of population reservoirs fed by numerous sources, and which use pheromone communication to focus on susceptible host trees. In the absence of such population reservoirs, the chances of success of an invasive population appears extremely low.

Allee effects and high dispersive behaviour: Antagonist forces in potentially invasive bark beetles

Jean-Claude Grégoire[1], Marius Gilbert[2]

[1]Université Libre de Bruxelles, Bruxelles, Belgium, [2]Fonds National de la Recherche scientifique, Bruxelles, Belgium

Introduction: Among the numerous records of Scolytine beetles established in new areas after having crossed a geographic barrier, there is no mention of aggressive, tree-killing *Ips* or *Dendroctonus* species. The continental European species, *Ips typographus*, in particular, has been regularly intercepted in the UK, the US and Canada but there is no record of successful establishment of this species.

Methods: An "invasion" experiment was performed within the distribution area of the species but in an area (Champagne, France) devoid of spruce and hence devoid of *Ips typographus*. 35 m^3 of infested timber was introduced from Belgium in a pine and oak stand and beetle dispersal was followed using pheromone traps. In parallel, the reservoir of beetles in the air was followed in a 180 km transect of pheromone traps starting in spruce area and ending deep in the spruce-free area.

Results: Out of the estimated 300,000 insects released, only 5,000 were caught, mostly in the near vicinity of the infested timber. The catches along the transect steeply declined with the distance to the spruce area.

Conclusions: It is hypothetised that the conditions for success of highly dispersive species such as *Ips typographus* lie in the presence of population reservoirs fed by numerous sources, and which use pheromone communication to focus on susceptible host trees. In the absence of such population reservoirs, the chances of success of an invasive population appears extremely low.

Economic threshold for the management of *Plutella xylostella* with granulovirus in cauliflower

Sevgan Subramanian[1], R. J. Rabindra[2], Natarajan Sathiah[3]

[1]International Centre of Insect Physiology and Ecology, Nairobi, Kenya, [2]Project Directorate for Biological Control, Bangalore, India, [3]Tamil Nadu Agricultural University, Coimbatore, India

Introduction: Resistance to insecticides and some bio pesticides by *Plutella xylostella* (DBM) has resulted in the search for alternative options in its management. The *P. xylostella* granulovirus (PlxyGV) has emerged as an effective option for DBM management. However use of PlxyGV would be economical only when the pathogen is applied at the right crop stage and at economic threshold levels.

Methods: Field level economic threshold for application of PlxyGV at the reproductive phase of cauliflower was evaluated in two different sites of Tamil Nadu with application of virus at thresholds of >5, >10, >15 and >20 larvae per 10 plant. Observations on the DBM population and cauliflower yield in different treatments were undertaken.

Results: PlxyGV was very effective in the management of DBM and it was comparable to weekly application of Quinalphos 25EC. Due to higher cost of PlxyGV applications than Quinalphos, the benefit cost ratio with insecticide was much higher than the virus. The net returns from the virus application decreased both at lower thresholds due to higher cost of plant protection and at higher thresholds due to the increased damage by the pest. Based on net income per ha and plant protection cost, PlxyGV application at threshold of 10-12 larvae per 10 plant was optimum with the net return just equal to the plant protection cost.

Conclusion: An economic threshold level of 10 – 12 larvae per 10 plants in the reproductive phase is suggested for the use of PlxyGV in the management of DBM in cauliflower.

A geographic mosaic of selection in a generalized plant-pollinator-herbivore system

Jose M Gomez[1], Francisco Perfectti[1], Jordi Bosch[2], Juan P M Camacho[1]

[1]University of Granada, Granada, Andalusia, Spain, [2]CREAF, Barcelona, Catalunya, Spain

Selection mosaic is central to the Geographic Mosaic Theory of Coevolution. Most information on coevolving interactions, however, is coming from specialized organisms. In contrast, an accurate understanding of the effect of geographically varying evolutionary dynamics on the evolution of generalist organisms is still lacking, despite this kind of organisms are the most frequent at nature. In flowering plants, pollinators and herbivores are important selective agents driving the evolution of many floral traits. In this study we investigate the selection mosaic caused by pollinators and herbivores in the generalist herb *Erysimum mediohispanicum*, by quantifying in eight populations from SE Spain the selection exerted by these organisms on several plant traits (flower number, stalk height, corolla shape and diameter, and corolla tube length and width). We found that different populations were under different selective regimes, and the traits affected by selection depended on the predominant local pollinators and the intensity of mammal herbivory. This spatial variation in selection scenarios results in populations with strong selective regimes (hot spots) intermingled with populations with weak selective regimes (cold spots), suggesting the occurrence of a selection mosaic for *E. mediohispanicum*. Four important features characterized this geographic mosaic: 1) The interactions with generalist organisms, contrary to the conventional wisdom, produced strong selection; 2) There was divergent selection across populations as a consequence of spatial changes in main pollinators; 3) The outcomes of the geographic mosaic depended on a balance between mutualistic and antagonistic selection; 4) The selection mosaics operated at fairly small spatial scales**.**

Structures and uptake mechanisms of vitellogenins in cockroaches

Makio Takeda, Mohamed El-Sayed El-Mogy, Tufail Muhammad

Kobe University, Kobe, Hyogo-ku, Japan

The reproductive success of insects depends on vitellogenin (Vg, the major yolk protein precursor) biosynthesis and its internalization by Vg receptors (VgRs) into the developing oocytes. The Vg is synthesized extraovarially in the fat body cells and transported through hemolymph to the oocytes where it is deposited by membrane-spanning receptors, the VgRs, through receptor-mediated endocytosis. Once sequestered by growing oocytes, the Vg is sent to yolk bodies, where it is processed for storage, thus providing main nutritional reserves necessary for the embryo development.

We have characterized the molecular structures of four Vg molecules, the two (Vg1 and Vg2) being that of the American cockroach, *Periplaneta americana* (Tufail et al., 2000, 2001 2005), whereas, the two (Vg1 and Vg2) being that of the Madeira cockroach, *Leucophaea maderae* (Tufail and Takeda, 2002; Tufail et al., 2007). We also demonstrate the synthesis and expression pattern of both the transcript and the protein, and clarify, on molecular basis, that how Vgs undergo a complicated pattern of post-transcriptional processing. The data on phylogenetic analysis suggests that Vgs are still phylogenetically bound, although divergence exists among them, and can be used as a molecular marker.

Also, we report cloning/characterization of two VgRs from ovaries of the two cockroach species, *P. americana* (Tufail and Takeda, 2005) and *L. maderae* (Tufail and Takeda, 2007) and confirm that a ~7.3 kb transcript was specifically expressed in ovarian tissues at high levels throughout ovarian development, especially in previtellogenic ovaries and in ovaries before adult emergence. RNA *in situ* hybridization and immunocytochemistry localized VgR mRNA and the protein only in germ line-derived cells, the oocytes, and revealed that VgR gene transcription and translation begin very early during oocyte differentiation in the germarium. Furthermore, we observed the timing of uptake of both *Vg* genes products using immunoblotting in *P. americana*, and found that the receptor-endocytotic mechanism starts functioning soon after the ligand becomes available.

We will report the structure and functions of Rab5 protein, a small Ras-like GTPase, involved in Vg uptaking endocytosis in *P. americana* oocyte.

Ancient diversification and evolution of large circular dsDNA viruses of insects

Johannes A. Jehle[1], Monique M. van Oers[2], Regina G. Kleespies[3], Just M. Vlak[2], Yongjie Wang[1]

[1]Agricultural Service Center Palatinate, Neustadt/Wstr., Germany, [2]Laboratory of Virology, Wageningen University, Wageningen, Netherlands, [3]Institute for Biological Control, Julius Kuehn, Darmstadt, Germany

Numerous viruses have been identified in different insect species. Among these, the baculoviruses are one of the largest and most diverse groups of viruses. Presently, 43 baculovirus genomes have been sequenced. They share 29 homologous genes, which are considered as the baculovirus core genes. Their evolutionary relationship to other large circular dsDNA viruses infecting insects and crustacea has not been elucidated. Here we will provide new insight into the diversification and evolution of large circular DNA viruses based on comparative analyses of their genomes. The genomes of two nudiviruses, the beetle-infecting *Oryctes rhinoceros* nudivirus (OrNV) and the cricket-specific *Gryllus bimaculatus* nudivirus (GbNV), have been cloned and sequenced. They are 127,615 bp (OrNV) and 96,944 bp (GbNV) in size, respectively. In-depth genome sequence comparisons revealed that homologues of 20 baculovirus core genes are conserved in the genomes of OrNV, GbNV, and in *Heliothis zea* nudivirus 1. These 20 genes are associated with transcription (*p47*, *lef-8*, *lef-9*, *lef-4*, *vlf-1*, and *lef-5*), replication (*dnapol* and *helicase*), virion structure (*p74*, *pif-1*, *pif-2*, *pif-3*, *vp91*, *vp39*, *38K*, *19kda* and *odv-e56*), and with yet unknown functions (*ac68*, *ac81* and *p33*). The four *pif* genes (*p74*, *pif-1*, *pif-2* and *pif-3*) of baculoviruses are involved in virus binding to and in entry into midgut epithelial cells and hence are essential for successful infection of insect hosts *per os*. Genome wide analysis indicated that the baculoviruses and nudiviruses share a common ancestor and form monophyletic group. The phylogeny and evolution of these viruses will be discussed.

Comparative study on the morphology of egg pods, egg development and hatching of three *Hieroglyphus* species (Acrididae: Orthoperta)

Riffat Sultana, M.Saeed Wagan

Department of Zoology, Jamshoro, Pakistan

Comparative study of egg pods of agriculturally important grasshoppers were carried out in Pakistan between the years 2005-2006. Searches were made of oviposition sites under laboratory condition. The three principal grasshopper species found at these oviposition sites were *Hieroglyphus perpolita* (Uvarov), *H.oryzivorus* Carl and *H. nigrorepletus* I. Bolivar.

1. Female usually lays a heap of eggs in grounds, eggs usually enclosed in a sac, consisting of the hardened secretion cemented with grains of earth; such mass of eggs is called egg-pod. The pods are sub-cylindrical and slightly curved. The weight (3.64±0.60gm) and width (22.82±2.21mm) of *H.perpolita* is significantly greater than that of *H.oryzivorus* (1.30±0.03gm) and *H.nigrorepletus* (0.185±0.003gm) whereas length of *H.oryzivorus* (34.68±0.84mm) is significantly greater than that of *H.perpolita* (27.78±0.78mm) and *H.nigrorepletus* (18.38±1.15mm).

2. Eggs cylindrically elongated, large slightly bent in the middle and rounded at ends. The size, length (6.37±0.06mm) and weight (0.128±0.01mm) of eggs of *H.perpolita* is significantly greater than that of *H.oryzivorus* (0.0054±0.0001gm), (4.52±0.07mm) and *H.nigrorepletus* (0.005±0.00006gm), (4.55±0.0063mm) weight and length respectively. Similarly there was significant difference between the weight of dry eggs and fresh laid eggs of *H.perpolita.* The egg-pod is full of eggs without any empty space. There are more eggs at the base and their number decreased towards the top.

3. The major hatching occurred with in few weeks i-e 57.43to 100% in *H.perpolita* from June to August but mostly in the month of June, 76.85% to 100% in *H.oryzivorus* from July to September (mostly in August) and 69.09% in *H.nigrorepletus* from July to August mostly in mid July hatching then stopped.

The present study described the detailed of morphological variation in egg pods of these species although the genus is same, and examines some of the factors which influences egg laying in *Hieroglyphus* whose development has been dealt with elsewhere. Present study is being reported for the first time.

Introduction on a geometric approach in the study on the patterns of divergence in ecological relevant traits in an adaptively radiated wolfspider genus from Galapagos

Charlotte De Busschere, Léon Baert, Jean-pierre Maelfait, Frederick Hendrickx

University, Ghent, Belgium

Adaptive radiation is the process in which an ancestral species induces a range of species adapted to different niches and characterized by unique features to explore these niches. Although this is a well studied topic, there is still a lot of uncertainty about the underlying processes for example when the geographical distribution is not an adequate barrier to obstruct gene flow. Whether divergence in ecological traits is merely influenced by ecological processes (ecological opportunity) or rather by the potential of species to produce alternative phenotypes is crucial for understanding the mechanisms of speciation. This research is focused on the genus *Hogna.* On the Galapagos, populations of this genus are primarily diverged in function of the geographical position of the islands and secondly in function of the habitat in a repeated pattern. Populations are recently diverged and give the potential to get insight in the first steps of speciation. These populations are difficult to distinguish morphologically and constitute several species, until now 3 species are described *H. albemarlensis, H. galapagoensis* and *H. snodgrassi.*

The main goal is to contrast the degree of divergence in both ecological and molecular traits to explain the observed patterns of this differentiation. Furthermore we would like to know to what extent divergence in ecological traits can lead to reproductive isolation. Practically, this research involves morphometric methods, biometric measurements and genetic analyses. In this poster some preliminary morphometric methods are explained to analyze shape differences in carapax, epigynum and other structures.

Impacts of frost on beech (*Fagus sylvatica* L.) susceptibility to Scolytine ambrosia beetles

Sylvie La Spina, Charles De Canniere, Abdoul-Kader Sawadogo, François Mayer, Jean-Marc Molenberg, Jean-Claude Gregoire

Université Libre de Bruxelles, Brussels, Belgium

Introduction: Beech (*Fagus sylvatica* L.) stands in Southern Belgium have suffered in the early 2000S from a steady decline, puzzling by its geographical extent, gravity and suddenness. Bark exudations and necroses broke out on the trunks, along with fungi and the appearance of xylophagous insect galleries (the ambrosia beetles *Trypodendron* spp., *Anisandrus dispar*). These insects are generally considered secondary, normally attacking weakened or dead trees. The hypothesis of a sudden cold wave in November 1998 affecting trees not yet prepared to winter conditions is highly supported by meteorological (sudden drop of temperature in mid-November 1998), and symptomatological observations (orientation of the necroses, damages correlated with altitude and wind exposition).

Methods: Frost related injuries were artificially inflicted to beech trees, by application of different levels of cold shocks on the bark, using dry ice. Beech attractiveness to scolytids was studied by using interception traps established at the base of the trees. Volatile substances produced by necrotic zones were identified, after trapping on adsorbant substrates, by gas chromatography and mass spectrometry (GC-MS). Beech susceptibility to insect attacks was estimated by the colonization success of scolytids caged on the trunk.

Results: Ambrosia beetle attacks were observed in spring 2007 inside the treated zones. Results of year 2007 and 2008 will be presented and discussed.

Proteomic identification of parasitism-specific proteins in *Plutella xylostella* larvae

Kyung-Han Song, Min-Kyo Jung, Jai-Hoon Eum, Sung-Sik Han

Korea University, Seoul, Republic of Korea

Introduction: *Cotesia plutellae,* an endoparasitoid wasp of the diamondback moth *Plutella xylostella*, uses several strategies, such as the injection of viruses, venom, and serosal membrane-derived cells called teratocytes to overcome the innate immune system of the host; however, the proteome profiles related to these immune deficiency systems have not been clearly defined. This study was carried out to investigate the differently expressed proteins in parasitized *Plutella xylostella* larvae in order to determine the parasitism- specific proteins.

Methods: The parasitism-specific proteins in the host hemolymph were analysed by two-dimensional polyacrylamide gel electrophoresis and Q-TOF MS/MS. Real-Time PCR were performed to investigate mRNA expression level of pxSerpin 2.

Results: A total of 350 protein spots were detected in the 2-D gels, and approximately 50 spots were determined to have been differentially released into the parasitized DBM larvae every 48 h. Among them, 24 potential candidates, including translationally controlled tumor protein, apolipophorin-III, pxSerpin 2, fatty-acid binding protein, and signal transduction histidine kinase, were identified through quadrupole time-of-flight tandem mass spectrometry and sequence homology. These proteins were classified to 6 groups such as immunity, Signaling-related, lipid metabolism, enzyme metabolism, glycolysis, and structure. Among them, gene of pxSerpin 2 was cloned and investigated expression profile during parasitism. Real-time PCR analysis of pxSerpin 2 revealed that there was a poor correlation between the mRNA level and protein abundance.

Discussion: Our results suggested that these parasitic proteins were related to suppress the innate immune responses from host.

Female immunity, sperm length and sperm death

Luc Bussiere[2], Gioia Schwarzenbach[1], Andrew Pemberton[1], Paul Ward[1]

[1]University of Zurich, Zurich, Switzerland, [2]University of Stirling, Stirling, United Kingdom

Reproduction and immune defence are major fitness components, and they interact phenotypically. However, few studies have investigated genetic in addition to phenotypic correlations. We selected replicate lines of the yellow dung fly, *Scathophaga stercoraria*, for the expressed level of phenoloxidase (PO), an important enzyme in insect immune responses. There were correlated responses to selection: flies in high PO lines have shorter sperm and spermathecal ducts than flies in low PO lines. Although most of the theory linking immunity and reproduction has focussed on the potential for energetic trade-offs to regulate investment in each function, instead we found support for a direct role for PO in selecting on reproductive morphology. Specifically, we show that longer sperm are more susceptible to stress, and that they are more likely to die than short sperm within the sperm storage organs of wild-type females having high PO levels. This has implications for sexual conflict research and the relationship between immunity and sex, and may also help explain inconsistent findings on the adaptive significance of longer sperm.

The efficiency of regulation of brood size in securing resources for reproduction in the burying beetle, *Nicrophorus quadripunctatus*

Tomoyosi Nisimura, Masahiro Kon

The University of Shiga Prefecture, Hikone, Shiga, Japan

Introduction: In burying beetles, the adults are attracted to small vertebrate carcasses. After intra-sexual competition, a larger male-female pair remains to bury a carcass as a resource for their brood. They provide extensive parental care and adjust their brood size to match the carcass size. In the field, however, it was not examined whether regulation of brood size causes sufficient size of the offspring at the adult stage to secure a carcass.

Methods: In the burying beetle *Nicrophorus quadripunctatus*, the body size was measured for all adults collected with baited traps in the field. In baited traps with soil, moreover, a various size of carcasses were placed and the adults were allowed to breed.

Results: In the field, the sizes of breeding adults were larger than those of adults that searched carcasses. In the reproduction, a positive relationship was found between the brood size and the size of carcasses. When the carcass was small, however, the size of the grown adult on it would appear too small to secure carcasses for breeding. Moreover, it was revealed that the ratio of the total mass of brood to the carcass size was higher when the brood size on the carcass was larger.

Conclusions: In *N. quadripunctatus*, despite of the regulation of brood size, small carcasses caused that the offspring size would appear too small to secure a carcass, which might be concerned with the assimilation efficiency.

Molecular systematics of the genus *Dacus* Fabricius (Diptera: Tephritidae)

Massimiliano Virgilio[1], Marc De Meyer[1], Ian M. White[3], Thierry Backeljau[2]

[1]Royal Museum for Central Africa, Tervuren, Belgium, [2]Royal Belgian Institute of Natural Sciences, Brussels, Belgium, [3]Natural History Museum, London, United Kingdom

Introduction: The genus *Dacus* Fabricius includes economically important fruit flies distributed in the Afrotropical and Indo-Australian regions. A recent classification of the African fauna, based on morphological characters, resolved 177 species subdivided in seven subgenera. However, phylogenetic relationships within the genus still need to be fully clarified due to high levels of homoplasy in morphological characters.

Methods: 106 representatives of 34 African *Dacus* species (from five subgenera) were sequenced at one or more mitochondrial (COI, 16S) and nuclear (Period) gene fragments,. Phylogenetic relationships were inferred by Maximum Likelihood methods.

Results: Analyses of a concatenated dataset of representatives of 25 taxa resolved two major bootstrap supported clades. Clade A included species of the subgenera *Dacus* (n=12), *Leptoxyda* (n=3), *Didacus* (n=1) and *Psilodacus* (n=1). Clade B included other representatives of the subgenera *Leptoxyda* (n=6) and *Didacus* (n=2) and a species of the subgenus *Lophodacus* (*D. hyalobasis*). A number of bootstrap supported subclades was also resolved. *D. humeralis*, *D. chiwira*, *D. diastatus, D. durbanensis*, *D. famona* and *D. kariba* (all belonging to the group Humeralis of the subgenus *Dacus*) formed a subclade within clade A. However, specimens of *D. humeralis* from East (Kenya, Tanzania, Uganda) and West African locations (Benin, Congo D.R., Ivory Coast) formed separated clusters, possibly as a consequence of cryptic speciation.

Conclusions: The molecular phylogeny of 25 *Dacus* species shows a number of discrepancies with classifications based on morphological characters. Molecular taxonomy seems to represent a valuable complementary tool towards a more stable classification for the genus *Dacus* Fabricius.

Comparative efficacy of Ivermectin and Cypermethrin against *Hyalomma anatolicum* ticks (Acari: Ixodidae)

Muhammad Sajid, Muhammad Khan, Zafar Iqbal, Ghulam Muhammad

University of Agriculture, Faisalabad, Punjab, Pakistan

The objective of this paper is to describe the current status of the *in vitro* and *in vivo* effectiveness of the two acaricides viz; Ivermectin and Cypermethrin against prevalent tick species (*Hyalomma anatolicum*) of bovines. To this end, four hundred and eighty live engorged female *Hyalomma anatolicum* ticks were collected from the animals and separated into two equal groups viz; I & II for the efficacy trial of Ivermectin (Ivomec, Merial, France) and Cypermethrin pour-on (Cipermetriven, Ivan Labs, Spain), respectively. Each group was further divided into four sub-groups (A through D) to administer various concentrations of each drug. The ticks were counted after an immersion period in order to compare the efficacy of the two compounds. For an *in vivo* trial, three hundred and sixty bovines were selected on the basis of criteria as (i) having tick burden at the rate of >100 ticks per animal (ii) age of animals is more than 1year (iii) No history of application of acaricide to any of infested animals. The comparison of the two groups was done on day 0, 5, 10, 15 and 20 after treatment of the two test acaricides. The results of the study indicated better *in vitro* and in vivo efficacy of cypermethrin pour-on as compared to ivermectin against *Hyalomma* ticks. The results, thus obtained provide some useful tools in decision making of tick control providing the basis for testing the findings on provincial and national levels in future studies.

A complex world: Direct and indirect interactions between plants, decomposers and herbivores

Adela González Megías

Universidad de Granada, Granada, Spain

One of the main characteristics of food webs is their complexity. A myriad of organisms can interact direct and indirectly among them. In most systems plants interact with other plants and also with herbivores and decomposers. To fully understand food web complexity and functioning, it is important to determine the intensity of these interactions between all these organisms. Arid systems are ideal for this purpose because food webs are simpler than in other more productive ecosystems. I established a full factorial experiment in the field using an annual plant, *Moricandia moricandioides*, as a model system, and manipulating the presence of belowground decomposers, and above- and belowground herbivores. The manipulation of herbivores and decomposers affects other herbivores, parasitoids, and plant traits. Decomposers and herbivores negatively affect sap-suckers associated to *M. moricandioides*. There was also an important effect of decomposers and aboveground herbivores on flower visitors. Herbivore mortality due to parasitoids was lower in plants with decomposers. Plant size and reproductive output are affected positively by decomposers and negatively by herbivores. Therefore, decomposers and herbivores can affect antagonist and mutualist organisms associated to plants through direct and indirect effects. This experiment points out the importance of considering above- and belowground interactions in any system to fully understand the processes determining not only food web functioning but also complexity.

Comparison of different methods of bioassay for detecting Calypso and Spinosad susceptibility in *Leptinotarsa decemlineata* (Say)

Maryam Azimi[1], Aliasghar Pourmirza[1], Mohammad hasan Safaralizade[1], Nouraddin Shayesteh[2]

[1]Urmia university, Urmia/west Azarbijan, [2]Islamic Azad University, Branch of Mahabad, Mahabad, Islamic Republic of Iran

Introduction: The Colorado potato beetle, *Leptinotarsa decemlineata* (Say) is one of the most important pests of potato throughout the world. This pest cause seriously damages by defolation.

Methods: In this study susceptibility of CPB adults to Calypso and Spinosad as safe alternatives for conventional insecticides was determined through contact and dipping assay techniques.

Results: For Calypso LC_{50} and 95% confidence limits values with contact and dipping techniques were 0.12 (0.88 – 0.02) and 32.96 (71.86 – 19.16) ppm respectively. For Spinosad these criteria were 140.75 (328.06 – 93.61) and 1041.91 (2702.71 – 477) ppm in the same order. Contact technique, however, exhibited less variability in LC_{50} estimates and showed a higher degree of sensitivity than other method.

Conclusions: The results suggest that contact method is simple and sensitive test technique for measuring susceptibility of CPB adults to Calypso and Spinosad.

Compass orientation mechanisms in migratory butterflies

Rebecca Nesbit, Duncan Sivell, Jason Chapman

Rothamsted Research, Hertfordshire, United Kingdom

The butterflies *Vanessa cardui* (painted lady) and *V. atalanta* (red admiral) are frequent obligate migrants to northern Europe from the Mediterranean Basin. However, there remain significant gaps in our understanding of the behavioural mechanisms they have evolved to facilitate successful migrations.

We employed two different methods to investigate these mechanisms. Initially, we performed controlled flight-simulator experiments to test the ability of migrant *V. cardui* to orientate in a seasonally advantageous direction.

Our results provide convincing evidence that *V. cardui* reared under autumn day length conditions and flown with visual access to the sun exhibit a mutual SSW orientation. However, when the sun was not visible to butterflies in the simulators, their orientations were random. These results imply that *V. cardui* has an inherited preferred migration direction in the autumn (towards the SSW), and that it uses a sun compass to orientate its flight heading. Further experiments have been performed to test whether this sun-compass mechanism is time compensated.

In addition, we are using data from two vertical-looking entomological radars located in southern England. We have examined the displacement directions and flight headings of free-flying butterflies (likely to be *V. atalanta* and *V. cardui*) hundreds of metres above ground level. We provide evidence that they are migrating at altitude in seasonally adaptive directions.

Taken together, our results indicate that European migratory butterflies use a sun compass to direct their flight headings in seasonally-advantageous directions, and they frequently migrate at high altitudes, taking advantage of fast-moving, favourable winds.

Within host competition and virulence amongst pathogens: A race to the finish or a pound-for-pound fight.

Peter Staves, Rob Knell

Queen Mary University of London, London, United Kingdom

In nature multiple infections are the rule; when sampling hosts for pathogens often they are infected by a number of invaders. Coinfecting pathogen strains will vary in their respective virulences, and the competitive interactions between such strains are thought to drive the evolution of virulence within pathogen populations. While it has been suggested that a pathogens intrinsic virulence is correlated with competitive ability, there is a lack of empirical evidence to support this, as previous studies report. It is generally assumed that within host competition selects for increased virulence when competition is for a limited resource. The best competitor is the pathogen that makes the best use of a host and, as such, causes the most harm.

This assumption however is based on only one method of competition. Pathogens can compete within a host in a number of ways, indirectly or directly. When the competition between strains is direct (i.e. a pound-for-pound fight), the best competitor is the one that most successfully interferes with its opponent. As a result the “race” for host exploitation may suffer, leading to competitors that do less damage. Using the wax moth *Galleria mellonella*, the fungal pathogen *Metarhizium anisopliae* and the nematode *Steinernema feltiae* as a model coinfection system, we test these assumptions. We provide empirical data for both intra- and inter-specific coinfections, using multiple fungal strains of varied intrinsic virulence, and show how this relates to competition and competitive ability between these taxa.

The development of combined heat and controlled atmosphere quarantine treatments for phytosanitary pests of South African fruit crops

Shelley Johnson

University of Stellenbosch, Stellenbosch, South Africa

Phytosanitary pests of fruit crops grown in South Africa have lead to many rejections of fruit consignments presented for export to trading partners. Effective post-harvest non-chemical control treatments against these pests are required, as alternatives to chemical mitigation treatments such as fumigation with methyl bromide, and to sustain trade with other countries. The controlled atmosphere and temperature treatment system (CATTS) technology was developed in the United States and has been tested for commercial use against a number of phytosanitary pests affecting pome and stone fruit in the US. Developing CATTS treatments for specific pests on specific commodities is expensive since it requires infesting and treating large quantities of fruit. In order to determine the most tolerant pest species and developmental stage to CATTS, without the expense of in-fruit treatments, simulated-CATTS treatments using a water bath system have been developed by CATTS researchers. This controlled atmosphere water bath system (CAWB) was used to test combined heat and controlled atmosphere treatments on serious phytosanitary pests of South African export fruit, namely, *Macchiademus diplopterus*, (grain chinch bug), *Phlyctinus callosus*, (banded fruit weevil) and *Thaumatotibia leucotreta* (false codling moth). The effects of exposure to elevated levels of carbon dioxide and reduced levels of oxygen, combined with increasing temperature, on *M. diplopterus* and *P. callosus* adults, and *T. leucotreta* egg and larval stages are presented with a view to expand the testing of effective treatments on infested fruit in CATTS chambers and to evaluate fruit quality.

Phylogeny of apoid wasps

Michael Ohl, Volker Lohrmann, Silke Mosel

Museum of Natural History, Berlin, Germany

Apoid wasps, traditionally known as the family Sphecidae, is a morphologically and behaviorally highly diverse taxon of aculeate Hymenoptera. It comprises about 10,000 described species in about 280 genera. Apoid wasps share a number of plesiomorphic characters and can only be recognized by the unique combination of apomorphies of Apoidea (bees + apoid wasps) *and* the lack of the apomorphies of the bees. Cladistic analysis both based on morphological and molecular characters confirm that apoid wasps is paraphyletic with respect to bees. This is reflected in a newly proposed classification of Apoidea: Ampulicidae + (Sphecidae s.str. + (Crabronidae + bees)). Heterogynaidae is an enigmatic taxon of only eight described Old World species. It has been considered as the most basal taxon in Apoidea, but recent analyses have shown that it is a highly derived group of parasitic wasps deeply nested in Crabronidae. The Crabronidae, including about 9000 species of apoid wasps, is usually considered to be the sister group of bees, but this is weakly supported. Monophyly of Ampulicidae and Sphecidae s.str. has good support, but the relationships within the highly diverse Crabronidae is contradictory.

Rearing of codling moth *Cydia pomonella* (L.) for research purposes in South Africa

Matthew Addison, Dalene Stenekamp

Department of Conservation Ecology and Entomology, Faculty of AgriSciences, Stellenbosch University, Stellenbosch, South Africa

Codling moth is mass reared in South Africa for research purposes. Current maximum production is 250 000 individuals per week. The moths are primarily used in a sterile insect technique (SIT) program which involved the treatment of 120 Ha of commercial apple and pear orchards. Due to various constraints an agar and maize meal based diet was used. Research on the diet included the assessment of the impact of maize meal containing *Bacillus thuringiensis*, the use of wheat flour to replace maize meal and the testing of a number of gelling agents. The codling moth culture has allowed for research to be carried out on entomopathogenic nematodes and parasitic wasps (*Trichogrammatoidea* spp.). In addition the diet has been used to culture false codling moth *Thaumatotibia leucotreta* (Meyrick) and carnation worm *Epichoristodes acerbella* (Walker) for research purposes.

Climatic and biotic influences on the distributions of *Calliphora augur* and *Calliphora dubia* (Diptera: Calliphoridae)

Aidan P. Johnson[1], James F. Wallman[1], Melanie S. Archer[2]

[1]*Institute for Conservation Biology, School of Biological Sciences, University of Wollongong, NSW 2522, Australia,* [2]*Department of Forensic Medicine, Monash University, 57-83 Kavanagh St, Southbank Vic 3006, Australia*

Introduction: Documenting the known and potential distributions of insects is crucial to understanding their quarantine risk and role in agriculture, pest management, epidemiology and forensic entomology. This study focused on determining and interpreting the distributions of two endemic Australian blowflies, *Calliphora augur* (Fabricius) and *Calliphora dubia* (Macquart).

Methods and Results: We examined the effect of climatic factors on the maximal distributions of *C. augur* and *C. dubia*. Comparative laboratory and field experiments were used to derive parameters defining the distributions of these sister species, particularly in relation to temperature and moisture. The results showed that *C. dubia* had an increased tolerance to dry stress and high temperatures in comparison with *C. augur*. No difference was seen between species in the impact of cold temperatures on the development of maggots to the pupal stage. CLIMEX software was used to model the distributions of *C. augur* and *C. dubia* in relation to climate. Model parameters, determined from the literature, fieldwork and laboratory work, were entered into CLIMEX. The results accorded with those of a bait trapping transect extending from Berry (New South Wales) to Adelaide (South Australia). The distributions generated also greatly overlapped with distribution maps derived from insect collections and the literature, and extended these distributions significantly. Discrepancies are probably due to the inability of CLIMEX to accommodate non-climate related parameters, such as competition.

Conclusions: This study showed that distribution modelling software, such as CLIMEX, has great promise as a tool in forensic entomology.

Conservation priority setting and insects: How, where, how often?

Mar Cabeza, Anni Arponen, Heini Kujala, Astrid van Teeffelen, Ilkka Hanski

University of Helsinki, Helsinki, Finland

Choosing which areas to protect, or what to manage and how is no easy task. Many conservation implementations are a legacy of opportunistic actions, resulting from political and economic constraints that have led to inefficient, ineffective conservation. Systematic conservation planning has emerged in response to this reality, and has helped us move from ad-hoc decisions to a quantitative decision-making process. This process identifies conservation priorities that achieve explicit quantitative objectives in a cost-efficient manner. However, these tools are rarely applied to insects. This is perhaps because insects are rarely the target of large conservation plans or because we seldom have comprehensive data for groups of insects. But it is not because insects would not be suitable targets for such an approach. In this study we give an overview of a variety of available tools, applicable to different questions, scales, and numbers of species. We provide examples using Finnish butterflies: a national conservation priority map for 100 species, a regional plan for management options showing trade-offs between plant and butterfly species, and a local example with an endangered butterfly, assessing optimal management locations under different urban planning scenarios. There is no evidence to expect that targeting other taxa will simultaneously protect insects and therefore we encourage the inclusion of insects in large conservation priority assessments. This is possible by using quantitative conservation planning approaches and utilising modeling advances to cover for incomplete or biased data.

Mechanisms of odor information processing: Investigating representations of odor mixtures in the antennal lobe

Linda S. Kuebler, Shannon B. Olsson, Bill S. Hansson

Max Planck Institute for Chemical Ecology, Jena, Germany

Natural odors are often complex blends of several different compounds. Despite this fact, most studies concerning odor detection and coding in insects have focused on single components. The first olfactory neuropil in the insect brain, the antennal lobe (AL), modifies the final representation of odors in the assembly code carried by projection neurons to higher-order brain centers. The neural representation of odor mixtures in the AL may be simply the sum of its components or non-linear due to odor information processing. The phenomenon of a non-linear response to a mixture that is not predictable from the basis of responses to its components is called a mixture interaction. Our goal is to investigate interactions and different response characteristics in the AL in order to reveal relationships between host odor mixtures and single plant volatile components. Using a novel stimulus delivery system as well as coupled intracellular recording and calcium imaging experiments in the hawkmoth *Manduca sexta*, we addressed the question: what are the mechanisms of odor information processing at different levels in the antennal lobe? Preliminary results suggesting mixture interactions among host volatile odors in the general olfactory neuropil will be presented.

Factors influencing weather station ambient temperature corrections in forensic entomology

Aidan P. Johnson[1], Melanie S. Archer[2], James F. Wallman[1]

[1]Institute for Conservation Biology, School of Biological Sciences, University of Wollongong, NSW 2522, Australia, [2]Department of Forensic Medicine, Monash University, 57-83 Kavanagh St, Southbank Vic 3006, Australia

Introduction: Forensic entomologists use weather station data to retrospectively estimate the ambient temperatures at a death scene prior to discovery of the body. Correlation 'corrects' the weather station data, thus estimating scene temperatures. Archer (2004), in one of the first validation studies in forensic entomology, found a significant effect of time after body discovery on the accuracy of this technique.

Methods: We expanded Archer's study by examining additional factors that might influence weather station temperature corrections: 1) length of correlation period (2, 5, 10 days); and 2) distance between weather station and body discovery site (2 – 15 km). 24 hypothetical body discovery sites were clustered around four weather stations in New South Wales and Victoria, Australia. Temperature loggers at each site collected data every 30 minutes for approximately one month. This experiment was carried out twice: in early 2006 and 2007. We assumed that all hypothetical bodies lay *in situ* for five days before discovery.

Results and Conclusions: The results of this ongoing study so far indicate that neither correlation period length nor distance affects the accuracy of retrospective scene temperature estimation. This suggests that 1) forensic entomologists can use a shorter correlation period in the analysis of their data; and 2) at the distances examined here, weather stations closer to death scenes may not produce a more accurate result than those further away. We will also report on the results of a third factor, frequency of collection of weather station records, investigated using the same data set.

Influence of *Ageratum conyzoides* (L.) extract on the orientation of larvae and oviposition of adult *Helicovepra armigera* (Hüb.) (Lepidoptera: Noctuidae)

Ashok Singh, P. R. Ragesh

Department of Zoology, University of Delhi, Delhi-110 007, India

Introduction: *Helicoverpa armigera* is a pest of major economic concern worldwide. This insect has developed resistance against all the synthetic insecticides, and even against *Bt.* Plant derived products are viable alternative for the sustainable management this insect. *Ageratum conyzoides* (L.) is an annual plant having insecticidal property against agricultural pests. Present study was initiated to assess the effect of *Ageratum conyzoides* extract on the behaviour of this pest.

Methods: Hexane extract of dried aerial parts of *Ageratum conyzoides* was prepared in evaluated against *H. armigera*. The orientation response of the larvae was studied in a straight tunnel olfactometer. The ovipositional bioassay of adult females was conducted in a glass jar covered with muslin cloth. Test extract was applied on one half of the muslin cloth, and the other half was applied with hexane.

Results: Present study shows that hexane extract of *Ageratum conyzoides* elicit significant influence on orientation of larvae, and oviposition of adult *H. armigera.* Lower concentration of extract did not elicit response from larvae but repellency was significant for the higher concentration. Interestingly in choice situation, females laid significantly higher number of eggs on the surface treated with lower concentration but lower number of eggs was recorded at higher concentration as compared to control surface.

Conclusion: *A. conyzoides* contains non-polar chemicals that influence the orientation of larvae and oviposition of adult *H. armigera.* Further study is on progress to isolate and identify the deterrent compounds of *A. conyzoides,* which can be exploited in the management program of *Helicoverpa armigera*.

Nocturnal activity in carrion-breeding blowflies (Diptera: Calliphoridae) in south-eastern Australia

Bryan D. Lessard, James F. Wallman

Institute for Conservation Biology, School of Biological Sciences, University of Wollongong, NSW 2522, Australia

Introduction: The incidence of nocturnal activity in carrion-breeding blowflies is unclear. Limited studies, so far restricted to the northern hemisphere, have produced contradictory results. However, clarification of this topic is important because it is often assumed in forensic entomological casework that flies are not active and thus cannot oviposit at night. Estimates of time since death could be substantially affected in cases where such an assumption is incorrect.

Methods and Results: We investigated nocturnal oviposition in south-eastern Australia using piglet carcasses placed in the field. Night time experiments were carried out under conditions of new moon, full moon, and artificial light. Nocturnal oviposition did not occur on any carcass. Interestingly, the carrion beetle, *Ptomophila perlata* (Silphidae), was active at night in dense vegetation under both the full moon and artificial lighting. Even in the absence of flies, this species could therefore be a potential indicator of nocturnal corpse placement. Laboratory studies were also done to monitor diurnal and nocturnal blowfly activity under differing light intensities. A significant association was found between the time of day and degree of activity for all light intensities, as well as between activity and light intensity irrespective of time of day. We also investigated the influence of time of day and light intensity on oviposition in the laboratory.

Conclusions: Overall, our results support the general assumption that nocturnal oviposition is unlikely to occur in the field under typical circumstances in south-eastern Australia, However, laboratory data suggest that this may still be possible under certain scenarios.

Are oil palm plantations green deserts? Invertebrate biomass, diversity and function in oil palm plantations in Sabah, Malaysia.

Ed Turner, Jake Snaddon, William Foster

Department of Zoology, University of Cambridge, Cambridge, United Kingdom

Introduction: The area of oil palm plantations has expanded dramatically in recent decades and now covers approximately 10.7 million hectares worldwide: an increase of over 168% since 1960. Despite the threat to global biodiversity of oil palm expansion, remarkably few studies have assessed the impact on the environment of conversion of forest to oil palm plantation.

Methods: We studied the impact on overall invertebrate biomass and abundance, of forest conversion to oil palm in Sabah, Malaysia. The effect of habitat conversion was investigated for invertebrates living in the leaf litter, the canopy and common epiphytes by collecting arthropods using a variety of standard sampling techniques. We also investigated the impact of oil palm expansion on the diversity of leaf litter and epiphyte invertebrates and on leaf litter decomposition in these habitats.

Results: We found that oil palm expansion has a dramatic overall effect on the invertebrate community as well as on the rate of decomposition.

Conclusion: Our results highlight the overall negative effect that oil palm expansion has on invertebrates and demonstrates that more research needs to focus on management to enhance biodiversity and ecosystem functioning in plantations. We discuss our results with reference to plantation management and sustainability.

Post-campaign assessment of desert locust pesticide pollution at loading sites in West Africa

Wim C. Mullié[1], Gerrit van de klashorst[1], James W. Everts[2]

[1]FAO, Sub-regional Desert Locust Office, Dakar, Senegal, [2]FAO, AGPP, Rome, Italy

Introduction: During the 2003-2005 locust control campaign in West- and NW Africa, *c*. 13 million litres of pesticides were sprayed against Desert Locust, *Schistocerca gregaria* (Forsk.). Products used were mainly organophosphates. In 2006, an inventory was conducted in several Sahelian countries to assess soil pollution due to accidental spillage. The inventory and subsequent risk assessment was made by the so-called QUEST teams (QUality and Environment Survey of Treatments) in collaboration with the Africa Stockpiles Programme (ASP).

Methods: Targets in Niger, Mali, Mauritania and Senegal were large pesticide storage sites and aerodromes where spray planes were loaded. Assessments were visual and field officers were interviewed; recording on special forms. The ASP assessment method was adapted specifically for soil pollution. Field collected samples were transported refrigerated, then frozen until analysed. If needed, two depths were sampled to assess infiltration. Three pesticides (chlorpyrifos, fenitrothion and malathion) were analysed by gas chromatography (GC) and confirmed by GC-mass spectrometer.

Results: All sites examined by residue analysis were contaminated, ranging from slight (0.5-10 mg of pesticide/kg of soil to very heavy (> 1000 mg of pesticide/kg of soil). The size of polluted areas ranged from 1 - 3500 m^2. Some sites smelled badly up to 1500 m distance. Although most sites were fenced, no hazard warning signs were present, and many sites were close to habitations and accessible to humans and livestock.

Conclusion: Several heavily polluted sites need to be cleaned up and measures should be taken to prevent access by the general public and livestock.

Metabolic resistance to synthetic insecticides in the B and Q biotypes of *Bemisia tabaci* (Hemiptera: Aleyrodidae)

Shai Morin[1], Iris karunker[1], Michal Alon[1], Einat Laor[1], Juergen Benting[2], Ralf Nauen[3], Bettina Lueke[3], Tanja Ponge[3], Emmanouil Roditakis[4], John Vontas[5], Kevin Gorman[6], Ian Denholm[6]

[1]Hebrew University of Jerusalem, Rehovot, Israel, [2]Bayer AG, Corporate Development-Innovation, Leverkusen, Germany, [3]Bayer CropScience AG, Monheim, Germany, [4]Plant Protection Institute of Heraklion, Heraklion, Greece, [5]Agricultural University of Athens, Athens, Greece, [6]Rothamsted Research, Harpenden, United Kingdom

The two most damaging biotypes of *Bemisia tabaci*, B and Q, have evolved strong resistance to a range of synthetic insecticides. This resistance may result from changes in the sensitivity of insecticide target sites or increased rate of insecticides detoxification by metabolic enzymes. Here, we investigated the possible involvement of seventeen metabolic genes: the cytochrome P450 monooxygenases (P450s), the glutathione S-transferases (GSTs) and the carboxylesterases (COEs) in *B. tabaci* resistance to imidacloprid (neonicotinoid), pyriproxyfen (juvenile hormone analog) and chlorpyriphos (organophosphate). For studying imidacloprid resistance, the expression levels of 11 P450 genes were compared by real-time PCR (qPCR) across nine B and Q strains showing strong resistance, moderate resistance or susceptibility to imidacloprid. We found that constitutive over-expression (up to ~17-fold) of a single P450 gene, *CYP6CM1,* was tightly related to imidacloprid resistance in both biotypes. In studying pyriproxyfen resistance, we compared by qPCR the expression levels of 17 metabolic genes in two resistant and one susceptible Q biotype strains. We found that constitutive over-expression (up to ~35-fold) of a single GST gene, *GST_2*, was tightly related to pyriproxyfen resistance in both resistant strains. In studying chlorpyriphos resistance, our qPCR analysis showed that one COE gene, *coe1*, was over-expressed (~4-fold) in a chlorpyriphos B biotype resistant strain when compared to a susceptible strain. Taken together, these data show that metabolic resistance by over-expression of detoxification genes may be a major mechanism of resistance to synthetic insecticides in both the B and Q biotypes of *B. tabaci*.

Mimics and magnets: The importance of colour and ecological facilitation in floral deception

Craig I. Peter[1], Steven D. Johnson[2]

[1]Department of Botany, Rhodes University, P.O. Box 94, Grahamstown, 6140, South Africa, [2]School of Biological and Conservation Sciences, University of KwaZulu-Natal, Private Bag X01, Scottsville, 3209s, South Africa

Introduction: Plants that lack rewards can attract pollinators if they share attractive floral signals with rewarding plants. These deceptive plants should benefit from flowering in proximity to rewarding plants, because pollinators are locally conditioned on floral signals of the rewarding plants (mimic effect) and because pollinators are more abundant close to rewarding plants (magnet effect).

Methods and Results: We tested these ideas using the non-rewarding South African plant *Eulophia zeyheriana* (Orchidaceae) as a study system. Field observations revealed that *E. zeyheriana* is pollinated exclusively by a single species of *Lipotriches* (Halictidae) closely associated with the flowers of the rewarding sympatric plant *Wahlenbergia cuspidata* (Campanulaceae). The pale blue colour of the flowers of *E. zeyheriana* differs strongly from flowers of its congeners, but is similar to the flowers of *W. cuspidata.* Analysis of petal spectral reflectance using a bee vision model showed that bees are unlikely to be able to distinguish the flower colour of the two species. UV-absorbing sunscreen applied to the orchid flowers to alter their colour, resulted in a significant decline in pollinator visits indicating the importance of flower colour for attracting pollinators. Surveys of natural orchid populations, as well as a translocation experiment indicate that pollination success in the orchid was strongly affected by proximity to patches of *W. cuspidata.*

Conclusion: Flower colour and location of *E. zeyheriana* plants relative to rewarding magnet patches are key components of the exploitation by this orchid of the relationship between *W. cuspidata* and pollinating *Lipotriches* bees.

CpGV resistance of codling moth: new isolates with improved efficacy

Johannes A. Jehle, Karolin E. Eberle, Sabine Asser-Kaiser, Stefanie Schulze

Agricultural Service Center Palatinate, Neustadt/Wstr., Germany

The *Cydia pomonella* granulovirus (CpGV, Baculoviridae) is one of the most important biocontrol agents of the codling moth (CM) a worldwide pest of apples, pears and walnuts. It is worldwide used one more than 150,000 ha. Since 2003, CM populations with an up to thousand-fold decreased susceptibility to commercial CpGV products have been observed in Germany, France and several other countries. Meanwhile several CpGV isolates overcoming CpGV resistance have been identified. Here, we report the biological parameters describing their efficacy in CpGV susceptible and CpGV resistant codling moth larvae as well as their genetic differences to the conventionally used CpGV-M. A detailed genome comparison of two CpGV isolates overcoming CpGV resistance with the conventional CpGV-M will be provided. This comparison provide some clues about the potential factors influencing the virulence of CpGV.

Genetic variability of the sorghum plant bug, *Stenotus rubrovittatus* in Japan: its relationship with increasing populations in rice fields

Tetsuya Kobayashi[1], Tamito Sakurai[1], Mitsutaka Sakakibara[1], Tomonari Watanabe[2]

[1]National Agricultural Research Center for Tohoku Region, Daisen, Akita, Japan, [2]National Agricultural Research Center, Tsukuba, Ibaraki, Japan

Introduction: Since the first damage to rice by *Stenotus rubrovittatus* was reported in limited areas in the early 1980's, the area of rice fields infested by this species has been increasing. To determine whether new infestations originated from endemic populations or immigrants, the genetic structure and differentiation of *S. rubrovittatus* populations from across Japan was studied.

Methods: Samples were collected from 35 sites including undamaged areas in Japan. Sequence polymorphisms of mitochondrial COI genes and variations of six microsatellite markers on nuclear DNA were used to analyze genetic diversity, gene flow and phylogenetic relatedness of local populations.

Results: Northern (Tohoku) populations contained a unique group of mtDNA haplotypes at high frequencies of more than 50%. Haplotype diversity of mtDNA was high in northern populations, decreased toward the south and was quite low in southern populations. A neighbor-joining tree based on the microsatellite polymorphisms showed that northern populations are ancestral, and eastern (Kanto) and southernmost (Kyushu) populations diverged from them. Genetic differentiation between populations from highly damaged and undamaged areas was not detected.

Conclusions: Japanese populations of *S. rubrovittatus* are genetically differentiated along a geographical gradient, rather than in relation to the history of rice infestations. The increase in damage to rice caused by *S. rubrovittatus* is probably caused by increases in endemic populations and not by immigration from other regions.

Chemical mediation and organization of fig and fig wasp communities

Magali Proffit[1], Bertrand Schatz[2], Martine Hossaert-McKey[2], Steve Johnson[1]

[1]University of KwaZulu-Natal, Pietermaritzburg, South Africa, [2]CEFE-CNRS, Montpellier, France

Introduction: Encountering partners is a crucial phase in the functioning of highly specialized and obligatory interactions. All of the ~750 *Ficus* species (Moracea) are usually associated with at least one specific species of pollinating wasp (Chalcidoidea, Agaonidae), which also strictly depends on its host *Ficus* for reproduction. In these interactions pollinators use the chemical message produced by the plant to locate it. In addition, many non-pollinating wasp species, also specific, exploit this mutualism. In this study we investigated the role of chemical mediation in organisation of wasp communities associated with *Ficus* species.

Methods: By detailed monitoring of the species present on figs, we tried to establish the temporal succession of different species of non-pollinating fig wasps associated with two *Ficus* species. Using gas chromatography/mass spectrometry (GC-MS) we characterise and compare the chemical message produced at receptivity by several *Ficus* spp. to attract their pollinators. In addition, electroantennographic methods were used to detect the compounds within the message produced by figs at receptivity that elicit signals in the antennae of their pollinators.

Results: The temporal succession is associated with the production of different olfactory signals, to which the different species of wasps differentially respond.

Conclusion: Specialisation on different developmental stages of the fig is probably one of the principal mechanisms explaining the coexistence of different non-pollinating wasp species in association with a single pair of mutualists. Our work highlights the role of chemical mediation in fig and fig wasp communities.

New baculovirus products offer solutions for the biological control of *Cydia pomonella* and *Cryptophlebia leucotreta*

Philip Kessler, Daniel Zingg

Andermatt Biocontrol AG, Grossdietwil, Switzerland

Baculoviruses are insect pathogenic viruses that are ideal and valuable agents for biological insect pest control. They are very selective, do not produce toxins or residues, and are generally regarded as safe.

The *Cydia pomonella* granulovirus (CpGV), for example, is being applied worldwide not only in organic but also in IP orchards for the control of the codling moth (CM), *Cydia pomonella*. The development of resistance towards the CpGV-Mexican isolate has recently been reported to occur in isolated orchards after intensive sprayings over numerous years. Results are presented on the efficacy of the newly developed CpGV products “MADEX Plus” and “MADEX I12”. “Madex Plus” was developed through laboratory selection on larvae from a resistant CM population. Furthermore, a new Iranian isolate “I12” has been tested on resistant CM populations. Both products revealed good efficacy on resistant and on non-resistant codling moth populations both in the laboratory and in the field. CpGV is a good example of how baculoviruses can be used as an effective and sustainable control tool against insect pests.

Recently, a new product based on *Cryptophlebia leucotreta* granulovirus (CRYPTEX) has been approved for use against the false codling moth (FCM) (*Cryptophlebia leucotreta*) in citrus production in South Africa. Field trials demonstrated that the application of CRYPTEX reduces FCM below the damage threshold and therefore offers an alternative control measure against an economically important pest.

Factors influencing the Sirex-Pine interaction in South Africa

Brett Hurley[1], Bernard Slippers[1], Kier Klepzig[2], Mike Wingfield[1]

[1]FABI, University of Pretoria, Pretoria, South Africa, [2]Insects, Diseases, Invasive Plants (IDIP), USDA, Pineville, Louisiana, United States

The woodwasp *Sirex noctilio* and its fungal symbiont *Amylostereum areolatum* have been introduced and become established in many regions of the world where the pest is non-native. *Deladenus siricidicola*, a nematode parasitic to *S. noctilio* in its native range has been introduced as a biological control agent into many countries to reduce the impact of *S. noctilio*. Success with this nematode in these non-native environments has been variable. Research in the summer rainfall region of South Africa, where success with *D. siricidicola* has been poor, has shown that moisture content of the wood influences the success of the nematode. Moisture content of the wood at time of inoculation in this region is lower than in winter rainfall regions where *D. siricidicola* has been more effective. However, it was also apparent that moisture content is not the only factor determining nematode success. Incompatibility between *D. siricidicola* and *A. areolatum* strains has been observed in the laboratory and this could be a major barrier to nematode establishment in the field. Furthermore, bluestain fungi are commonly present in Sirex-infested trees. These fungi could compete with *A. areolatum* for resources and affect development of *D. siricidicola* populations. These barriers to the successful establishment of *D. siricidicola* in its non-native environment have not previously been investigated deeply. Their existence highlights the fact that a multi-faceted approach is needed to achieve effective control of *S. noctilio*, and this must include the introduction of multiple biological control agents.

The joint use of chemical and biological control agents: How the effects of pesticides on natural enemies can be elucidated?

Elisa Viñuela

Technical University of Madrid (UPM), Madrid, Spain

Introduction: In recent years, IPM programs based on the use of natural enemies and pesticides to control agricultural pests have rapidly increased in importance all over the world. In these programs pesticides used to manage a pest on a particular crop must be harmless to the biological control agent used in that crop. Studies to elucidate the effects of pesticides on biological control agents were first initiated in Europe by the IOBC in 1974. Today they are essential for registration of pesticides within the European Union.

Methods: Standard Methods have been developed by the IOBC to measure the effects of pesticides on different developmental stages of parasitoids and predators (see http://www-iobc-wprs.org.). The protocol first requires a natural enemy to be exposed to a pesticide on an inert surface and then on leaves in the lab. It then requires extended semi-field and field studies in a sequential scheme. Furthermore, persistence studies (aged residues) or exposure through different uptake routes are also performed. First tier laboratory studies require only two indicative species. On the other hand, further studies require an additional two more species to those used in the first tier.

Results: The safest pesticides are usually of natural origin or mimics of insect growth regulators. Eggs and pupae are generally more compatible with pesticides than the exposed stages (larvae of predators and adults of parasitoids).

Conclusions: As toxic effects depend on the mode of action of the pesticide to the natural enemy used, studies must be performed on a case-by-case basis.

Population dynamics and infestation levels of *Xylosandrus compactus* (Coleoptera: Curculionidae) on coffee in Hawaii

Elsie Burbano, Mark Wright

Department of Plant and Environmental Protection Sciences, University of Hawaii, Honolulu, Hawaii, United States

Introduction: The Asian black twig borer (BTB), *Xylosandrus compactus* (Coleoptera: Curculionidae), is among the most serious pests of coffee in Hawaii. This beetle attacks over 224 plant species including native forest trees. The control method used currently is sanitation by pruning. This tactic reduces vegetative plant material and many farmers do not use adequate methods to destroy infected material, thereby leaving an important reinfection source on the ground. Traps originally designed for the Japanese beetle, baited with ethanol 95 % can serve as a monitoring and research tool to assess seasonal phenology.

Methods: A series of ten Japanese beetle traps were deployed in twelve coffee farms in Kona, Hawaii at different elevations. The traps were baited with 95 % ethanol to monitor the BTB population and checked monthly for 19 months. Infested coffee branches were collected for each farm, number of borer tunnels per branch and populations of all BTB stages were quantified.

Results: There is a seasonal effect and plant stress effect on BTB population fluctuations. BTB populations show seasonal fluctuations throughout the year; populations are higher during the dry season.

Conclusion: BTB population levels are directly related to plant stress, including harvesting, dry season or lack of fertilizer. Traps baited with ethanol can be an important tool for monitoring adult insect populations as part of an integrated pest management program. These traps could also serve as a physical control tactic.

Population dynamics and infestation levels of *Xylosandrus compactus* (Coleoptera: Curculionidae) on coffee in Hawaii

Elsie Burbano, Mark Wright

1Department of Plant and Environmental Protection Sciences, University of Hawaii, Honolulu, Hawaii, United States

Introduction: The Asian black twig borer (BTB), *Xylosandrus compactus* (Coleoptera: Curculionidae), is among the most serious pests of coffee in Hawaii. This beetle attacks over 224 plant species including native forest trees. The control method used currently is sanitation by pruning. This tactic reduces vegetative plant material and many farmers do not use adequate methods to destroy infected material, thereby leaving an important reinfection source on the ground. Traps originally designed for the Japanese beetle, baited with ethanol 95 % can serve as a monitoring and research tool to assess seasonal phenology.

Methods: A series of ten Japanese beetle traps were deployed in twelve coffee farms in Kona, Hawaii at different elevations. The traps were baited with 95 % ethanol to monitor the BTB population and checked monthly for 19 months. Infested coffee branches were collected for each farm, number of borer tunnels per branch and populations of all BTB stages were quantified.

Results: There is a seasonal effect and plant stress effect on BTB population fluctuations. BTB populations show seasonal fluctuations throughout the year; populations are higher during the dry season.

Conclusion: BTB population levels are directly related to plant stress, including harvesting, dry season or lack of fertilizer. Traps baited with ethanol can be an important tool for monitoring adult insect populations as part of an integrated pest management program. These traps could also serve as a physical control tactic.

Drosophila tracheal cells can sense hypoxia and induce terminal branch sprouting

L Centanin[1], A Dekanty[1], NM Romero[1], TA Gorr[2], P Wappner[1]

[1]Instituto Leloir, Universidad de Buenos Aires, CONICET, Buenos Aires, Argentina, [2]Institute of Veterinary Physiology, Vetsuisse Faculty and Zurich Center for Integrative Human Physiology, Zurich, Switzerland

The Drosophila tracheal system is a network of ramified tubes that deliver oxygen to every tissue in the organism. In larval stages, tracheal terminal branches are plastic and have the capacity to sprout-out projections towards oxygen-starved areas, in a process analogous to mammalian angiogenesis. It was reported that this oxygen-dependent effect relies on the upregulation of the fibroblast growth factor (FGF) homolog Branchless in hypoxic target tissues, which binds its receptor Breathless expressed in tracheal cells. Here, I will summarize our work with the group of P. Wappner on the role of the key mediator of survival during O_2 deprivation, the hypoxia-inducible transcription factor HIF, in tracheal sprouting and FGF signaling.

Transgenic, HIF-reporter expressing 3rd instar larva showed that terminal branches of tracheal cells can respond to hypoxia with a seemingly much higher sensitivity than any other cell type in the animal and, thus, are well endowed to sense incremental changes in oxygen tension via HIF. Moreover, the extra-sprouting phenotype was regulated by the Drosophila HIF-alpha homolog Sima, and antagonized by the oxygen sensing prolyl-4-hydroxylase product Fatiga (gene: *fga*). *fga* mutants displayed an extra-sprouting phenotype that was even stronger than that observed in wild type individuals exposed to hypoxia. This extra-sprouting phenotype is, to our knowledge, the first demonstration that loss-of-function of a HIF-prolyl hydroxylase can provoke an angiogenic-like phenotype. Thus, it seems reasonable to expect that conditional knock-down of mammalian prolyl-4-hydroxylase domain (PHDs) proteins in an appropriate cell type will promote angiogenesis. Upon Sima protein accumulation in tracheal cells of mildly hypoxic larvae, this transcription factor was able to induce the Breathless FGF receptor. Upregulation of Breathless, in turn, was sufficient to provoke extra sprouting. This cell-autonomous response enhances tracheal sensitivity to increasing levels of the ligand Branchless as a cardinal step in hypoxia-dependent sprouting of the fly respiratory system. Given the critical requirement of endothelial cell HIF for angiogenesis, it should now be tested if the autonomous and HIF-dependent induction of receptors for the vascular endothelial growth factor (VEGF) in these cells mediates a similar priming of the mammalian angiogenic response to hypoxia.

Circadian circuits in the fly's visual system

Elzbieta Pyza

Department of Cytology and Histology, Institute of Zoology, Jagiellonian University, Krakow, Poland

Introduction: In the fly's visual system, L2 interneurons in the first optic neuropil (lamina) show circadian changes in morphological plasticity. Their dendrites and axons change size and shape during the day and these rhythms are also maintained under constant darkness. Since the L2 cells do not express "clock genes" they must receive circadian information directly or indirectly from a circadian clock. To learn how circadian information is transmitted to target neurons in the visual system we examined terminals of clock neurons, containing pigment-dispersing factor (PDF), together with cells located next to them and L2 cells.

Methods: We used immunocytochemistry to examine the cyclical expression of with PDF and marker proteins specific for neurons and glial cells. For the same reason we also used *Drosophila* transgenic lines with expression of GFP targeted to different cell types. Flies were fixed at different times of the day, their brains sectioned and examined by confocal microscopy.

Results: The results obtained showed that accumulation of specific proteins detected in neurons in the lamina and medulla increases during the day, while in the glial cells neighbouring them the abundance of specific proteins is higher during the night.

Conclusions: Circadian information from the pacemaker seems to be delivered to neurons in the visual system through different types of glial cells, which synchronize the activity of neurons in modular units of the lamina and medulla.

Toxicity evaluation of Spinosyn, Chloropryfos methyl, Methoxyfenozide, insecticide Gel(IG), mineral oils (MO), insecticidal emulsion (IE) against *Phyllocnistis citrella* Stainton (Lepidptera: Gracillariidae)

Behnam Amiri-Besheli, Fatemeh Asgharnejad

Faculty of Agric. Univ. of Mazandaran, Sari/Mazandaran, Islamic Republic of Iran

Different methods have been used to control the citrus leafminer (*Phyllocnistis citrella*) but the bioinsecticides are realized to be the best and effective pesticides. The main aim of this experiment was to determine the efficacy of Spinosyn , Chloropryfos-methyl , Methoxyfenozide , insecticide Gel(IG), mineral oils (MO), Insecticidal emulsion (IE) on the control of citrus leafminer (CLM), *Phyllocnistis citrella* Stainton (Lepidoptera:Gracillariidae) in lab condition at 24, 48, 72 and 96 h post treatments. Leaves of Citrus with second and third instars of leafminer larvae were used in all tests and the larval mortality were monitored. Analysis of variance showed that there were significant differences between treatments and control, and also significant differences were found among treatments. LSD & Tukay-Test among above treatments has shown that Chloropryfos-methyl and Spinosyn and Methoxyfenozide with 86.7± 3. 2 and 80.5± 8.1 and 68.3± 7.1 percentage mortality were more effective than MO, IG and IE with 57.7 ± 8.3 and 54.8±7.5 and 30.6±4.2 percentage mortality and significant different with control (P< %1) respectively. LSD & Tukay-Test among 72 and 96 h post treatments with 60.5 ± 7 and 69.5 ± 7.5 percentage mortality are more effective than 24 and 48 h post treatments with 31.6 ±6 and 54.7 ± 7.7 percentage mortality respectively.

Toxicity evaluation of Spinosyn, Chloropryfos methyl, Methoxyfenozide, insecticide Gel(IG), mineral oils (MO), insecticidal emulsion (IE) against *Phyllocnistis citrella* Stainton (Lepidptera: Gracillariidae)

Behnam Amiri-Besheli, Fatemeh Asgharnejad

Faculty of Agric. Univ. of Mazandaran, Sari/Mazandaran, Islamic Republic of Iran

Different methods have been used to control the citrus leafminer (*Phyllocnistis citrella*) but the bioinsecticides are realized to be the best and effective pesticides. The main aim of this experiment was to determine the efficacy of Spinosyn , Chloropryfos-methyl , Methoxyfenozide , insecticide Gel(IG), mineral oils (MO), Insecticidal emulsion (IE) on the control of citrus leafminer (CLM), *phylocnistis citrella* Stainton (Lepidoptera:Gracillariidae) in lab condition at 24, 48, 72 and 96 h post treatments. Leaves of Citrus with second and third instars of leafminer larvae were used in all tests and the larval mortality were monitored. Analysis of variance showed that there were significant differences between treatments and control, and also significant differences were found among treatments. LSD & Tukay-Test among above treatments has shown that Chloropryfos-methyl and Spinosyn and Methoxyfenozide with 86.7± 3. 2 and 80.5± 8.1 and 68.3± 7.1 percentage mortality were more effective than MO, IG and IE with 57.7 ± 8.3 and 54.8±7.5 and 30.6±4.2 percentage mortality and significant different with control (P< %1) respectively. LSD & Tukay-Test among 72 and 96 h post treatments with 60.5 ± 7 and 69.5 ± 7.5 percentage mortality are more effective than 24 and 48 h post treatments with 31.6 ±6 and 54.7 ± 7.7 percentage mortality respectively.

A molecular phylogeny of Strepsiptera

Dino McMahon, Jeyaraney Kathirithamby

University of Oxford, Oxford, United Kingdom

The first molecular phylogeny of Strepsiptera is investigated using approximately 3 kb of genomic data, with representative taxa being taken from diverse genera across the major extant strepsipteran families. The resulting hypothesis is broadly consistent with traditional taxonomic classifications, although interrelationships between families are discordant with a recent cladistic analysis based on morphology. Tree shape is investigated with reference to key innovations that occurred during the evolution of this unique system, and in light of the pattern of host associations. The concept of morphological stasis as an order-wide phenomenon is also discussed.

Incidence of *Ceratitis capitata* (Wiedemann) (Diptera: Tephritidae) on native fruit trees of southern Mozambique: The role of habitat quality

Silvia Mausse, Romana Bandeira

Eduardo Mondlane University/Faculty of Agronomy and Forest Engineering/Department of Forestry, Maputo, Mozambique

Introduction: This study was conducted during the year 2003 and 2004 in three Districts of southern Mozambique aiming at assessing *Ceratitis capitata* incidence on native fruit trees per site and to determine sites similarity concerning insect species diversity.

Methods: Field surveys were performed by sampling 30 x 30 m quadrangular plots established in three locations per site. The locations were selected among those with natural occurrence of native fruit trees for sampling fruit insect pests. *Ceratitis capitata* population density was compared with that of other insect pests on same host tree species.

Results: *Ceratitis capitata* was one of the most constant fruit pest. Highest infestations of native fruit trees were caused by *C. capitata* on *Garcinia livingstonei* and *Annona senegalensis* fruits. Constance of *C. capitata* by site was higher in Manhiça, site that observed highest fruit infestation by this insect pest. Findings in the Matutuíne site gave indications of competition between insect pest species with low insect pest diversity and high numbers of the dominant curculionid *Endaeus floralis* on *A. senegalensis* fruits. The other sampling sites were divese in fruit insect pest species. We discuss implications of habitat condition on *C. capitata* incidence.

Structure of the arthropod community during flowering in mango, *Mangifera indica* L. (Anacardiaceae: Terebinthales) cv Ataulfo in the Soconusco region of Chiapas, Mexico

Ricardo Magallanes-Cedeno, Jorge Ulises Lopez-Ley, Amalia Concepcion Mejia-Barrios, Alfonso Perez-Romero, Martha Elena De Coss-Flores, Mario Ernesto Cabrera-Alvarado

Universidad Autonoma de Chiapas, Huehuetan, Chiapas, Mexico

Introduction: According to mango growers in Chiapas, the reduction in yield observed since 1996 is caused by thrips, therefore pesticides are regularly sprayed at blooming. Previous research indicate, however, that abundance of thrips has no relationship with fruit set. This research was conducted to obtain an understanding of the arthropod community in the mango flower habitat, required to support an IPM program.

Methods: Two different samplings were taken twice a week in six orchards around Huehuetan, Chiapas; the sampling unit was one panicle, and a sample size of 40 was obtained from ten trees in each orchard. Flying and non-flying arthropods were collected by different procedures. Specimens were identified by family and, up to this point, as morphospecies. Samplings started at beginning of blooming and continued until panicles were no longer visited by arthropods from December 2006 to January 2007.

Results: Arthropods visiting mango flowers integrate a community of three classes, Entognatha (Order Collembola), Insecta (Orders Odonata, Mantodea, Orthoptera, Psocoptera, Thysanoptera, Hemiptera, Diptera, Trichoptera, Lepidoptera, Neuroptera, Coleoptera and Hymenoptera) and Arachnida (Order Araneida) including about 72 families and 139 morphospecies. Differences in communities were found associated to the use of chemicals.

Conclusions: Only two species of Thysanoptera, one of Hemiptera and two of Hymenoptera are mentioned as potential pests by mango growers, but in communities as diverse like these perhaps none of them reach economical levels, although more research is needed to understand such interactions.

This research was partially supported by CONACYT and SAGARPA, Mexico.

Developing sampling systems for monitoring pest population levels on deciduous fruits in the Western Cape, South Africa

Kenneth Pringle

University of Stellenbosch, Stellenbosch, South Africa

Introduction: Sampling plans have been developed for monitoring pest population levels in apple orchards and table grape vineyards in South Africa.

Methods: The sampling plans are based on inspecting appropriate secondary sampling units for the presence of pests or their damage on a set number of evenly spaced primary units in blocks of apple orchards or vineyards. Operating characteristic curves were used to determine the precision of decisions regarding intervention. The results for *Eriosoma lanigerum* (woolly apple aphid) are used to illustrate the interpretation of the monitoring data on apples, while those for *Planococcus ficus* are used for illustrating interpretation of monitoring data on vines.

Results: Decisions regarding intervention against *E. lanigerum* were not markedly compromised by simply classifying the 25 trees as infested or uninfested, as opposed to counting colonies in leaf axils. The presence-absence system greatly reduced the time spent monitoring *E. lanigerum* population levels. In vineyards *P. ficus* cordon infestation preceded bunch infestation by three to five months. Therefore, cordon infestation can be used as a warning for pending bunch infestation. Control measures against *P. ficus* should be planned in the case of chemical control and initiated in the case of augmentative biological control at 2% cordon infestation.

Conclusions: A basic generic sampling plan can be used to monitor pest activity in apple orchards and table grape vineyards, the only difference being the definition of the primary and secondary sampling units.

Consortium for the Barcode of Life: An African perspective

Daniel Masiga

International Centre of Insect Physiology and Ecology (icipe), Nairobi, Kenya

Introduction: The Consortium for the Barcode of Life (CBOL) promotes DNA barcoding as a tool for identification of species. The primary objective of DNA barcoding is the adoption of a standardized gene targets for species identification. This provides a simple, but powerful tool for identifying known species and the discovery of new ones. The utility of such a scheme depends on agreed data standards that give confidence that data have been generated consistently and reliably.

Methods: Acquisition of DNA barcode data complies with a community consensus-developed BARCODE data standard, which has as key components: i) a DNA sequence ≥ 500 basepairs sequenced bidirectionally with less than 1% ambiguous base calls, (ii) a trace file, (iii) detailed collection records, (iv) a voucher specimen, with catalog numbers and details of holding institution, (v) identifier of specimen (vi) PCR primers, and (vii) digital image of the specimen. The Barcode of Life Data System (BOLD) is currently the main repository of primary DNA Barcode data, and the keyword "BARCODE" has been reserved by the International Nucleotide Sequence Database Collaboration (INSDC: DDBJ/EMBL/GenBank) for published sequence submissions that are compliant with the data standards, as collaboration with CBOL.

Results: A growing number of barcoding projects of relevance to Africa have been initiated. These include arthropods of medical and veterinary importance, crop pests and projects of interest to biodiversity and conservation. Although the numbers are relatively small, they already demonstrate the utility of DNA barcoding for identifying specimens.

Conclusions: Considering the small and falling number of experienced taxonomists in Africa, DNA barcoding provides a technology for more reliable understanding of the taxonomic status of several African taxa, including arthropods of major agricultural, veterinary and medical importance.

Inner anatomy of intercastes soldier-neotenic reproductives in *Prorhinotermes simplex* (Isoptera: Rhinotermitidae).

Jan Šobotník[1], František Weyda[2], Robert Hanus[1], Irena Valterová[1]

[1]Institute of Organic Chemistry and Biochemistry, Academy of Sciences of the Czech Republic, Praha, Czech Republic, [2]Institute of Entomology, Biology Centre, Academy of Sciences of the Czech Republic, Budějovice, Czech Republic

Introduction: After application of juvenile hormone analogue (JHA) to group of pseudergates (false workers), majority of treated specimen changes into intercastes pseudergate-soldier. We studied circumstances of occurrence of intercastes soldier-neotenic reproductive, and compared their inner anatomy with natural castes.

Methods: Intercastes soldier-neotenic reproductives moulted from pseudergates receiving JHA only by contact with treated specimen (and not being directly treated). Part of them was fixed and studied using methods of transmission electron microscopy; remaining individuals were kept living in group of nest-mates to evaluate their reproductive potential.

Results: Frontal gland is always quite small (compared to soldiers), present as sac-like organ in the head (never observed in neotenics). Labial glands are strongly modified, namely proportions of particular types of central secretory cells differ from all common castes. Epidermal glands are well-developed (more than in sterile castes) and of the same ultrastructure as observed in neotenics; unmodified epidermal cells always exist (while disappeare in neotenics). The size of corpora allata and gonades (both, testes and ovaries) is comparable to young neotenics - much larger than in sterile castes, but smaller than in functional reproductives. Neither gut nor fat body is influenced by JHA. Intercastes soldier-neotenic reproductive are not able to inhibit differentiation of further neotenic reproductives, and are not able to reproduce.

Conclusion: Although some intercastes show significant development of reproductive organs and other tissues specific to reproductives (e.g. epidermal glands), they are not able to fill reproductive role.

Financial support by Czech Science Foundation (project 206/06/1643) is gratefully acknowledged.

Bistrifluron: A new benzophenyl urea insecticide for both agricultural and non-agriculture use

Si Yong Kim, Chang Seop Cho, Tae-Joon Kim, Kyoung-Sung Kim

AgroLife Research Institute, Daejeon, Democratic People's Republic of Korea

Introduction: Bistrifluron inhibiting chitin biosynthesis is a new benzophenyl urea insecticide developed by Dongbu HiTek. Diverse field trials demonstrated that bistrifluron shows a very high control efficacy not only on agricultural insects, especially lepidopterous species, but on non-agricultural insects including mosquitoes and termites. Bistrifluron has good toxicological, environmental and eco-toxicological profiles, and it has been commercialized since 2006 in Korea for agricultural uses. Dongbu HiTek has tried to resister bistrifluron in 18 countries worldwide.

Methods: Many field trials have been conducted to determine the biological activity against various species of whiteflies and lepidopterous insects. The efficacy of bistrifluron has been evaluated against *Culex pipiens pallens* and *Reticulitermes speratus* under laboratory and field conditions.

Results: Bistrifluron showed a highly controlling efficacy to *Trialeurodes vaporariorum* and *Bemisia tabaci* at 50-100g ai/ha in greenhouse crops. Lepidopterous insects of *Spodoptera exigua* and *Plutella xylostella* were completely controlled at 75-150g ai/ha in vegetable crops. In orchard crops, *Stathmopoda masinissa* and *Phyllonorycter ringoniella* were effectively controlled at 100-400g ai/ha. More importantly, no cross-resistance to the organophosphorous insecticides was found. There have been no crop injuries detected to the wide range of crops. Showed LC_{90} of 0.0092 ppm under laboratory conditions, bistrifluron is able to control *C. piniens pallens* at 0.05 ppm under field conditions in 8 days. Special formulation, the above-ground-bait, could be required to control *Reticulitermes speratus* at 0.5%(w/w) of bistrifluron.

Conclusions: Bistrifluron is a new insecticide possessing a wide spectrum for both agricultural and non agricultural insects. For stand-alone application, Dongbu HiTek has introduced 10% EC bistrifluron with the trade name of HANARO® in the Korean market since 2006 for controlling lepidopterous insects for agricultural uses. Diverse efforts have been tried to commercialize bistrifluron for other crops and non-agricultural uses in the world.

Genetics of biological control: The diversity of *Teretrius nigrescens*, predator of the larger grain borer, *Prostephanus truncatus.*

Bonaventure Omondi Aman[1], Daniel Masiga[1], Fritz Schulthess[1], Johnnie van den Berg[2]

[1]International Centre of Insect Physiology and Ecology, Nairobi, Kenya, [2]North West University, Potchefstroom, South Africa

Introduction: The larger grain borer, an alien invasive post harvest pest, has spread to all regions of Africa, since its introduction two decades ago, becoming the single worst insect pest of stored maize in the continent. Biological control was considered a key tool in the integrated management of the pest and two populations of *Teretrius nigrescens,* from Costa Rica and Mexico were released in several areas between 1991 and 1996. However, the effectiveness of the predator has been inconsistent between populations and locations, with greater successes in hot-humid areas.

Methods: The genetic diversity among populations of the predator recovered from four agro-ecological zones in Mexico and Costa Rica and those recaptured from Africa was investigated. The cytochrome oxidase 1 (COI), COII and ribosomal Internal Transcribed Spacer (ITS1, 5.8S and ITS2) were amplified, and sequenced. Sequence alignment and analysis of potential diagnostic restriction sites were done.

Results: Two distinct clusters were detected, the cool highland and warm lowland populations clustered together irrespective of their geographical separation. The two genetic forms produced distinct profiles of the COI gene using *Rsa*I, *Bst*YI and *Aci*I enzymes. Intragenomic variation was detected in ITS1 and ITS2 while COII and 5.8S were monomorphic.

Conclusion: It is therefore possible that there exist ecological or geographical types of *T. nigrescens*, specialised to different environmental conditions. We propose a simple molecular identification procedure for strain-specific monitoring of the predator populations. Microsatellite markers have been developed for biotyping the populations.

Detection of plant DNA in the gut of omnivorous predators by molecular markers.

Nuria Agusti, Lorena Pumariño, Rosa Gabarra, Oscar Alomar

IRTA, Plant Protection, E-08348 Cabrils (Barcelona), Spain

Introduction: Identification of refuge plants that are source of natural enemies is a very important tool for the application of conservation biological control. This tool could allow studying crop colonization of either predator natural populations or pests. The main problem with the markers traditionally used (dyes, rubidium, proteins, etc.) is that only those individuals or plants that have specifically been marked can be identified but not others. The use of molecular markers to detect plant DNA in the gut of omnivorous natural enemies allows not only its detection, but also the identification of which plant species they have been feeding on.

Methods: *Macrolophus caliginosus* Wagner (Heteroptera: Miridae) is an omnivorous predator used in biological control of insect pests in horticultural crops. This study discusses the detection of plant DNA in the gut of this predator and other predator and pest species using the tomato plant as a model. For this purpose, two types of markers were tested: one tomato-specific and a universal one which amplifies all plants but giving different PCR product sizes.

Results: Both markers allowed amplification of DNA tomato fragments within the gut of *M. caliginosus* but not in all cases. Results are discussed depending on the type of material ingested, molecular marker used, and the feeding physiology of the insect.

Conclusions: The development of these techniques can facilitate the study of plant-insect interactions, conservation and crop colonization.

Cloning of vitellogenin gene of the giant water bug, *Lethocerus deyrollei*

Yoshiki Nagaba, Muhammad Tufail, Makio Takeda

Kobe University, Kobe, Japan

The Giant Water Bug, *Lethocerus deyrollei,* the largest aquatic insect in Japan is an endangered species. Nevertheless, basic biology of this bug is not well known. For conservation of this bug, the yolk protein precursor, Vitellogenin (Vg) was investigated. A 5865bp cDNA encoding 219.7kd Vg was cloned and sequenced from the fat body. The cleaved Vg polypeptide subunits were isolated from the female hemolymph and oocytes by SDS-PAGE, and their N-terminal sequences were decided by Edman degradation to determine the regions in the cleavage site. The developmental expressions around seasons and the temporal expressions in reproductive season of the Vg mRNA were investigated by Northern blot analysis. Similarly SDS-PHAGE was carried out for seasonal changes in the protein pattern.

Positional cloning of genes conferring pyrethroid resistance in *Anopheles funestus*, malaria vector in Africa

Charles Wondji[1], John Morgan[1], Helen Irving[1], Maureen Coetzee[2], Hilary Ranson[1], Janet Hemingway[1]

[1]Liverpool School of Tropical Medicine, Liverpool, United Kingdom, [2]Vector Control Reference Unit, National Institute for Communicable Diseases, NHLS, Johannesburg, South Africa

Introduction: A major QTL *rp1* conferring pyrethroid resistance to the malaria vector *Anopheles funestus,* was previously identified. Here we present a fine-scale mapping of *rp1*, the identification and characterisation of the genes conferring this resistance.

Method: 650 F6 and F8 individuals from reciprocal crosses between susceptible and resistant strains were genotyped with SNPs and microsatellite markers for QTL mapping. A BAC clone containing *rp1* was sequenced and annotated. Quantitative PCR was carried out to study the expression pattern of the P450s genes and the *in vitro* metabolic activity of the candidate enzymes on pyrethroids was assessed.

Results: *rp1* was the major QTL explaining 85% of the genetic variance to pyrethroid resistance. Two other QTLs of minor effect *rp2* and *rp3* were detected. Fifteen genes were identified in the 120kb BAC clone containing the *rp1* QTL with a cluster of 10 P450 genes among which CYP6P9 and CYP6P4 were duplicated. These two genes were significantly differentially expressed between susceptible and resistant strains. Enzymes from these genes actively metabolise pyrethroid *in vitro*. Specific mutations associated with resistance were identified in CYP6P9 and CYP6P4. For each gene, two A/G SNPs were identified and genotyped for over 650 specimens. The G/G genotypes confer resistance at 100% and these could be used to design a diagnostic assay to detect this metabolic resistance.

Conclusion: CYP6P9 and CYP6P4 are the main genes conferring pyrethroid resistance in the laboratory strain FUMOZ-R and will now be analysed in field populations.

The landscape in agroecosystems and the ecological services provided by stingless bees

Vera L. Imperatriz-Fonseca, Judith E. Slaa, Marilda Cortopassi-Laurino, Denise de A. Alves, Jacobus C. Biesmeijer

[1]University of São Paulo, São Paulo, São Paulo, Brazil, [2]University of Leeds, Leeds, United Kingdom, [3]University of São Paulo, São Paulo, São Paulo, Brazil, [4]University of São Paulo, São Paulo, São Paulo, Brazil, [5]University of Leeds, Leeds, United Kingdom

The importance of pollination services provided by stingless bees (Meliponini) has been highlighted by several authors. Meliponini comprises many species that differ highly in body size, colony size and foraging strategy, which offers a wide range of pollinators for different floral species. Stingless bees can be managed in rational hives and several experiments have shown that they can be used for pollination of certain crops. However, Meliponiculture has not been developed on as large a scale as Apiculture, and only a fraction of all species is available in rational hives. The presence of natural nests close to the crop provides free pollination services. Most stingless bees require trees for nesting. Therefore, the landscape of the agroecosystem and the structure of the bordering area determine the nesting possibilities of these potential pollinators.

Using 50 Brazilian studies, we extracted the most commonly reported nest trees for several ecosystems, and analyzed the possibility of preferences for using tree species to nidify.

For each habitat, nests were found in many tree species. However, some trees were more commonly reported to house stingless bee nests, which could be used for selective reforestation in and around agroecosystems. Different stingless bee species have different habitat requirements, with some species requiring true forested areas, whereas others benefit from more open areas. Given the current problems in apiculture and the difficulty of quickly rearing large numbers of stingless bee hives, it is important to further develop this free pollination service in agricultural systems through habitat restoration and landscape recovering.

Pre-release monitoring of the larger grain borer *Prostephanus truncatus* and its predator *Teretrius nigrescens* in Kenya

Bonaventure Aman Omondi[2], Josephine Songa[3], Fritz Schulthess[1], Daniel Masiga[2], Johnnie van den Berg[1]

[1]International Centre of Insect Physiology and Ecology, Nairobi, Kenya, [2]North West University, Potchefstroom, South Africa, [3]Kenya Agricultural Research Institute, Nairobi, Kenya

Introduction: The larger grain borer, (LGB), *Prostephanus truncatus*, is the worst pest of farm stored maize in Africa since its introduction some 20 years ago. Biological control of the pest has been. Biological control of the pest was successful in West Africa and parts of Kenya initially. This study was a pre-release survey of *P. truncatus* and *T. nigrescens* in five ecological zones in Kenya.

Method: Twenty six-month monitoring and three month were done in 2005 - 2007 in five regions in Kenya pheromone baited flight traps. A second three-month life sample recovery was done around the first release area to recover *T. nigrescens.* Monthly flight patterns were determined and related to weather parameters based on regression models.

Results: In general, LGB flight activity increased with altitude. The predator was not recovered outside the warm lowland coastal and eastern regions. The strongest possible effects of respective mean monthly weather parameters and LGB flight activity were observed after two months delay. Temperature, relative humidity and vapour pressure deficit were the most important parameters determining LGB flight activity in all regions.

Conclusion: *T. nigrescens* established in the warm coastal areas of Kenya since last release. Its inability to disperse outside initial release region may be due to geographical barriers, unsuitable weather or independent introductions of LB into the hinterland. Biological control of the LGB in Kenya needs to incorporate focus on augmentative releases suitably adapted strains of natural enemies for respective agroecological zones.

What ecological niche models can tell us about invasive species' distributions

Mark Robertson[1], Marc De Meyer[2], Townsend Peterson[3], Mervyn Mansell[4]

[1]Department of Zoology & Entomology, University of Pretoria, Pretoria, South Africa, [2]Royal Museum for Central Africa, Entomology Section, Tervuren, Belgium, [3]Natural History Museum and Biodiversity Research Center, University of Kansas, Lawrence, United States, [4]United States Department of Agriculture, APHIS, Pretoria, South Africa

Introduction: Ecological niche models and species distribution models have been applied to a variety of problems in biology. Ecological niche models have considerable value in identifying regions that may be at risk from invasive species. These models can either be used to identify areas that are likely to be invaded by a species that has already been introduced to a region or in cases where a species has not yet been introduced. For these organisms, absence data are unreliable and thus cannot be used in model calibration or evaluation. This limits the type of modelling technique that can be used and has important implications for evaluation of the predictions. This study examines some of the advances and limitations in the application of ecological niche models to invasive species.

Methods: We used three correlative modelling approaches (GARP, Maxent and PCA) to generate ecological niche models for three invasive species of fruit fly. These models were used to predict the potential distributions of these species in regions that may be invaded in future.

Results: Ecological niche models were used successfully to identify regions that may be at risk of invasion by three fruit fly species. Model agreement was generally high and models performed well against test data.

Conclusions: Ecological niche models show considerable promise in assessing risks associated with invasive species but invasion risk cannot be determined directly from species potential distributions.

Life history patterns of an important predator in orchards, the common earwig, determines pest control efficacy

Bruno Gobin[1], Gertie Peusens[1], Kurt Jordaens[2], Rob Moerkens[2], Herwig Leirs[2]

[1]Zoology Department, pcfruit, Sint-Truiden, Belgium, [2]University of Antwerp, Antwerp, Belgium

Boosting populations of naturally occurring beneficial arthropods requires detailed knowledge on presence, life stages and interactions with orchard management. This is especially important in beneficials with a univoltine life cycle, which may suffer cumulative side-effects throughout their lifetime. Furthermore, correlation with pest life cycles and interaction with pesticides should be taken into account to optimize biological control potential.

Earwigs (*Forficula auricularia*) are important generalist predator of top fruit summer pests. Detailed population monitoring of earwigs revealed the presence of two molecularly distinct subspecies with different reproductive strategies –having a single or double brood per season. Both can occur either sympatric or allopatric, affecting the ensuing population dynamics and predatory impact. Different occurrence of egg-laying does not affect timing of appearance above ground. Migration from undergrowth to tree is steered by temperature rather than by prey seeking as we see no difference in orchards with specific pest spectra. The production of a small second brood in summer has an important effect on total population at the main mating and pair bonding period in September. We identified two critical periods in earwig phenology, during which earwig numbers reduce considerably. Winter mortality and the availability of nest sites are the main limiting factor in earwig population development and can be experimentally manipulated. A second loss of substantial amounts of earwigs occurs at the moult from 4th instar nymphs to adults. This reduction is density dependent and might be linked to intraspecific competition rather than predation or parasitism.

Spread of the invasive ladybird *Harmonia axyridis* in the Czech Republic and Denmark

Oldřich Nedvěd[1], Tove Steenberg[3], Susanne Harding[4]

[1]Faculty of Science, University of South Bohemia, Ceské Budejovice, Czech Republic, [2]Institute of Entomology, Biology Centre, Ceské Budejovice, Czech Republic, [3]Faculty of Agricultural Sciences, University of Aarhus, Lyngby, Denmark, [4]Faculty of Life Sciences, University of Copenhagen, Frederiksberg, Denmark

Introduction: *Harmonia axyridis* (Coleoptera: Coccinellidae) is an invasive alien ladybird in several continents. In late 2007, the established range in Europe extended to Denmark in the north and to the Czech Republic in the east.

Methods: Systematic field observations by professional entomologists, as well as random recordings by volunteer naturalists contributed to a database of records including site, date, environment, and colour morphs.

Results: By early 2008 the Czech database included 125 records, covering 57 (out of a possible 650) KFME grid squares (approximately 11x11 km). Most of these *H. axyridis* records were from large cities (probably introduced by transportation) and to the northwest of the country, where they probably spread naturally from Germany. There were 865 individuals recorded in total, 16% were melanics (12% *spectabilis*, 4% *conspicua*). Two individuals from the Czech Republic were identified as the nominal *axyridis* morph. In Denmark, large numbers of larvae and pupae has been recorded from Copenhagen in late 2007. Small numbers (8 records) of adults have been found in the southern parts of the country. 769 individuals have been recorded in total, 7% were melanics (6% *spectabilis*, 1% *conspicua*), Two individuals of *axyridis* morph were found.

Conclusions: We predict that *H. axyridis* will continue to spread rapidly in Europe, particularly northwards and eastwards. Although there may consequently be a reduction in pest insects, our records support that this species may have significant detrimental impact. The records of the *axyridis* colour morph in the Czech Republic and Denmark are unique within Europe and so this requires further study.

Assessing the effects of endosulfan, imidacloprid and indoxacarb on *Chrysoperla carnea* (Neuroptera: Chrysopidae) in laboratory using IOBC and life table methods

Golamreza Golmohammadi, Mir Jalil Hejazi, Shahzad Iranipour, Seyed Abolghassem Mohammadi

University of Tabriz, Tabriz, Islamic Republic of Iran

Introduction: Common green lacewing, *Chrysoperla carnea* (Stephens) is a polyphagous predator used in greenhouses. It is also very common in many agricultural systems. Compatibility of Insecticides with biological control agents is of most concern to practitioners of integrated pest management. Lethal and sublethal effects of imidacloprid, indoxacarb and endosulfan were assessed on *C. carnea* in laboratory, using the IOBC and life table methods.

Method: First instar larvae of *C. carnea* were treated with imidacloprid (12 mg ai/L), indoxacarb (86 mg ai/L) and endosulfan (181 mg ai/L) using glass petri dishes. Twenty four hours after treatment, the surviving larvae were individually transferred to 60 mm diameters plastic petri dishes and monitored daily until adults appeared. The resultant adults from the surviving treated larvae were kept separately in pairs of males and females; and their eggs were collected and counted daily. The total effects were estimated using IOBC and life table methods.

Results: All three insecticides tested showed significant adverse effects on the developmental time and survival of the 1st instar larvae ($p<0.01$). There were no significant differences in population growth parameters, namely gross reproductive rate, net reproductive rate, intrinsic rate of increase, doubling time, mean generation time and finite rate of increase among the treatments. Based on the IOBC classification method, imidacloprid, endosulfan and indoxacarb were classified as slightly harmful to 1st instar *C.* carnea.

Conclusion: If results similar to laboratory findings are obtained in field conditions, these insecticides might be suitable candidates for use in IPM programs.

Road-building and use in the western Amazon Basin, Part 2: Employing data from applied conservation research to address basic questions about species richness patterns of Neotropical Mordellidae (Coleoptera)

Christy Jo Geraci[1], Terry L. Erwin[1], Valeria Aschero[2]

[1]Smithsonian Institution, Washington, DC, United States, [2]Instituto Argentino de Investigaciones de Zonas Aridas, Mendoza, Argentina

Introduction: The terre firme forest of eastern Ecuador has very high tree and insect species richness. We predict that degree of host tree specialization is a factor governing phytophagous beetle diversity in the canopy, but this hypothesis remains to be tested. One of the by-products of the Ecuador Canopy Biodiversity Project (ECBP) is the discovery of a rich community of tumbling flower beetles (Mordellidae) in the two forest macroplots. Our objectives were to 1) describe morphospecies and classify them into genera using morphology and DNA, 2) build a geodatabase of Mordellidae and tree distributions within each macroplot, and 3) examine spatial and temporal patterns in morphospecies occurrences to identify generalists and host tree specialists.

Methods: A total of 2761 Mordellidae specimens were sorted into morphospecies, imaged, and databased. Two specimens (if available) of each species were chosen for DNA barcoding. Morphospecies were grouped into morphogenera based on gross morphology. The coordinates of both forest macroplots, along with the locations of all 200 sampling stations and the trees surrounding each station, were georeferenced using ESRI ArcGIS software. These data were used to find associations between beetles and trees.

Results and Conclusions: We designated 388 morphospecies based on morphological characters. There was a large turnover in morphospecies composition but no significant difference in species richness across seasons (Anova 1-way $p>0.05$). The majority of morphospecies showed limited distributions, but three (#004, 021, and 038) are widespread, abundant, and classified as generalist pollen vectors. DNA barcoding and evaluation of morphogenera monophyly is still underway.

Larval requisition behavior for food trophallaxis in the termite *Reticulitermes speratus*

Kazutaka Kawatsu[1], Kenji Matsuura[2], Kenji Fujisaki[1]

[1]Kyoto University, Kyoto, Japan, [2]Okayama University, Okayama, Japan

Introduction: Termite larvae may achieve higher fitness to increase trophallaxis by workers, since differentiation into nymphal line is considered to depend on their nutritional and hormonal conditions. Larvae have legs so that they can move by themselves, while they depend on workers for food. Therefore, some sort of behavior for trophallaxis can be expected in the larvae. We studied larval behavior in *Reticulitermes speratus* and hypothesized that larvae would try to control food intake by requisition to nursing workers to stimulate trophallaxis. We also investigated that intensity of requisition behavior is affected by larval nutritional conditions.

Methods: Larval behavior and trophallaxis were recorded by videotaping. To correlate larval behavior with their hungry level, we changed food availability of the larvae before experiment and set up three situations: uric acid or only distillation water with workers, complete isolation from workers. Larvae were then transferred to the observation nest with workers and filmed for 60 min.

Results: it was often observed that larvae actively and quickly approached workers (active approach). Trophallaxis was positively correlated with active approach and it was occurred after this behavior. Intensity of active approach significantly decreased with improvement of larval food availability.

Conclusion: Larvae require for trophallaxis by active approach. It would be expected that workers react against larval requisition, because it may results in producing more nymphs and bringing less ergonomic efficiency. We concluded, however, that the larval behavior is an important element of requisition for trophallaxis because it reflects larval nutritional condition.

Insects in the ancient Chinese custom and faith

Xue-xin Chen, Qiong Wu, Ya-ping Yao

Zhejiang University, Hangzhou, Zhejiang, China

There is no question that insects have shaped and molded human civilizations. Throughout history insects have managed to permeate our spiritual, cultural, and scientific endeavors. As China with a long history and many nationalities, ancient Chinese had made a great contribution to the knowledge of cultural entomology and the connotations of Chinese insect culture are of great diversity. Insects are used in a variety of ways to entertain, to evoke emotions, to convey ideas, and to amaze. Cricket-fighting is an ancient and very popular form of entertainment in China, and sound-making insects are kept as pets. There are many insect-associated love stories in Chinese literature, perhaps the most famous one is a story about a pair of lovers turning into butterflies and flying out of the control of their families (Liang Shan-bo and Zhu Ying-tai). The symbolic character of insects is ingrained in the ancient Chinese cultures. A mantis symbolized cruelty and mystery, the cicada a symbol of resurrection, a tettigoniid a symbol of more offspring, and the butterfly a symbol of joy. There are more than one hundred traditional festivals associated with insects in the history of China. A number of insects are used as or part of ancient Chinese names. Students are so-called “booklice”. The Chinese also believe the similarities of existence found ubiquitous throughout the living world including those between insects and humans.

Queen selection in the stingless bee *Scaptotrigona* aff*. depilis* (Hymenoptera: Apidae: Meliponini)

Cristiano Menezes, Tiago Maurício Francoy, Vera Lucia Imperatriz Fonseca

University of Sao Paulo, Ribeirao Preto, Brazil

Introduction: The selection of queens by colonies of eusocial bees is probably under strong selective pressures since the choice of an inadequate queen would considerably diminish the fitness of the colony. Due to the great size variability among virgin queens, this feature probably is under selection because it directly interferes with the reproductive capacity. This work aimed to investigate whether queen selection occurs in the stingless bee *Scaptotrigona* aff. *depilis*, and whether it is related to the size of the queens. Differences between the size of virgin queens and of chosen physogastric queens would be an important evidence for size selection.

Methods: We collected 30 virgin queens and 30 physogastric queens from 30 colonies of *S.* aff. *depilis*. Both the thoraces (three different measurements) and the heads (four different measurements) of the queens were taken as reference for the bees' size.

Results: Using a Principal Component Analysis, we found that the group of physogastric queens is more uniform and restricted in its distribution than the group of virgin queens. Besides an overlapping of the two groups, the physogastric queens are concentrated in a limited portion of virgin queens' distribution.

Conclusions: We postulate that this "concentration" is a consequence of queen selection. Experimental tests are being performed to investigate the importance of queen size for the colonies, and how colonies choose their queen.

Rapid radiations in vespoid Aculeata

Erik Pilgrim, James Pitts, Carol von Dohlen

Utah State University, Logan, UT, United States

Members of the vespoid lineages exhibit diverse lifestyles, from pollen feeding to parasitism to predatory behavior and from solitary to highly eusocial. Fossils indicate many lineages date to the early Cretaceous. While most vespoid families display multiple autapomorphies supporting their monophyly, solid synapomorphies to outline relationships among families are lacking. Analyses of our recently collected molecular data mirror the morphological characters, such that we find short internodes between lineages whose relationships have been ambiguous based on morphology, suggestive of a rapid radiation at the family/subfamily level. Maximum-parsimony analysis of a four-gene data set cannot resolve the radiation; however, likelihood-based Bayesian analysis of the combined-gene dataset, with genes modeled individually, resolves the radiation with confidence. Genes analyzed individually show a consistent pattern of short, deep internodes, suggesting the rapid radiation is true and not an artifact of conflict among gene partitions. The sampled genes show a range of variation that in combination provides signal from deep to shallow divergences. We subjected the molecular data with fossil-based calibrations to Bayesian relaxed molecular clock analyses to define the likely geological interval of the rapid radiation and correlate it with contemporary environmental/ecological variables, in an attempt to identify possible triggers for the radiation. In addition, we focus on the case of a single family, Pompilidae, in which morphology-based phylogenetics also has been difficult and our molecular data indicate a dramatic and rapid diversification; in this case, however, the radiation dates to a more recent period, most likely in the early Tertiary.

Temperature and starvation limit fig wasp abundance and distribution

Marié Warren

University of Pretoria, Pretoria, South Africa

Introduction: Determining what limits the distribution and abundance of a species is challenging. Two species of fig wasp utilise the flowers of *Ficus sycomorus* L. Both the pollinator (*Ceratosolen arabicus* Mayr) and the cuckoo wasp (*Ceratosolen galili* Weibes) are widely distributed across the range of *F. sycomorus*. However, it has been stated that *C. galili* is less abundant in drier areas. Here, we examine thermal tolerance, desiccation and starvation resistance of these two sympatric wasp species.

Methods: Figs that were close to releasing wasps were collected in Sukuza, Kruger National Park, South Africa. For each species, 30 freshly emerged female wasps were used for experiments examining critical thermal minima, maxima, desiccation and starvation resistance.

Results: Although the onset of chill coma is not significantly different between the species, recovery from chill coma is (faster and) at a lower temperature (by 2^{o}C) for *C. arabicus*. *C. arabicus* is also able to withstand higher temperatures than *C. galili*. Therefore, the thermal range of *C. arabicus* is greater than that of *C. galili*. Both species have similar survival times under desiccating conditions. However, *C. arabicus* appears to be more starvation resistant than *C. galili*.

Conclusion: Thermal tolerances and starvation resistance may determine the limits to the distribution and abundances of these fig wasp species.

Sperm precedence and its implication on evolution of prolonged copulation in *Dysdercus koenigii*

Kamal Gupta

Department of Zoology, Deshbandhu College, University of Delhi, Delhi, India

Introduction: Adults of *Dysdercus* exhibit certain unique features in their reproductive behaviour. Both males and females mate 5-7 times in their entire life span. Each mating lasts 2-3 days.. The females remain receptive to mating throughout their life span. Both males and females show relatively nonspecific mate selection behaviour.

Methods: A dose of Gamma radiation was selected which induced sterility in males but did not impair mating behaviour. In the first set of experiment the female was allowed to mate with normal and sterilized males in a sequence. The sperm utilization pattern in there females was assessed by calculating P_2 value. . In the second set of experiment the female was allowed to mate for 24 hr and then mating was forcefully terminated. The females were allowed to mate with normal or sterilized male.

Results: Our studies indicated that in *Dysdercus* insemination took place during first 24 hr of mating. However a female if mated for longer duration showed an enhanced fertility and an ordered oviposition behaviour. Studies pertaining to sperm utilization pattern of doubly mated females indicated sperm precedence behaviour. The P_2 value was 0.966. This reflected that sperms of last mating were utilized by the female for fertilization.P_2 value in the females of second set was 0.85 This indicated that a female if mated with two males in same mating cycle utilized the sperms contributed by the last male.

Conclusion: The significance of sperm precedence in evolution in prolonged copulation in *Dysdercus* was discussed.

Positional cloning of densovirus-resistance genes in *Bombyx mori*

Keiko Kadono-Okuda[1], Katsuhiko Ito[2], Kurako Kidokoro[1], Kimiko Yamamoto[1], Hideki Sezutsu[1], Keiro Uchino[1], Isao Kobayashi[1], Andrew Kalyebi[1], Toshiki Toshiki[1], Susumu Katsuma[2], Toru Shimada[2], Kazuei Mita[1]

[1]National Institute of Agrobiological Sciences, Tsukuba, Ibaraki, Japan, [2]The University of Tokyo, Bunkyo, Tokyo, Japan

Introduction: *Bombyx mori* densovirus (BmDNV) multiplies in the columnar cell nuclei of the midgut epithelia of the silkworm, *Bombyx mori*. It is classified into two species, BmDNV-1 and BmDNV-2 or Z (denso-like virus). Some silkworm strains are absolutely resistant against BmDNV-1 and/or BmDNV-2. Four unlinked mutations, *nsd-1*, *Nid-1*, *nsd-2* and *nsd-Z*, which were discovered in different *Bombyx* strains, control nonsusceptibility to infection by BmDNV-1 or 2. However, none of them had yet been isolated as responsible genes. The identification of these genes will provide important information for understanding the host- and tissue- specificity and infection mechanisms of the corresponding viruses. Since significant *Bombyx* genome information had accumulated, we undertook map-based cloning of the genes, *nsd-2, nsd-1 and Nid-1*.

Methods: Fine mapping of the genes and narrowing of the candidate regions were performed by linkage analysis of the virus-selected BC_1 populations. Germline transformation was adopted to prove the candidate genes.

Results and Conclusions: We isolated the *nsd-2* and *nsd-1* candidate genes, and narrowed the candidate region for *Nid-1* to 79 kb. The virus-resistance of *nsd-2* is caused by a 6 kb deletion in the ORF of a gene encoding a 12-pass transmembrane protein expressed only in midgut. Germline transformation with a wild type ($+^{nsd-2}$) transgene expressed in the midgut restored susceptibility, showing that the defective membrane protein is responsible for resistance. This is the first report of positional cloning of a mutant gene in *Bombyx* and the first isolation of an absolute virus resistance gene in insects.

Pollination by sexual deception in orchids

Florian Schiestl

Institute of Systematic Botany, Zürich, Switzerland

Sexually deceptive orchids mimic the sex pheromones of their insect-pollinator species, and pollination occurs when the males attempt to copulate with the orchid flowers. Pollination is highly specific and the floral odor is often of primary importance for pollinator attraction. Sexual deception is widely distributed, and can be found among terrestrial as well as epiphytic orchids, and in many floristic regions. My talk addresses the following topics: 1) What are the mechanisms of pollinator attraction? 2) Why has sexual deception evolved? 3) What are the evolutionary consequences? 1) Mechanisms of pollinator attraction are well understood in certain genera, and have proven to be surprisingly diverse. In the Australian genus *Chiloglottis,* few specific compounds attract the pollinators, thynnine wasps, whereas in many European *Ophrys* species, several more commonly found compounds are responsible for attraction of the pollinators, often solitary bees. 2) Since pollination via pollinia, a typical feature of orchids, is an efficient but also risky pollination mode, orchids may often suffer high pollen loss. In a comparative study, we have shown that sexually deceptive orchids have better pollen transfer efficiency than their related food deceptive species. This result can be explained by the high pollinator-specificity found in sexually deceptive orchids, a possible evolutionary driving force for the evolution of this pollination system. 3) This high specificity has consequences for the speciation within these orchids. As orchids evolve to mimic the sex pheromones of different pollinator species, reproductive isolation is a by-product of the adaptation towards specific pollinators, since sex pheromones often act on a species-specific basis.

Yield losses due to natural infestation of *Vicia faba* by l*iriomyza* spp., in Central Sudan

Faiza Salah[1], Elamin M Elamin[2], Elameen Eltoum[1], Dominique Bordat[3]

[1]Dept. Crop Protection, Faculty of Agricultues, Gezira University, Medani, Sudan; [2]Agricultural Research, Medani, Sudan; [3]CIRAD, Montpellier, France

The limiting factor for faba bean in the Gezira area proved to be the leaf miners (LM). This study was carried out at the Experimental Farm of the Faculty of Agricultural Sciences, University of Gezira, during the seasons, on two faba bean varieties: Shambat and SML. Two experiments were conducted: one for each variety where two treatments were laid out in a RCB design with six replicates. The first treatment was the natural infestation of LM (insecticide-untreated), and the second was protected by the IGR Trigard 75% W.P. (insecticide-treated). In both seasons, the untreated plots were heavily infested by the leaf miners, while the protected plots were lightly infested. Infestation resulted in yield losses of 22.8% and 42.2% for Shambat variety, in season I and II, respectively, and 29.1% and 27.6% for SML variety following the same order of seasons. Moreover, there were highly significant differences ($P<0.01$) in plant height and number of pods between the treated and the untreated plots. Negative correlations between the percentage of leaf infestation and plant height in the treated plots were detected.

Control of tomato pests under protected cultivation in the hot and seasonally humid tropics

Hans-Michael Poehling, Nasser Halaweh

Institute of Plant Protection and Plant Diseases, Leibniz Universität Hannover, Hannover, Germany

Introduction: Tomato production in the hot and seasonal humid tropics suffers from a number of detrimental pests. Thrips and white flies are of special importance because they damage by feeding activity and vector virus diseases such as Capsicum Chlorosis Virus or Tomato Yellow Leaf Curl Virus. All year round tomato production under those climatic conditions is only possible using protected cultivation systems, which was the topic of an international joint research project (see www.sus-veg-thai.de) located in Bangkok, Thailand.

Methods and Results: First basically we worked out life-table parameters for *Ceratothripoides claratris*, the most important thrips pest in the greenhouses, and we studied in detail its virus transmission capabilities and the heritability of its competence for virus transmission. A second set of experiments dealt with thrips and white fly control. Greenhouse cladding with UV absorbing plastics (roofs) and nets (side walls) inhibited immigration of thrips and white flies very efficiently. Thrips infestation and virus spread was reduced with an efficacy up to 90%. Accidental introduced thrips and white flies could be further controlled by a package of measures such as systemically plant translocation of neem ingredients and natural enemies, such as Entomopathogenic fungi.

A third focal point was the universal validity and mechanism of the UV effects, studied in laboratory experiments, with different herbivorous insects and natural enemies as well. Obviously most insects tested that search visually for hosts need a stimulation of UV sensitive photoreceptors to properly orientate in space and to differentiate colours.

Mating behaviour and evidence of the existence of a contact pheromone in *Monochamus leuconotus* (Pascoe) (Coleoptera: Cerambycidae)

Dumisani Kutywayo[2], David Hall[1]

[1]Natural Resources Institute, Chatham, Kent, United Kingdom, [2]Coffee Research Institute, Chipinge, Zimbabwe, Zimbabwe

Introduction: *M. leuconotus* is an important pest of coffee in several African countries currently controlled by uprooting and swabbing. New methods of control are required. Mating behaviour and evidence of the existence of a contact pheromone in *M leuconotus* were studied under laboratory conditions.

Methods: Behavioural interactions involved before, during and after mating were taken from twenty pairs of male and female *M leuconotus* in plastic boxes containing coffee twigs as food under laboratory ambient conditions over an eight-hour period. Male behavioural response within 10 minutes of exposure to dead unwashed female, dead hexane-washed female and dead hexane-extract recoated female in plastic box arenas was monitored.

Results: Males exhibited reproductive behaviour of licking, mounting, abdominal bending, copulation and mate guarding after initial antennal or tarsal contact with the females. Females were motionless during copulation but walked freely during pre-or post copulation mounting. Males mated more than once with same female and with different females. Males completed the full range of mating behaviour with dead unwashed and dead recoated females but did not recognise hexane-washed females

Conclusions: Mating behaviour in *M leuconotus* males is initiated after antennal or tarsal contact with conspecific females. Male recognition of dead unwashed and dead recoated females suggests the presence of a contact pheromone on the body surface

Plant damage to horticultural crops by zoophytophagous mirid predators

Cristina Castañé, Oscar Alomar, Jordi Riudavets, Judit Arnó, Rosa Gabarra

IRTA-Cabrils, 08348-Cabrils (Barcelona), Spain

Predatory mirid bugs have a mixed plant-prey diet in which the predatory aspect is principal in relation to their phytophagy, since most of them are unable of developing their immature stages and reproduce in a strict plant diet. However, these predators need the plant for oviposition and as a dietary complement to the prey.

The injuries they cause to plants are directly related with prey scarcity, although environmental conditions (temperature, humidity and impossibility to migrate) may have a synergistic effect. Two types of damage can be described: deformities of plant parts (pits and dimples on green tomato fruits or young zucchini fruits, and yellow spots on red tomato fruits by *Dicyphus tamaninii* or *Macrolophus caliginosus*; necrotic rings in tomato stems and shots by *Nesidiocoris tenuis*) and yield reduction due to nutrients extraction (*N. tenuis* in tomatoes).

They are important pest control agents in horticultural crops due to their high prey consumption and their polyphagy, despite the risk for causing damage to crops. It is important to have a deep understanding of the mechanisms implicated in crop damage in order to take advantage of their high biological potential.

Until recently, *N. tenuis* has been considered a tomato pest while nowadays it is commercially produced for *Bemisia tabaci* control. When confined in hermetic greenhouses with severe scarcity of prey it produces important yield loses. However, when there is enough prey and/or they can emigrate to search for it, only deformities as some necrotic rings appear in the crop.

Egg structures and embryological features of heel-walkers (Mantophasmatodea)

Ryuichiro Machida[1], Toshiki Uchifune[2], Koji Tojo[3], Tadaaki Tsutsumi[4], Mike D. Picker[5], Leonie Pretorius[6]

[1]Sugadaira Montane Research Center, University of Tsukuba, Sugadaira Kogen, Ueda, Nagano 386-2204, Japan, [2]Yokosuka City Museum, Fukadadai, Yokosuka, Kanagawa 238-0016, Japan, [3]Department of Biology, Faculty of Science, Shinshu University, Matsumoto, Nagano 390-8621, Japan, [4]Department of Environmental System Management, Faculty of Symbiotic Systems Science, Fukushima University, Fukushima, Fukushima 960-1296, Japan, [5]Zoology Department, University of Cape Town, Rondebosch 7700, Cape Town, South Africa, [6]ARC-Plant Protection Research Institute, Private Bag X 134, Queenswood, Pretoria 0121, South Africa

Egg structures: Eggs of *Karoophasma biedouwensis*, *Sclerophasma paresisensis*, *Hemilobophasma montaguensis*, and Austrophasmatidae gen. sp. were examined. The egg is ellipsoidal and more than 2 mm long. Anterior *ca*. 15% "cap region" and "body region" are distinguished. The egg membrane is composed of: 1) the fibrous thin outermost surface layer which forms a polygonal pattern on the egg surface, 2) the chorion which is composed of the exochorion with numerous long outer projections and endochorion vertically crossed by numerous striations, and 3) the fine vitelline membrane. The organization of egg membranes being specialized in the cap region, three zones 1-3 are distinguished: the posteriormost zone 1 is equipped with circular-arranged micropyles; the mid zone 2 is weak in structure, to be torn at hatching.

Embryonic development: As we have not succeeded in breaking the egg diapause yet, our knowledge on the mantophasmatodean embryology has not progressed after XXII ICE 2004, where we reported some prekatatrepsis stages of *Sclerophasma paresisensis*. The mantophasmatodean embryonic development is characterized by some features such as the typical short-germ-band embryogenesis and the special type of blastokinesis in which the embryo largely elongated at the egg surface shifts its position deeply into the yolk.

Phylogenetic remarks: Among the orthopteroid groups, it is only Grylloblattodea that possess a set of basic features of the egg membranes and the special manner of blastokinesis as shown in Mantophasmatodea, strongly suggesting the assemblage "Mantophasmatodea + Grylloblattodea."

Entomopathogenic fungus for the control of adult Anophelines in Tanzania

Tanya Russell[1], Ladslaus Mnyone[1], Dickson Lwetoijera[1], Gerry Killeen[2]

[1]Ifakara Health Research and Development Centre, Ifakara, United Republic of Tanzania, [2]Durham University, Durham, United Kingdom

Malaria is one of the most prevalent infectious diseases in the tropics. Annually, more than 500 million people become infected, with >1 million deaths. Malaria control efforts are limited by the development of *Plasmodium* resistance to drugs, *Anopheles* resistance to synthetic insecticides, the logistical difficulties in retreating insecticide-treated bednets and a general lack of funding in resource-poor countries. As such, there is an ongoing need for research into novel techniques which can be used to control vector mosquitoes. Our aim is to develop formulations of entomopathogenic fungi that can be incorporated into existing integrated malaria control programs. The fungal formulations will first be developed strategically. During laboratory trials we will identify the optimal fungal strain or co-formulation, concentration and delivery methods. This information will be used to design focused experimental hut trials to examine the efficacy of the most promising fungal formulations in the field. Sequentially, we plan to evaluate the efficacy of the newly developed technique at a village scale. The village scale trial will compare the biodemographics of the mosquito populations before and after the implementation of the fungus in two villages in rural Tanzania. The information derived from this work will highlight the efficacy of the formulations under real-life situations and provide essential information that will allow fungus formulations to be scaled up for use in national control programs.

Effects of environmental stress on efficacy of *Beauveria bassiana* for stored-product pest suppression

Jeff Lord

USDA-ARS, Manhattan, Kansas, United States

Manipulation of environmental conditions is perhaps the most benign of the pest control practices that are currently in wide use for stored-product insects. Several resulting changes favor the performance of *Beauveria bassiana* as a mycoinsecticide. Perhaps most surprising is that for many insects, the fungus's efficacy is best under dry conditions that are stressful to the insect. We have demonstrated this phenomenon for larval and adult *Rhyzopertha dominica* and *Tribolium castaneum*, larval *Plodia interpunctella*, and adult *Sitophilus oryzae* and *S. zeamais.* We did not find an efficacy enhancement with desiccation of adult *Cryptolestes ferrugineus*, larval *Lasioderma serricorne* or larval *Oryzaephilus surinamensis*. Temperatures from ca. 10-26°C favor the fungus primarily due to its lower temperature optimum for growth than those of the target insects. The effects of modified atmospheres are less clear. With *T. castaneum* as our test insect, oxygen reduction to 5% as opposed to CO_2 elevation to 40% for the first 72 h of fungus exposure resulted in greater larval mortality than fungus exposure under ambient atmospheres. Both treatments slowed beetle development, which would favor fungal efficacy. CO_2 elevation, but not O_2 reduction affected the mortality of adults that were exposed to the fungus. CO_2 elevation significantly reduced *B. bassiana*'s germination and growth rates, but oxygen reduction did not. Stresses are associated with a plethora of physiological effects, and determining those that influence fungal efficacy will be a long term venture

Incidence of *Ceratitis capitata* (Wiedemann) (Diptera: Tephritidae) on native fruit trees of southern Mozambique: the role of habitat quality

Silvia Mausse, Romana Bandeira

Eduardo Mondlane University/Faculty of Agronomy and Forest Engineering/Department of Forestry, Maputo, Mozambique

Introduction: This study was conducted in three Districts of southern Mozambique aiming at assessing *Ceratitis capitata* incidence on native fruit trees per site and to determine sites similarity concerning insect species diversity.

Methods: Field surveys were performed by sampling 30 x 30 m quadrangular plots in three locations per site. The locations were selected among those with natural occurrence of native fruit trees for sampling the fruit pests. *C. capitata* population density was compared with that of other insect pests on same host tree species.

Results: *C. capitata* was one of the most constant species. Highest infestations of native fruit trees were caused by *C. capitata* on *Garcinia livingstonei* and *Annona senegalensis* fruits. Constance of *C. capitata* by site was higher in Manhiça, site that observed highest fruit infestation by this insect pest. Findings in the Matutuíne site gave indications of competition between insect pest species with low insect pest diversity and high numbers of the dominant curculionid *Endaeus floralis* on *A. senegalensis* fruits. The other sampling sites were divese in fruit insect pest species. We discuss implications of habitat condition on *C. capitata* incidence.

Release of locust flight with neurochemicals

Stevenson Paul A., Buhl Edgar, Schildberger Klaus

University of Leipzig, Leipzig, Germany

Introduction: A central question in behaviour is how central pattern generators (CPGs) are activated? Our experiments refute the generally excepted notion that the CPG for insect flight is activated by octopamine and reveal an alternative, cholinergic mechanism.

Methods: Neurochemicals were applied to the deafferented thoracic ganglia of adult locusts in solution, or via micropipettes by pressure or ionophoresis. Flight activity was monitored by myograms. Amines were depleted using reserpine and this checked by immunocytochemistry.

Results: In addition to octopamine, the amines adrenaline, noradrenalin, dopamine, tyramine and histamine, but not serotonin, or the precursor amino acid tyrosine, all initiated fictive flight. Fictive flight was also initiated by acetylcholine's non-hydrolizable analogue carbachol, the muscarinic agonist pilocarpine and the acetylcholinesterase inhibitor eserine, but not by nicotine. While neither aminergic antagonists, nor amine depletion prohibited flight initiation by natural wind stimulation or cholinergic agonists, this was reversibly blocked by the muscarinic antagonist atropine. Finally, selective electrical stimulation of an identified descending giant interneurone (TCG) initiated flight within 25 ms, indicating direct activation of the CPG, and this action was selectively and reversibly blocked by atropine.

Conclusions: We suggest that flight initiating interneurones release acetylcholine which acts via muscarinic receptors to activate the flight CPG, various amines may facilitate this and tune the motor pattern, but are not essential.

Ecology of natural enemy-prey interactions: What can we learn for practical biocontrol?

Nick Birch

SCRI, Dundee, United Kingdom

The value of biocontrol as an 'ecological service' to agriculture is conservatively valued at around \$24/ha/year or approximately $\$4x10^{10}$ per year globally for all cropped land (Costanza et al., 1997). Globally, farmers spend c. $\$32 \times 10^9$/year (2004 figures) on pesticides, of which c. 25% are insecticides. Due to this intensive use of pesticides more than 500 species of insect and mite pests are now resistant to pesticides (FAO 1998) and more than 3 million pesticide-related poisonings to humans occur annually (WHO), highlighting the dangers of relying on this approach alone. As a result of environmental, economic and legislative pressures, pesticides are increasingly being used within IPM frameworks, with the aim to reduce pesticide inputs and increase and stabilise yields. IPM approaches should promote more sustainable crop protection by added value of components, although this is not always achieved (Pretty, 2005). Unfortunately, the rate of success (control target pests, reduce/replace pesticide use, provide economic and stable crop yields) for classical biocontrol initiatives as components of IPM is often only <10% (Gurr and Wratten, 1999), particularly in more variable open field environments.

In this review, possible reasons for failures and successes of biocontrol as a part of IPM will be examined. The role of genetics and evolution at three trophic levels (crop and uncultivated plants, herbivores, natural enemies), the need to understand complex interactions involving functional ecology at different scales (plant, field/farm, landscape) and the challenge to understand the 'black box' of multiple genotype x environment interactions will be discussed. Multidisciplinary case studies will be presented as examples which combine the use of molecular ecology, genetics, chemical ecology, insect behaviour, field experimentation and modelling. The aim is to build up an understanding of complex agro-ecosystems so that trophic interactions providing key 'ecological services' for biocontrol can be made more effective for farmers operating under diverse growing conditions and scales.

Adaptation to chronic nutritional stress in *Drosophila*

Tadeusz Kawecki, Munjong Kolss, Geraldine Schwaller

Department of Ecology and Evolution, University of Lausanne, Lausanne, Switzerland

Climate change does not only affect thermal and water regime experienced by insects, but many other aspects of insect ecology, including the quantity and quality of food. Adaptation to nutritional stress is thus an important aspect of evolutionary response to climate change. Using experimental evolution in Drosophila melanogaster we attempt to understand the physiological basis and life history consequences of adaptation to nutritionally poor food. During over 40 generations of selection for tolerance to chronic larval nutritional stress, our experimental fly populations significantly improved their egg-to-adult viability on poor food, without any reduction in viability on normal food. They evolved genetically smaller size and shorter developmental time. However, on both normal and poor food their relative pupal lipid content remained the same as that of unselected control populations. Despite their smaller size, the adults also show the same lifespan and no detectable decline in fecundity. This result contrasts with life history correlates of adaptation to survive periods of acute adult starvation. Our results also indicate an evolutionary trade-off between larval and adult tolerance to nutritional stress – the selected lines survive less well on poor food as adults. Finally, the selected lines show reduced associative learning performance. Thus, tolerance to nutritional stress is associated with a complex pattern of trade-offs, which may limit the potential of insect populations to adapt to climate change. We are currently studying the physiological and genomics basis of those trade-offs.

Studies on the external ultrastructure of the antennal sensilla of the adult female blackfly, *Simulium chutteri* Lewis (Diptera: Simuliidae)

Vuyisile L. Hobololo, Alan Hall, Chris Van Der Merwe

[1]ARC-Onderstepoort Veterinary Institute, Onderstepoort, 0110, South Africa, [2]University of Pretoria, Department of Veterinary Tropical Diseases, Faculty of Veterinary Sciences, Onderstepoort, 0110, South Africa, [3]University of Pretoria, Laboratory for Microscopy and Microanalysis, Pretoria, 0002, South Africa

Introduction: *Simulium chutteri*, endemic to Southern Africa, is the most important blackfly pest of livestock in South Africa. The ability of olfactory stimuli reception to influence blackfly host location behaviour has been confirmed by previous studies. However, sensory structures of *S. chutteri* responsible for stimuli reception, which elicit host location behaviour, have not yet been studied.

Methods: Wild populations of live adult female blackflies, *S. chutteri* were sweep-netted from sheep grazing in open fields along the Vaal River in the Christiana-Bloemhof area, South Africa. Live specimens were anaesthetized with diethyl ether and prepared for scanning electron microscopy (SEM) by fixation in 2.5% gluteraldehyde buffered at 0.075M sodium phosphate at pH of 7.4. After dehydration through a graded ethanol series, the specimens were critical point dried and mounted on SEM stubs with double-sided tape. Conductivity of the specimens was enhanced using RuOч vapour. Examination and micrography was done on a JEOL JSM 840 SEM, and a JEOL JSM 6000F SEM was used to obtain high resolution micrographs.

Results: Five types of sensilla were found on the antennal flagellum of *S.chutteri*, namely Type 1 sensilla chaetica (T1), Type 2 sensilla chaetica (T2), sensilla trichodea (ST), sensilla basiconica (SB) and the grooved sensilla basiconica (GSB). T1's are uniporous, thick-walled, outwardly curving sensilla protruding and occurring only around the antennal tip, whilst the T2 are thick-walled, grooved spines, outwardly curving, similarly structured as T1's, but shorter and located on the general flagellar surface. ST are thin-walled, porous, evenly distributed over the flagellum and most numerous and inwardly recurving sensilla. SB are thin-walled, consisting of two sub-types, some tapering and some club-like, shorter in the flagellomere ends than mid-region of antennal segments. GSB are thick-walled, multiporous, grooved and sparsely distributed on all flagellomeres mostly associated with SB at distal ends of flagellomeres.

Conclusions: Morphology of Type 1 and Type 2 sensilla chaetica have functional adaptations of contact chemoreceptors, whilst the structural adaptability of sensilla trichodea, sensilla basiconica and grooved sensilla basiconica is of olfactory reception.

Studies on the external ultrastructure of the antennal sensilla of the adult female blackfly, *Simulium chutteri* Lewis (Diptera: Simuliidae)

Vuyisile L. Hobololo, Alan Hall, Chris Van Der Merwe

[1]ARC-Onderstepoort Veterinary Institute, Onderstepoort, 0110, South Africa, [2]University of Pretoria, Department of Veterinary Tropical Diseases, Faculty of Veterinary Sciences, Onderstepoort, 0110, South Africa, [3]University of Pretoria, Laboratory for Microscopy and Microanalysis, Pretoria, 0002, South Africa

Introduction: *Simulium chutteri*, endemic to Southern Africa, is the most important blackfly pest of livestock in South Africa. The ability of olfactory stimuli reception to influence blackfly host location behaviour has been confirmed by previous studies. However, sensory structures of *S. chutteri* responsible for stimuli reception, which elicit host location behaviour, have not yet been studied.

Methods: Wild populations of live adult female blackflies, *S. chutteri* were sweep-netted from sheep grazing in open fields along the Vaal River in the Christiana-Bloemhof area, South Africa. Live specimens were anaesthetized with diethyl ether and prepared for scanning electron microscopy (SEM) by fixation in 2.5% gluteraldehyde buffered at 0.075M sodium phosphate at pH of 7.4. After dehydration through a graded ethanol series, the specimens were critical point dried and mounted on SEM stubs with double-sided tape. Conductivity of the specimens was enhanced using RuOч vapour. Examination and micrography was done on a JEOL JSM 840 SEM, and a JEOL JSM 6000F SEM was used to obtain high resolution micrographs.

Results: Five types of sensilla were found on the antennal flagellum of *S.chutteri*, namely Type 1 sensilla chaetica (T1), Type 2 sensilla chaetica (T2), sensilla trichodea (ST), sensilla basiconica (SB) and the grooved sensilla basiconica (GSB). T1's are uniporous, thick-walled, outwardly curving sensilla protruding and occurring only around the antennal tip, whilst the T2 are thick-walled, grooved spines, outwardly curving, similarly structured as T1's, but shorter and located on the general flagellar surface. ST are thin-walled, porous, evenly distributed over the flagellum and most numerous and inwardly recurving sensilla. SB are thin-walled, consisting of two sub-types, some tapering and some club-like, shorter in the flagellomere ends than mid-region of antennal segments. GSB are thick-walled, multiporous, grooved and sparsely distributed on all flagellomeres mostly associated with SB at distal ends of flagellomeres.

Conclusions: Morphology of Type 1 and Type 2 sensilla chaetica have functional adaptations of contact chemoreceptors, whilst the structural adaptability of sensilla trichodea, sensilla basiconica and grooved sensilla basiconica is of olfactory reception.

Assessment of blackfly (Diptera: Simuliidae) abundance along the Vaal and Orange Rivers in South Africa with reference to potential biological control approaches

Chantel de Beer, Solly Boikanyo, Karin Kappmeier Green

ARC-OVI, Pretoria, South Africa

Introduction: Blackflies (Diptera: Simuliidae) are major pests in the livestock and labour-intensive farming systems in South Africa. Presently blackflies are controlled with the larvicide *Bacillus thuringienses* var. *israelensis* (b.t.i.). As part of the establishment of an environmentally friendly and cost effective Integrated Pest Management program (IPM) against blackflies, investigations were initiated to support the present blackfly control strategy in South Africa. Emphasis was placed on potential predators and parasites of the blackflies' aquatic stages.

Methods: Thirteen sites along the Orange river, 12 along the Vaal river and one site along each of three tributaries to the Vaal river were monitored seasonally for one year. The abundance of the aquatic stages of blackflies and potential predators on rocks and vegetation in the river were determined using the 10-point visual ranking system of Palmer (1994) and the South African Scoring system (SASS 5), respectively. The abundance of algae, which may influence the efficacy of b.t.i, was also monitored.

Results: The four most abundant blackfly species were *Simulium damnosum* s.l,, *S. adersi*, *S. chutteri* and *S. nigritarse sl.* The most important families of predators identified were Coenagrionidae, Aeshnidae, Corydalidae, Hydropsychidae and Muscidae. Hydropsychidae was the only family recorded in high numbers. Nematode and Protozoan infection of the blackfly larvae and pupae were noted. The most abundant algae were species of *Baccillariophyceae* and *Chlorophyceae.*

Conclusion: The contribution of each of these potential predators and parasites needs to be evaluated for possible integration into an IPM approach.

Neonicotinoid resistance status of green peach aphid, *Myzus persicae* (Sulzer) (Hemiptera: Aphididae), in Turkey

A. Sibel Velioglu[1], Cem Erdogan[1], M. Oktay Gurkan[2], Graham D. Moores[3]

[1]Plant Protection Central Research Institute, Department of Physiology and Toxicology, Ankara, Turkey, [2]University of Ankara, Faculty of Agriculture, Department of Plant Protection, Ankara, Turkey, [3]Rothamsted Research, Harpenden, United Kingdom

Imidacloprid is the first authorized neonicotinoid in Turkey (1994). Following this, in 1996 acetamiprid, in 2000 thiamethoxam and in 2004 clothianidin were also authorized. Neonicotinoids are used heavily in vegetable, ornamental, cotton and similar important agro-ecosystems in green house and field conditions against aphids, whiteflies and other important pests. Related to their low cost advantage, usage rates are increasing more and more in Turkey, like in some other countries. Therefore, reduced susceptibilty rates are begun to monitor on pests in many agro-ecosystems.

Myzus persicae, is a polyphagous pest, which can easily found in many agro-ecosystems in Turkey. During this study, different populations that collected from heaviest insecticide used vegetable green houses and fields were assessed for cross-resistance risks refer to their LC_{50} values of authorized neonicotinoids of Turkey. Furthermore, same populations were also investigated on the relations of two metabolic enzymes - carboxylestrease and glutathione-S-transferase - with cross-resistance formation.

During our studies, 9 different populations from two important agricultural regions were used to determine LC_{50} values against imidacloprid, acetamiprid, thiamethoxam and clothianidin. Conducted systematic bioassay studies showed that; determined LC_{50} values for imidacloprid and acetamiprid has been higher than the values of thiamethoxam and clothianidin. The resistance rates of some populations were determined as follows; over than 200 fold in acetamiprid, 100 fold in imidacloprid, 10 fold in thiamethoxam and 20 fold in clothianidin. Related to the metabolic enzymes, carboxylesterase activity observed with both techniques the gel electrophoresis and the kinetic microplate assay. On the other hand the glutathione-S-transferase measured just with kinetic microplate assay.

Outbreak of erythrina gall wasps and control strategies based on their biology

Man-Miao Yang[1], Gene-Sheng Tung[2], Yen-Chiu Lan[3], En-Cheng Yang[4], Chia-Chin Hsu[2], Chun-Chern Fangjian[1]

[1]Department of Entomology, National Chung Hsing University, Taichung 402, Taiwan, [2]Division of Forest Protection, Taiwan Forestry Research Institute, Taipei 100, Taiwan, [3]Department of Resources and Environment, Tainan 709, Taiwan, [4]Department of Entomology, National Taiwan University, Taipei 106, Taiwan

Introduction: Since the report of erythrina gall wasp (EGW), *Quadrastichus erythrinae* (Hymenoptera: Eulophidae) in 2004, it has widely spread into various countries in Asia, pacific islands, and recently found in Florida. EGW form galls on the leaflets, petioles, and tender shoots of coral trees (*Erythrina* spp.). Heavy infestation causes curling of leaves and shoots, decline of plant health, defoliation, and possible death. Besides the emergent treatment, study of its basic biology is important for a better control of this significant invasive pest.

Methods: Various aspects of studies were conducted to understand basic biology of EGW, including life history, mating behavior, gall development, natural enemies, progressive stages of infestation, visual preference of adults, and investigation of population fluctuation in various regions of Taiwan. Further control strategies are recommended based on these results.

Results: The life cycle of EGW is 24.4 ± 1.2 days under 30℃ and 70-80% Rh. Significant differences were found in adult life between feeding with water and with diluted honey. Modifications of gall tissue from normal part only involve with increasing layers of cells but not obvious differentiation. At least four species of possible natural enemy are found, including a confirmed external parasitoid of EGW larvae which is well established in various populations in Taiwan. The sex ratio of male to female is slightly higher than one. The preference in wave-length using calibrated color paper shows a discrepancy between male and female. Four stages of damage levels are determined and treatment strategies are advised for each stage.

Conclusions: A better understanding of fundamental biology is essential for successful management of invasive pests. Our results cast some light on effective controlling strategies of EGW and further practical studies, such as biological control using parasitoids, are needed.

Hypersensitivity reactions in rice cultivars and effects on the morphology and development of the African rice gall midge, *Orseolia oryzivora* Harris and Gagné (Diptera: Cecidomyiidae)

Adebayo Omoloye

University of Ibadan, Ibadan, Oyo State, Nigeria

Introduction: Hypersensitivity responses (HR) in plants are physical, nutritional and allelochemical features that change in a plant's physiological, biochemical or morphological constituents following damage or stress by invasion of a herbivore. HR is presumed to be beneficial to the eliciting host plants since they hinder the performance and/or preference of invading herbivore. The relevance of HR as a mortality factor acting upon the African rice gall midge, *Orseolia oryzivora* in the resistant Africa (Tog) rice was investigated

Methods: Morphological changes after infestation in five different rice cultivars were recorded and data on rice reactions: gall length, colour, time to gall initiation, rate of gall development, period of development at each instar, number of pupae that emerged per treatment and number of larvae that survived to each instar were taken.

Results: Gall setting was the main morphological response to attack by the AfRGM and this occurred at the first instar. Many larvae may colonize a tiller but only one survives usually to 2nd instar in the field. Gall length was significantly suppressed in the resistant *O. glaberimma* cultivars compared to the *O. sativa* cultivars. Larval mortality (98%) in resistant cultivars was significantly higher at the first instar compared to the susceptible check. The female reproductive anatomy was negatively affected by HR causing reduced potential fecundity (32); morphological distortion, 70% reduction of egg size of F1 emergent in resistant cultivars.

Conclusion: The combined effects of hypersensitive reaction and probably other heritable factors of which type and amount phytosterol content are implicated.

Tentative phylogeny of Ditrysian Lepidoptera based on molecular data from mitochondrial and nuclear genes

Marko Mutanen[1], Lauri Kaila[2], Niklas Wahlberg[3]

[1]Zoological Museum, Department of Biology, University of Oulu, Oulu, Finland, [2]Finnish Museum of Natural History, Zoological Museum, University of Helsinki, Helsinki, Finland, [3]Laboratory Genetics, Department of Biology, University of Turku, Turku, Finland

Introduction: The Lepidoptera is one of the four megadiverse insect orders, yet the interrelationships between the superfamilies within it are poorly resolved. This situation is particularly true in the suborder Ditrysia, which comprises more than 99% of all Lepidopteran species. This study primarily aims at resolving the family-group relationships of the Ditrysian Lepidoptera using data from eight molecular markers.

Methods: One mitochondrial and seven nuclear genes (a total of 6472 basepairs) were sequenced from over 250 species representing ≈37 Lepidopteran superfamilies, ≈95 families and ≈195 subfamilies. Parsimony and Maximum Likelihood trees were constructed using TNT and RAxML, respectively

Results: The results further support the monophyly of Ditrysian Lepidoptera. Systematic placement of many previously unplaced Ditrysian lineages is clarified and several major lineages are reassigned. Insights into the phylogeny of most advanced non-Ditrysian Lepidoptera are gained as well.

Conclusions: Large molecular and morphological datasets combined with quantitative cladistic analyses are shedding new light to Lepidopteran phylogeny. It is foreseeable that the ongoing molecular and morphological Lepidoptera phylogeny projects will contribute at stabilizing the systematics of many poorly understood major Lepidopteran lineages.

Insecticide resistance status of *Trialeurodes vaporariorum* (Westw.) (Hemiptera: Aleyrodidae) in Turkey and resistance related biochemical markers

Cem Erdogan[1], A. Sibel Velioglu[1], M. Oktay Gurkan[2], Graham D. Moores[3], Ian Denholm[3]

[1]Plant Protection Central Research Institute, Department of Physiology and Toxicology, Ankara, Turkey, [2]University of Ankara, Faculty of Agriculture, Department of Plant Protection, Ankara, Turkey, [3]Rothamsted Research, Harpenden, United Kingdom

The greenhouse production in turkey mainly focused on vegetable production, which represents approximately 95% of total greenhouse production. A whitefly species, *Trialeurodes vaporariorum*, is very harmful to the greenhouse vegetable growing. Control of the whiteflies is very difficult because of their fast reproduction capacity, their ability to give several offspring in a agricultural production season, behavioural preferences of the both the adults and larvae to live on under surface of the leaf, and also having many host plant.

Therefore, the chemical control methods are heavily used in whitefly control. For the last 20 year, approximately, whitefly control is based on conventional insecticides as organophosphorus, carbamates and synthetic pyrethroids.

During our studies, insecticides from organophosphorus, synthetic pyrethroids and neonicotinoids were used. Eight different whitefly populations collected from the Turkey's heaviest insecticide used greenhouses, and compared regarding to their LC_{50} values by leaf dip and systemic bioassay methods. All populations showed higher resistance rates to the synthetic pyrethroids rather than other groups. During the studies, an evaluation of cross resistance was done according to different sorts of pesticide groups. Also, the activities of the metabolic enzymes (EST and GST), which were used as biochemical markers, are determined with microplate assay and then the relation between determined values and resistances discussed.

Tribolium species as models for chemical ecology and proteomic studies in insects

Taofic Alabi[1], Frederic Francis[1], Georges Lognay[2], Edwin Depauw[3], Eric Haubruge[1]

[1]Gembloux Agricultural University,Functional and Evolutionary Entomology, Gembloux, Belgium, [2]Gembloux Agricultural University,Analytical Chemistry, Gembloux, Belgium, [3]University of Liege, Mass Spectrometry Laboratory, Liege, Belgium

Introduction: Insects constitute pests in food products. Most of them received considerable attention from entomologists to reduce their damages and related economical impacts. Public criticisms, increasing of insect resistance and bad health and environmental effects of traditional chemical controls provided the need for novel and global patterns of insect control based on knowlegde of all biology aspects. Particularly, the stored product pests including Tribolium castaneum and related species were very studied for their response to several conventional chemical and innovative biological control methods. To investigate the relation between stored product pests and their environment, T. castaneum was selected to develop several complementary approaches including chemical ecology and molecular biology to better understand their behaviour and physiology and to be able to promote potential new control strategies such as the use of semiochemicals.

Methods: *Tribolium* species were selected as models to investigate an integrated view of insect communication by smell and taste. Beside behavioural assays and volatile compound analysis using gaz chromatography and electrophysiology to identify active infochemicals, complementary proteomic approach to identify active proteins in sensory organs by 2-D electrophoresis and mass spectrometry technics were performed.

Results: Behavioural and electrophysiological observations on T. castaneum and closed species were related volatile analysis and lead to the conclusion that several molecules were actively involved in the chemical communication of these species. Moreover, proteomic studies using very recent available genomic data's on antennae and legs of Tribolium species allowed us to identify proteins involved in the insect infochemical perception (CSP and OBP).

Phylogeny of Zygaenoidea and the evolution of larval locomotion, chemical defence and mimicry

Shen-Horn Yen[1], Marc Epstein[2], Oliver Niehuis[3]

[1]Department of Biological Sciences, National Sun Yat-Sen University, Kaohsiung, Taiwan, [2]Plant Pest Diagnostics Branch, California Department of Food & Agriculture, Sacramento, CA, United States, [3]School of Life Sciences, Arizona State University, Tempe, AZ, United States

The family-level classification and phylogeny of superfamily Zygaenoidea has been controversial for long. Currently it comprises 12 families: Heterogynidae, Zygaenidae, Lacturidae, Phaudidae, Himantopteridae, Somabrachyidae, Epipyropidae, Cyclotornidae, Megalopygidae, Dalceridae, Aididae, and Limacodidae plus several genera that have not been properly associated with any family. The monophyly of this superfamily are weakly supported by two morphological characters, the retractile head of the larva (at least in the later instars) and the second abdominal spiracle of the pupa, which is covered by the wings, but recent molecular phylogenetic studies have shown that the parasitic Epipyropidae and Cyclotornidae are more related to the cossoids. In the present study, we will address the research history of Zygaenoidea and in particular focus on the evolutionary trends of larval locomotion, chemical defence mechanisms and the complex mimetic coloration. We will also focus on the evolution of a peculiar functional and morphological replacement of male claspering apparatus by pregenital sternite and tergite, which is possibly one of the key innovations leading to diversification of several clades of this superfamily.

Ultrastructural and biochemical alterations in *Spodoptera litura* larvae treated with destruxin from *Metarhizium anisopliae* (Metch.)

Kandregula Sowjanya Sree, Vadlamani Padmaja

Andhra University, Visakhapatnam, Andhra Pradesh, India

Destruxin is a cyclodepsipeptidic mycotoxin produced by the entomopathogenic fungus, *Metarhizium anisopliae* and is of use in insect pest management with respect to its potent insecticidal properties. The crude destruxin treated *Spodoptera litura* larvae showed a decrease in thiol content and a hike in oxidation of glutathione to glutathione disulfide and ascorbate to dehydro ascorbate in a time (1, 24, 48 hours) and dose (LD_{30}, LD_{50}, LD_{90}) dependent manner. Apart from this evidence of the adverse effect of destruxin, an increase in the protein carbonyl levels which indicate the extent of protein oxidation or damage and the free radical levels (Hydrogen peroxide and hydroxyl radical) was also noted. These provide a clear indication of oxidative stress induced by crude destruxin on *S. litura* larvae. These biochemical changes in the larval body correlated with the ultrastructural alterations in the salivary glands of the larvae treated with LD_{50} (0.147 µg/g body wt.) of crude destruxin for 24 hours. These changes were noted from the transmission electron microscopic observations. The gradual detachment and damage of the microvilli from the epithelial cell surface was very clearly observed. Epithelial cell vacuolization, bleeding of the epithelial cells into the salivary gland lumen and disruption of the epithelial cell membrane were amongst the other major ultrastructural changes. The present investigation focuses salivary glands also as the target organ of destruxin apart from the already reported midgut, Malphigian tubules and haemocytes. The current study unravelled the role of larval innate antioxidant defence system in augmenting resistance or susceptibility against crude destruxin and the mode of action of this toxic metabolite on the larval body.

Pest risk analysis of importation of banana propagation materials from Uganda to Rwanda

Solomon Gebeyehu

Private, Africa, South Africa

The pest risk analysis of the importation of propagation materials from Uganda to Rwanda for the purpose of improving banana production was studied. A qualitative pathway-initiated pest risk analysis was done using the Crop Pest Compendium database compiled by the Common Wealth Agriculture Bureau International. The database provided several pests of potential quarantine importance to Rwanda, of which three were analyzed for their potential to enter, establish, spread and cause economic impact. The objective was to demonstrate the importance of doing pest risk analysis and decide appropriate phytosanitary measures by Rwanda before allowing importation of banana propagation materials from Uganda.

Individual risk factors were summarized as overall risk category for each of the insects. *Araecerus fasciculatus* had an overall high risk category as the banana propagation material could be a pathway for the entry of the pest into Rwanda, and favorable environmental conditions for its establishment as well as cultural practices that can aid its rapid spread would lead to significant yield loss to a wide range of major host plants which are of economic importance in Rwanda, once introduced. *Thrips hawaiiensis* showed medium risk as banana propagation materials are not direct pathway for this pest and the risk could be reduced by avoiding leaf materials in the consignment with which the insect is associated. Pest risk category for *Ceratitis capitata* was low as the pest only attacks fruits/pods and not banana propagation parts. The principles of pest risk analysis for trade with plants and plant materials is discussed.

Natural polymorphism affecting learning and memory

Tadeusz Kawecki[1], Frederic Mery[2], Amsale Belay[3], Marla Sokolowski[3]

[1]Department of Ecology and Evolution, University of Lausanne, Lausanne, Switzerland, [2]CNRS, Gif sur Yvette, France, [3]Department of Biology, University of Toronto, Toronto, Canada

Although numerous mutants with impaired learning have been identified, we know little about the genetic basis of natural variation in learning performance. Yet, it is on the basis of this variation that evolution moulds the learning ability and memory of a species. We have shown that a natural polymorphism in the gene *foraging* affects the ability of *Drosophila melanogaster* to learn which oviposition substrate is of high quality. Using a classical conditioning paradigm where flies are trained to avoid an odour associated with shock we could also show that the *foraging* polymorphism has antagonistic effects on two aspects of learning performance. Flies carrying the 'rover' allele have better short-term performance, but poorer long-term memory than flies homozygous for the 'sitter' allele. The *foraging* gene encodes a cGMP-dependent protein kinase (PKG). Using the GAL4-UAS system we could show that the effects of *foraging* on learning are mediated by the activity of PKG in the mushroom bodies of the fly brain. The *foraging* polymorphism has several pleiotropic effects and is thought to be maintained by balancing selection. This study thus offers insights into how ecology and genetics may combine to maintain variation for and create associations between behavioural traits.

Control of Colorado potato beetle, *Leptinotarsa decemlineata* Say (Coleoptera: Chrysomelidae), with the neonicotinoid thiamethoxam

Philippos M. Ioannidis[1], Zois D. Zartaloudis[1], Ioannis Papageorgiou[2]

[1]National Agricultural Research Foundation– Plant Protection Institute, P.O. Box 60324, ZIP 570 01,Thermi, Thessaloniki, Greece, [2]Syngenta Hellas SA, Anthousas Ave, Attiki, ZIP 153 49, Athens, Greece

Introduction: The Colorado potato beetle (CPB) is the most serious pest of potatoes in many regions of the world including Greece. This pest has an extraordinary ability to develop resistance almost to all groups of insecticides used to control it. Effective insecticide resistance management strategy aims to apply the least – insecticide amount on the population in order to conserve susceptibility. The method of spraying thiamethoxam directly on the potato tubers before sowing provides excellent protection.

Methods: Thiomethoxam (Cruizer 350 FS) which has a systemic action was sprayed (0.5lt water spray volume) just before sowing (beginning of May) at doses of 14, 20 and 28g of commercial product per 100 kg seeds tubers. Several preliminary trials and field experiments were conducted and the experimental design was a completely randomised block design with four replications. Harvesting was conducted in the middle of September.

Results: All the doses applied gave excellent control 45 days after sowing. Potato plants were satisfactorily protected even 60 days after sowing with less than 10% compared to the untreated control with more than 50% leaf damage.

Conclusions: This method gives a very good protection even from the early beginning of the growing season; keeps clear the plants from CPB damage even if the weather conditions are not ideal for alternative foliage spraying. This method has also an advantage of controlling early attacks of aphids and low impact on beneficial insects as well. This crop protection technique is strongly recommended particularly in regions where CPB severely damages potatoes.

Circadian plasticity of neurons and synaptic contacts in the fly's visual system

Elzbieta Pyza, Jolanta Gorska-Andrzejak

Department of Cytology and Histology, Institute of Zoology, Jagiellonian University, Krakow, Poland

Introduction: In the fly's visual system L2 interneurons show circadian plasticity in size of their axons. In addition the number of tetrad synapses formed between the photoreceptors and the L2 cells change during the day. We examined if morphology of the L2 dendrites, postsynaptic sites of the tetrads, and expression of their synaptic proteins are controlled by clock genes.

Methods: Flies were fixed at different times of the day and their brains sectioned. The L2 dendritic trees was examined by confocal microscopy. The L2 cells were visualized by expression of GFP in result of activation of a UAS-*gfp* reporter construct by the GAL4 enhancer-trap line 21D. Immunocytochemistry was used to detect pre- and postsynaptic proteins of tetrad synapses.

Results: The L2 dendritic trees were largest at the beginning of the day and of the subjective day in constant darkness. The rhythm was abolished in per^{01} but its pattern was changed in cry^{b} mutants. The tetrad presynaptic and postsynaptic proteins showed daily rhythms of their abundance. Only in case of the postsynaptic protein the rhythm was circadian.

Conclusions: The lamina L2 dendrites show circadian remodeling of their shape and this rhythm is controlled by clock genes. The presynaptic elements of tetrad synapses seem to be controlled by daily changes of light while the postsynaptic ones by a circadian clock.

Movement of non-native phytophagous Hymenoptera in Asia

Gene-Sheng Tung[1], Man-Miao Yang[2], Chia-Chun Hsu[3], Chia-Chin Hsu[1], Yuh-Shyong Yang[4]

[1]Division of Forest Protection, Taiwan Forestry Research Institute, Taipei 100, Taiwan, [2]Department of Entomology, National Chung-Hsing University, Taichung 402, Taiwan, [3]Division of Silviculture, Taiwan Forestry Research Institute, Taipei 100, Taiwan, [4]Department of Biological Science and Technology, National Chiao-Tung University, Hsingchu 300, Taiwan

Introduction: Various invasive phytophagous hymenopterans were reported in Asia and some cause severe damages to their hosts. Among these, the erythrina gall wasp (EGW), *Quadrastichus erythrinae* (Hymenoptera: Eulophidae) is a notorious one which forms galls and causes acute and severe damages on coral trees (*Erythrina* spp.). We reported the spread of EGW in Asia, and analyze the movement pattern of this pest geographically and biologically. Moreover, other cases of invasive wasps are reviewed.

Methods: The species distribution model was used to evaluate the potential distribution of EGW. Phylogenetic analysis was conducted based on molecular data for samples from various populations of Taiwan and different countries.

Results: The temporal distribution of EGW shows a progressive pattern geographically from west forward east direction or from Indian Ocean to Pacific Ocean. Models indicated EGW is confined to tropical area, and the Infection-unreported areas with the occurrence of host records are potential regions of EGW attack. Furthermore, prediction of the future expansion of is discussed. The molecular data confirm the con-specific status of EGW which occurred in various populations on different host species of Taiwan. The relationships of EGW from different countries are discussed based on molecular phylogeny.

Conclusions: The result of this analysis provides a better understanding of the movement of invasive EGW and an alert of its future expansion. It also offers a model for the study of other recently occurred invasive hymenopteran pests.

Xylosandrus germanus: A long established, but emerging invasive pest in U.S. nurseries

Christopher Ranger, Michael Reding

USDA-Agricultural Research Service, Wooster, OH, United States

Since first being detected in the U.S in 1932, the exotic ambrosia beetle *Xylosandrus germanus* is increasingly being recognized as a key pest of nursery trees, particularly deciduous hosts. Despite being mainly considered as a secondary attacker, a growing body of evidence indicates *X. germanus* will colonize apparently-healthy trees. A series of experiments were conducted to elucidate the influence of abiotic and biotic factors on the colonization strategy of *X. germanus*. The impact of prolonged winter dormancy on host-attraction to *X. germanus* was assessed using kousa dogwoods, *Cornus kousa*. Groups of dormant *C. kousa* trees were held for varying lengths of time in cold storage to experimentally-induce progressive phenological stages. *Cornus kousa* trees ranging from dormant to post-dormant were then simultaneously placed adjacent to woodlots just prior to *X. germanus* peak flight activity. The influence of phenological stage on host-attractiveness and colonization by *X. germanus* will be described. Complementary experiments focused on the interaction between flood stress and pathogenicity of *X. germanus* fungal symbionts. Sweetbay magnolia, *Magnolia virginiana*, trees under adequate and flood-stress irrigation conditions were inoculated with either *Ambrosiella hartigii* or a second unidentified *Ambrosiella* sp. isolated from the mycangium of *X. germanus*. Volatiles collected and identified from the *M. virginiana* treatments were subsequently assessed for their attractiveness to *X. germanus*. Fungal pathogenicity and the attractiveness of host-plant volatiles to *X. germanus* will also be described. Understanding the influence and interaction among these factors is critical to improving the management and detection of *X. germanus* in the nursery agroecosystem.

Immunization studies in rabbits using gut membrane-bound proteins derived from *Rhipicephalus appendiculatus, R. evertsi evertsi* and *Amblyomma variegatum* female ticks

Helen Lydia Kutima, Adepapo Amoo, Mabel Imbuga, Philip Kutima

Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya

The objective of this study was to immunize rabbits with Gut Membrane-Bound Proteins (GMBP) derived from partially engorged *Rhipicephalus appendiculatus*, *R. evertsi evertsi* and *Amblyomma variegatum* female ticks and to assess whether the elicited immunity was protective against both homologous and heterologous tick instars and to isolate and identify the protective antigens.

Sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) of the GMBP antigens demonstrated protein bands with molecular weights ranging from 16 to 140 KDa. Thirty-seven, 45 and 39 protein bands were fractionated from *R. appendiculatus*, *R. evertsi evertsi* and *A. variegatum* GMBP antigens, respectively, all possessing molecular weights ranging from 14 to 140 KDa. Twenty-two of the isolated proteins were shared among the three tick species. Immunized rabbits acquired resistance to challenge infestation by all instars of the three tick species. Resistance was manifested by prolonged feeding, reduction in engorgement weights, egg mass weights, moulting and percentage hatchability and increased mortality. Immunization of rabbits with GMBP antigens generated protection and cross-protection against challenge infestation with homologous and heterologous instars, respectively. Cross-protection was more pronounced in the homologous than heterologous systems.

Enzyme-Linked Immunosorbent Assay (ELISA) technique detected circulating antibodies in the anti-sera to GMBP from homologous and heterologous systems one week after the primary dose. Ouchterlony double immunodiffusion reactions with anti-tick GMBP sera formed 2 to 3 precipitin lines with homologous GMBP antigens and one to two precipitin line(s) with each heterologous GMBP antigens. A line of complete identity was observed when anti-sera to GMBP antigens reacted with GMBP from homologous and heterologous tick species, suggesting common antigenic epitopes.

Western blot analysis on GMBP of *R. appendiculatus*, *R. evertsi evertsi* and *A. variegatum* with sera from immunized rabbits detected protein bands specific to the homologous GMBP antigens, and revealed considerable cross-reactions in the heterologous systems. These results suggested further the presence of common antigens. The presence of cross-reacting antigens conferred cross-protection.

The influence and control of invasive pests in commercial forestry plantations in South Africa

Bernard Slippers[1], Brett P. Hurley[1], Jolanda Roux[2], Michael J. Wingfield[1]

[1]Department of Genetics, Forestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, South Africa, [2]Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, South Africa

South Africa has approximately 1.5 million hectares of commercial plantations, consisting predominantly of *Pinus* spp., *Eucalyptus* spp. and their hybrids, and *Acacia mearnsii*. During the course of the past Century, a number of pests have impacted negatively on the productivity and sustainability of these plantations. These pests have included a large number of polyphagous native insects that have adapted to feed on the non-native plantation trees. Such pests include a number of Lepidopteran and Coleopteran defoliators and root feeders, the wattle mirid (*Lygidolon laevigatum*), the wattle bagworm (*Chaliopsis junodi*), and others. Most recently, the native cossid moth, *Coryphodema tristis*, has caused severe damage to *E. nitens* plantations. Despite the presence of natural enemies, sporadic outbreaks of these pests cause serious financial losses to the forestry industry. Of increasing concern is the introduction of non-native pests. Two of the earliest of these non-native pests to be detected in South African plantations were the Eucalyptus snout beetle (*Gonipterus scutellatus*) and the black pine aphid (*Cinara cronartii*), which caused extensive damage to *Eucalyptus* and *Pinus* plantations, respectively. In recent years, there appears to have been an increase in the number of introductions of non-native pests. Thus, three serious pests (*Sirex noctilio* on *Pinus* spp. and *Thaumastocoris peregrinus* and *Leptocybe invasa* on *Eucalyptus* spp.) have appeared in the last 15 years. Previously insecticides were typically used to control pests, but the negative environmental and financial considerations associated with this form of control has elevated the need and urgency for alternative management strategies. In this regard, biological control, host resistance and silvicultural measures are currently being applied and pursued.

The role of dopaminergic G protein coupled receptors (GPCRs) in the homeostatic regulation of the transient potassium current (I_A) in arthropod neurons

Deborah Baro, Merry Clark, Hongmei Zhang, Wulf-Dieter Krenz

Georgia State University, Atlanta, GA, United States

We are interested in how neuronal monoamine receptors transduce signals across time and space. Large, identified crustacean neurons provide excellent models for understanding the cellular properties of arthropod neurons in an intact network. The same neuron can be unambiguously identified and studied in every preparation, allowing for a detailed characterization of the spatiotemporal organization of neuronal GPCR transduction cascades. Unfortunately, because crustaceans are genetically intractable, tools for delving beyond the characterization of neuronal electrophysiological properties have been limited. Taking advantage of the extensive insect databases and the relatively close phylogenetic relationship between insects and crustaceans, we have cloned a variety of GPCRs and ion channels, including dopamine receptors and the shal channel, which mediates I_A. We study dopaminergic modulation of shal channels in two neurons, PD and LP, which exclusively express D2 and D1 receptors, respectively. Dopamine receptors are only located in a subset of nerve terminals where they modulate local proteins, as well as produce global biochemical signals that alter protein function in distant compartments, like the soma. In response to a brief application of dopamine, remote D2 and D1 receptors increase and decrease the density of the somatic I_A, respectively. On the other hand, prolonged exposure to DA induces a persistent, homeostatic adaptation in I_A that opposes the short term modulation (e.g., D2 activation decreases I_A density 10-12 hrs after DA is removed). We are currently testing the hypothesis that dopamine simultaneously and conversely alters shal channel phosphorylation and shal gene transcription to homeostatically regulate I_A density.

State-wide monitoring of mosquito insecticide resistance in Florida, USA

John Petersen

Florida A&M University, Panama City, Florida, United States

Introduction: Since 1999 a state-wide program of training workshops has increased the number of mosquito control programs that monitor mosquito response to pesticides currently in use in Florida. A standardized general procedure for insecticide resistance testing by the bottle bioassay has been published. The bioassay is based on exposure of adult mosquitoes to a diagnostic concentration of insecticide that is selected to discriminate between fully susceptible mosquitoes from those that show some level of genetic resistance.

Methods: 14 protocols have been developed detailing procedures for diluting "off-the-shelf" pesticides in A.C.S. acetone prior to testing by the bottle bioassay. Regional workshops were conducted in 37 locations throughout the state of Florida, contacting directly 46 different mosquito control programs that had not carried out insecticide resistance testing prior to our workshop.

Results: For each Active Ingredient (AI), dose response data obtained in our laboratory were subjected to probit analysis estimating the LC_{50} and LC_{95}. The diagnostic concentration we use for the bottle bioassay is defined as 2 times the LC_{95}. Baseline response of susceptible mosquitoes is determined using colony mosquitoes that have not been exposed to pesticides. Data from insecticide resistance bioassays by Florida mosquito control programs were posted to the Center's web site. This outreach program makes extensive use of the internet to disseminate standardized protocols and to share data that are the outcome of insecticide resistance testing.

Conclusions: Based on the outcome of bottle bioassays, operations supervisors can make informed, timely decisions about which products to use in mosquito control.

The efficacy of *Strychnos spinosa* (Lam.) and *Solanum panduriforme* (Incanum) fruit-extracts in controlling ticks in cattle

James Madzimure[1], Humphrey Hamudikuwanda[1], Brighton Mvumi[2], Thokozani Hove[3]

[1]Department of Animal Science, Faculty of Agriculture, University of Zimbabwe,, Harare, Southern Africa, Zimbabwe, [2]Soil Science & Agricultural Engineering, Faculty of Agriculture, University of Zimbabwe, Harare, Southern Africa, Zimbabwe, [3]Faculty of Veterinary Science, Paraclinical Veterinary Studies, University of Zimbabwe, P.O. Box MP 167, Mt Pleasant, Harare, Southern Africa, Zimbabwe

Introduction: Some Southern African farming communities have claimed that fruit-extracts of the plants *Strychnos spinosa* (Lam.) and *Solanum panduriforme* (Incanum) can be used to control ticks in cattle. In this study, the efficacy of these fruit-extracts for controlling ticks in cattle was evaluated.

Methods: Ripe *S. panduriforme* and mature but unripe *S. spinosa* fruits were pounded separately, soaked in cold water for 48 hours, and filtered through a muslin cloth to achieve concentrations of 5%, 10% and 20% (w/v). Treatments included the different concentrations of each plant species, Tickbuster (amitraz) spray (positive control) and no treatment (negative control). All the treatments were sprayed on 44 Mashona cattle at weekly intervals. Tick numbers were recorded before spraying and subsequently, daily for 43 days. Cattle blood samples were collected for piroplasms screening.

Results: Duration, post-treatment application, had an effect on tick numbers ($p < .0.05$) with tick numbers increasing with time after each spray. *S. panduriforme* was effective ($p < 0.05$) even at 5% concentration against the ticks *Rhipicephalus evertsi* and *Rhipicephalus appendiculatus*. The 10% *S. spinosa* was more effective ($p < 0.05$) than other extract concentrations against the tick *Boophilus decoloratus*. The treatments were ranked, in descending order of effectiveness, as Tickbuster, plant extract treatments, and untreated control. No piroplasms were detected implying that animals were not infected.

Conclusion: The results indicate that *S. panduriforme* and *S. spinosa* have some acaricidal effect on ticks in cattle with the former being more potent.

International activities related to Persistent Organic Pollutants (POPs) that are termiticides

Agneta Sundén Byléhn

UNEP/DTIE Chemicals, United Nations Environment Programme, Geneva, Switzerland

Introduction: Persistent organic pollutants (POPs) are chemicals of international concern since they undergo global environmental transport, persist for long periods in the environment, bio-accumulate and cause adverse effects to human health and wildlife. POPs include pesticides, industrial chemicals and unwanted by-products such as dioxins. Individual countries alone are unable to control the environmental pollution from these border crossing substances, which are found in regions where they have never been produced or used.

International Actions: Negotiations of a global legally binding instrument on POPs were started under the auspices of UNEP in 1998. The Stockholm Convention that entered into force in May 2004 aims at ultimate elimination of POPs. It presently covers twelve substances of which aldrin, chlordane, dieldrin, heptachlor, and mirex have, or are still, being used as termiticides. Other pesticides covered include DDT, endrin, hexachlorobenzene, mirex and toxaphene (camphechlor). Another set of pesticides are presently under review for inclusion under the Convention: chlordecone, endosulfane, alpha-and beta-hexachlorocyclohexane, lindane and pentachlorobenzene.

Results: UNEP / FAO collaboration on the POP termiticide issues in support of the Stockholm Convention resulted in 2000 in the establishment of the Global Termite Expert Group (GTEG), which presently has around 20 members from all regions of the world. GTEG has developed guidance and technical information to support states in implementing sustainable alternatives to POP termiticides. These and other materials are available at UNEP's website: http://www.chem.unep.ch/termites/Default.html.

Conclusion: The implementation of sustainable alternatives to POP pesticides depends heavily on guidance and technical support from the scientific and research communities.

Infection of ticks with borrelia cuts off olfactory orientation towards host kairomones

Torsten Meiners[1], Hans Dautel[2]

[1]Applied Zoology/Ecology, Free University of Berlin, Berlin, Germany, [2]Insect Services, Berlin, Germany

Nymphs of the blood-feeding tick *Ixodes ricinus* are known to move short distances towards host odour, although their main mode of host finding is ambushing passing vertebrates. Several chemicals have been identified that can mediate the olfactory orientation of the eyeless ticks that are vectors of *Borrelia sp.* causing Lyme borreliosis in humans. While tick nymphs parasitise both small and large vertebrates, large vertebrates like deer are incompetent as transmission reservoirs for *Borrelia sp.*. Thus, for borreliae transfer to a big mammal often means a dead end.

Here we investigate whether infested (*Borrelia afzelii*) ticks behave differently towards host (dogs, men) odours or certain volatile host compounds (CO_2; hexanoic acid) and whether differently infested ticks chose different heights for ambushing. We used a locomotion-compensator (servosphere) and CO_2-traps in the surroundings of Berlin, Germany, to test responses of uninfested and infested ticks to volatile kairomones. The choice of ambush heights was tested in semi-field stalk-arenas.

Uninfested ticks responded to all offered kairomones (but not to control air or plant volatiles) and chose a high ambushing position. Infested ticks on the contrary showed the same walking activity as uninfected ones, but did not orientate to any of the offered odours and chose a low ambushing position. Nymphs caught in the field by CO_2-traps showed a lower degree of infestation with *Borrelia sp.* than nymphs caught by flag sweeping. It is discussed how a possible “manipulation” of ticks by borreliae might contribute to enhance their chance of avoiding incompetent transmission reservoirs.

Fungus-growing termites maximize harvest and minimize host-symbiont conflict by growing *Termitomyces* fungi in monoculture

Duur K. Aanen[1], Henrik H. de Fine Licht[2], Alfons J.M. Debets[1], Niels Kerstes[1], Jacobus J. Boomsma[2], Rolf F. Hoekstra[1]

[1]Laboratory of Genetics, Wageningen, Netherlands, [2]Institute of Biology, Copenhagen, Denmark

Introduction: Although mutualistic symbiosis per definition provides a net benefit to the partners involved, these partners' interests are usually not completely identical. Also in the mutualistic symbiosis between fungus-growing termites and *Termitomyces* fungi, such conflicts of interest exist, for example over reproduction and the degree of symbiont mixing. Recently, a proximate mechanism on how these conflicts of interest are regulated has been proposed. The key to the proposed mechanism is the within-nest propagation mode of fungal symbionts by termites. The termites suppress horizontal fungal transmission by consuming modified unripe mushrooms (nodules) for food. However, these nodules provide asexual gut-resistant spores that form the inoculum of new substrate. This within-nest propagation implies that harvesting and inoculation are coupled. Furthermore, the inoculation of spores in high density ensures the fast establishment of a fungal colony in the new substrate.

Methods: I describe *in vitro* experiments to test the hypothesis that fusion between clonally related subcolonies, but not between non-clonally related subcolonies, leads to synergism. We compared the 'harvest' (number of nodules) of five monocultures (heterokaryons belonging to a single biological species of *Termitomyces* associated with *Macrotermes natalensis*) with the harvest of varying degrees of mixed cultures of these five strains (with two, three or five heterokaryons in all combinations) in a high density.

Results: In line with the prediction, we found a highly significant correlation between harvest and 'relatedness' (the chance to meet a clonally related subcolony in a mixture).

Conclusions: The results of these experiments imply that i) monoculture maximizes the harvest; ii) monoculture is self-maintaining as there is positive frequency-dependent selection; and iii) the termites and the resident fungus share the same short-term interest as the introduction of an unrelated fungus will initially lead to a lower harvest.

Chemical and behavioral ecology in insect parasitoids: How to behave in a complex odorous environment

Torsten Meiners, Monika Hilker

Applied Zoology/Ecology, Institute of Biology, Free University of Berlin, Berlin, Germany

Volatile cues released from the host habitat or the host itself play a key role in the foraging process of parasitoids. However, these resource-indicating odors encountered by parasitoids in their natural environment need to be detected within a huge variety of other environmental odors and are often both complex and variable mixtures themselves. Our studies address the question how egg parasitoids of herbivorous insects cope with the problems of complexity and variability of the infochemical web.

Two principal strategies to solve these problems will be shown. One strategy is to avoid areas with high odor complexity, and another one is to “dig through” all the odorous information. A successful way to disentangle complex odorous information is the combined use of innate odor preferences and learning which enhances the host finding success of a foraging egg parasitoid. A novel learning mechanism will be suggested where a chemical cue is “filtered” by a learning egg parasitoid in different odorous contexts, but a behavioral response to this cue occurs only when it is presented in a specific odourous context. Furthermore, our studies show that the spatial presentation of different volatile blends may substantially influence parasitoid orientation.

Research investigating how parasitoids actually cope with a very unstable infochemical environment can be utilised to improve the efficacy of current biological control programmes. This includes the development of novel approaches that manipulate plant diversity and environmental odor complexity and/or the use of infochemicals to control important agricultural and forest pests.

Interactions between the Bt-transgenic trait and inherent plant resistance mechanisms

Felix Wackers[1], Cristina Faria[1], Joerg Romeis[2]

[1]Lancaster University, LEC, Centre for Sustainable Agriculture, Lancaster, United Kingdom, [2]Agroscope Reckenholz-Tänikon Research Station ART, Zurich, Switzerland

Recent reports indicate that genetically modified cotton crops that express toxins derived from *Bacilus thuringiensis* (*Bt*) can suffer higher damage by *Bt*-insusceptible pests. While outbreaks of secondary pests in *Bt*-cotton have raised widespread concern, the underlying mechanisms remain poorly understood. Here we present a novel mechanism explaining increased susceptibility of *Bt* cotton to secondary pests. This will contribute to the sustainable use of transgenic varieties and effective resistance-management.

Techniques in determining the progressive stages of EGW infestation for galling pest control in Taiwan

Yen-Chiu Lan[1], Gene-Sheng Tung[2], Chia-Chin Hsu[2], Man-Miao Yang[3], En-Cheng Yang[4]

[1]Department of Resources and Environment, Leader University, Tainan, Taiwan, [2]Division of Forest Protection, Taiwan Forestry Research Institute, Taipei, Taiwan, [3]Department of Entomology, National Chung-Hsing University, Taichung, Taiwan, [4]Department of Entomology, National Taiwan University, Taipei, Taiwan

Introduction: The Erythrina Gall Wasp (EGW, *Quadrastichus erythrinae*), an Erythrina-specific galling species, has been first reproted in 2000 and listed in Global Invasive Species Database (GISD). EGW forms galls on the leaves, petioles, young shoots, and stems and has multivoltine and overlapping generations. Severe infestation causes obvious swelling and curling of young shoots, defoliation, and death of the tree. Field observation and experiments were proceeded to explore efficient pest control methods in Taiwan. Although the efficacy of chemicals is confirmed, the costs and labor are too intensive. Here we report a technique in the determination of progressive infestation stages and, therefore, better efficient strategies of pest control could be applied accordingly.

Methods: The experiments were performed from July 2006 to June 2007 in Taipei City and Tainan City. The number of galls and EGWs on the leaves and stems were counted from cut branches of infested Indian coral tree (*Erythrina variegata*). All the sampled branches were photographed. The number of galls and EGWs were plotted and the slops from liner regression were tested.

Results: Three significantly different regression lines were found. Contrast to the corresponding photograph, we may conclude that there are four progressive stages of infestation, the first three stages can be determined by gall numbers and symptoms of infested leaves and the fourth stages can be determined solely by the symptoms of infested branches.

Conclusions: The result provides a useful technique for field monitoring of infestation stages and field workers without expertise could implement it easily. The field information could be gathered instantly in determining strategies for pest control, once the infestation stage is determined, strategies for pest control could be decided.

Are neonicotinoid insecticides resistant to the evolution of resistance in aphids?

Steve Foster

Rothamsted Research, Harpenden, United Kingdom

Neonicotinoid insecticides now have widespread use for controlling insect pests. The commercial forerunner, imidacloprid, is active against species in the Hemiptera, Coleoptera, Diptera and Lepidoptera, but in agriculture is being used most intensively to control sucking pests (aphids, planthoppers, leafhoppers and whiteflies), and the Colorado potato beetle (CPB). Although resistance to imidacloprid is still relatively rare, it has evolved in tobacco and glasshouse whiteflies, CPB and brown planthoppers. Interestingly, there are no documented examples of neonicotinoid resistance, capable of causing control failures, in any aphid species even though these compounds have been in use for over fifteen years. Possible reasons for this lack of resistance are 1: neonicotinoids target the nicotinic acetylcholine receptors of nerve membranes, and these are thought to comprise complex heteropentamers of non-identical subunits that may well generate diverse binding sites for these insecticides in different sub-populations. As a result, a point mutation in one subunit may not be sufficient to confer insensitivity (resistance) across the entire population of nAChRs within the insect's nervous system. 2: in species carrying resistance it often appears to be mediated by increased activity of mixed function oxidases (MFOs) and this enzyme-based mechanism has not previously been implicated for resistance in aphids. Taken together, this may explain why resistance to neonicotinoids has been slow to evolve in aphids, although this should not lead to grower complacency since some species show a consistent low level reduced susceptibility to neonicotinoids, and this may represent the first steps toward the evolution of more potent resistance.

Analyzing complex trophic interactions in arthropod communities using DNA-based methods

Michael Traugott

University of Innsbruck, Innsbruck, Austria

DNA-based methods of parasitoid and prey detection have revolutionized the study of trophic interactions under natural conditions. For example, multiplex PCR-based parasitoid detection allows to effectively resolve the trophic connections occurring in a community of aphid parasitoids consisting of 12 primary and secondary parasitoid species. Besides determining host-parasitoid links, multiparasitism and primary parasitoid-hyperparasitoid links could be tracked at a species-specific level, providing unique insights into the trophic complexity of this parasitoid food web. Based on the parasitism rates found in field-collected aphids, another multiplex PCR system was developed to screen arthropod predators for aphid and parasitoid consumption. First results on spiders indicate, besides high levels of aphid predation, that these predators also extensively fed on adult parasitoids early in the season, revealing complex trophic interactions between the natural enemies of aphid pests.

DNA-based methods are also extremely valuable for resolving trophic links within soil food webs. For example, we have shown that besides predatory beetle larvae, centipedes (Geophilidae) are the main predators of eggs and larvae of scarabaeid beetles, serious pests within alpine grasslands. Moreover, scarab prey proved to be an important food source during summer, sustaining the predatory soil invertebrate community when earthworm prey was scarce.

Within a current project we take molecular approaches to determine trophic interactions one step further: using DNA-based gut content analysis trophic links between plants and elaterid larvae, soil-dwelling insects which feed on a variety of plants, will be determined to assess the impact of plant biodiversity on herbivore food choice.

The olfactory pathway in Attine ants

Christoph J. Kleineidam, Markus Ruchty

University of Wuerzburg, Wuerzburg, Germany

Temperature is decisive for brood development and social insects show behavioral adaptations to take care of their brood. Various behavioral responses to temperature fluctuations illustrate an amazing thermal sensitivity of e.g. ants. Recently, we showed that leaf-cutting ants can use thermal radiation for orientation and we searched for the sensillum receiving the adequate thermal stimulus.

In Sensilla coeloconica we found a very sensitive thermo-receptive neuron. Extracellular recordings of the neuronal activity revealed a phasic-tonic response and rapid adaptation. As thermal stimuli, we used both, convective heat (tempered air) and radiant heat (using a Peltier-Element) to describe the response properties. We found the sensillum to be direction sensitive to IR-radiation with best sensitivity in front of the sensillum. The sensory peg of the S. coeloconica is located in a chamber, embedded in the antennal cuticle (peg-in-pit sensillum), and only a tiny aperture within the thin apical cuticle of the sensillum connects it to the environment. This embedding probably attenuates rapid fluctuations of air temperature and results in the direction sensitivity to IR-stimuli. Based on both, response property of the receptor neuron and morphology, we conclude that the S. coeloconica of leaf-cutting ants are morphological IR-sensilla, suited to detect rapid changes in the thermal environment. This newly described IR-sensillum may allow ants to assess spatial information about their thermal environment.

Funding: DFG SFB 554/A6

Trick or treat - effects of an invasive plant on survival and resource sharing in Irish bumblebees

Anke Dietzsch, Jane Stout

Trinity College Dublin, Dublin, Ireland

Introduction: Invasive plant species have become a major concern in recent years because they alter native ecosystems and processes such as plant-animal interactions. Little is known about their impacts on pollinators. Pollinator communities may benefit if alien plants offer valuable resources or substitute declining native plants. Alternatively, they may be harmed by alien toxic secondary compounds, or by displacement of native plants.

Methods: We used *Rhododendron ponticum* as a model plant species to investigate its effects on native bumblebees. *R. ponticum* is severely invasive in Ireland and contains grayanotoxins. To test the suitability of alien floral rewards as bumblebee food we caged workers of *Bombus lucorum* and kept them under six feeding regimes. We also estimated and compared numbers of bumblebee colonies utilising invaded and uninvaded field sites by genotyping workers of *B. lucorum* and *B. pascuorum* at six microsatellite loci and reconstructing sisterhoods among the individuals.

Results: Neither nectar and pollen of *R. ponticum* nor food containing a toxin similar to grayanotoxin reduced the survival rate of bumblebee workers significantly compared to native nectar and pollen or commercial bee food. Invaded field sites were used by a higher number of colonies of both bumblebee species than uninvaded field sites.

Conclusions: Rewards of *R. ponticum* do not harm worker bumblebees, and represent a valuable foraging resource for native bumblebees. As a result, invaded plant communities can support more colonies of social bumblebees than native plant communities do, perhaps by the alien plant facilitating the establishment of bumblebee queens.

A largely unstudied wealth of galls, gall-inducers and associated insects on indigenous South African plants

Stefan Neser

Agricultural Research Council, Plant Protection Research Institute, Pretoria; and Forestry and Agricultural Reseach Institute, University of Pretoria, Pretoria, South Africa

Introduction: Despite a vast diversity of galls in both the unique Fynbos Floral Kingdom and in the Afrotropical Flora, southern Africa's gall fauna has received only little attention. Cecidomyiids on very diverse plant groups and eriophyoid mites seem to vie for the position as most speciose group of local gall formers.

Methods and results: Amongst galls from other groups recorded to date, the following are prominent: Lepidoptera (including some highly specialized cecidosids), Diptera other than gall midges (especially Tephritidae) and Coleoptera (mainly curculionoids, some also reported as inquilines). Galling thrips, psyllids, coccoids and aphids are probably poorly represented. A conspicuous near-absence of phytophagous cynipids and sawflies is balanced by a large number of members from at least six other hymenopteran families, often reared in species complexes from galls in which their actual roles remain unknown. Rearing insects from opportunistically collected galls and gall-like structures may lead to wrong conclusions about the initiators. This is especially true when the (primary) inducers may belong to uncommon groups of gallers, such as eriophyoids, non-soil inhabiting nematodes, and fungi. Complexes of several species may emerge from a single gall, and a variety of galls and gall inducers may occur on a single host-plant species.

Conclusions: There is a considerable backlog in collecting, studying, and describing galls and gall formers in southern Africa. Surveys by specialist collectors will no doubt yield a plethora of unknown and/or undescribed insect taxa, galls, and host associations, as well as possible surprises, especially within the endemic flora, succulents, and other desert plants.

Impacts of thinning ponderosa pine forests on pine bark beetles: Implications for mitigating climate change.

Monica Gaylord, Richard Hofstetter, Sky Stephens, Michael Wagner

Northern Arizona University, Flagstaff, Arizona, United States

Introduction: Most climate models predict that future droughts will become more frequent and severe in the southwestern United States and mitigating the impacts of climate change is an ongoing concern for forest managers. Thinning treatments in the southwestern United States are often suggested as an effective means of preventing bark beetle outbreaks by increasing water availability to remaining trees and by changing microclimate within stands. However, little research has been done across a range of stand densities to determine optimal basal area for tree resistance to bark beetle attacks.

Methods: Measurements on tree water stress and bark beetle resistance were collected from a range of thinning treatments (9.2– 34.4 m^2/ha) at two sites in ponderosa pine forests of northern Arizona. One site has been maintained at selected basal areas since 1962 and represents a long term thinning response. The second site was thinned in late fall of 2005 and represents a short-term thinning response.

Results and Conclusions: Stand resistance generally increased after thinning treatments. Water stress during the dry season was reduced in thinned stands at both sites. Our research suggests that thinning treatments mitigate water shortages in forest stands and decrease bark beetle associated mortality via immediate changes in microclimate and long-term changes in trees vigor. Stands with basal areas of < 23.0 m^2/ha appear to be less susceptible to bark beetle attacks. We will discuss how our results can be used to determine the impact of thinning treatments on forest stands under future climate change scenarios.

Cynipid–parasitoid interactions: Comparing three dog rose species along a geographical gradient

Annette Kohnen[1], Katrin Klinge[3], Volker Wissemann[2], Roland Brandl[1]

[1]University of Marburg, Marburg, Germany, [2]University of Giessen, Giessen, Germany, [3]University of Goettingen, Goettingen, Germany

Multitrophic interactions between plants, herbivores and natural enemies change with host species as well as geographic context. Thereby, the genetic variation between hosts affects not only herbivores but also the structure and dynamics of higher trophic levels.

In our study we examined interactions between the gall wasp *Diplolepis rosae* (L. (Hym.)) and its parasitoids on three dog rose species (*Rosa*, section Caninae) across Germany. Within 388 galls we found eight species of parasitoids (most common: *Orthopelma mediator* 18 %, *Glyphomerus stigma* 12 %, *Torymus bedeguaris* 9.1 %) and the inquilin *Periclistus brandtii* (12 %). Most galls were found on *R. rubiginosa* (mean: 5.9±1.4 bush^{-1}; *R. canina:* 1.8±0.1, *R. corymbifera*: 2.8±0.5; 133 bushes sampled). The abundance of galls bush^{-1} varied between sample localities ($F_{7,109}$=25, p<0.001), the rose species ($F_{2,109}$=25., p<0.001) and their interaction ($F_{14,109}$=2.9, p<0.001). The rate of parasitism and therefore the survival rate of *D. rosae* decreased with increasing gall volume ($F_{1,256}$=479, p<0.001) and varied between rose species ($F_{2,256}$=96, p<0.001). But in contrast to the abundance, the rate of parasitism was smallest for galls collected on *R. rubiginosa* (62 %, *R. canina*: 76 %, *R. corymbifera*: 76 %). Again the parasitism rate varied with sample locality ($F_{7,256}$=49, p<0.001), but showed no geographical gradient. Furthermore, host identity and locality showed a significant interaction ($F_{14,256}$=13, p<0.001). Overall our results show that host identity and geography interact in determining the structure of food webs.

The population dynamics of red date palm weevil *Rhynchophorus ferrugineus* Oliv. and other insects in date palm orchards in the Kharje area of Saudi Arabia

Hassan ALAyied, Hathal ALDafer

[1]King Abdulaziz City for Sicenec and Technology, Riyadh, Saudi Arabia, [2]King Saud University, Riyadh, Saudi Arabia

Introduction: Since long the red palm weevil, *Rhynchophorus frrugineus* Oliv is known to be the most serious pest of coconut and other cultivated palms in India and other South Asian countries. This insect entered the Gulf countries in mid 1980's and since then it has caused devastating impact on date palm cultivation. It has threatened the multi-million dollar date industry and has raised the question on the survival of a cultural icon of the Gulf countries. The larval stages of this insect feed voraciously within the trunk of the palms and kill the trees. There are a number of insects attacks the date palm tree trunks such as the longhorn date palm stem borer *Pseudophilus Testaceus* Gah. and *Oryctes* sp., besides red date palm weevil. Our study was conducted to understand the relationship between the red date palm weevil and the other two insects.

Methods: Twenty five fields were selected in al Kharje area (55 km South Riyadh, Saudi Arabia). Number of light traps and pheromone traps were distributed evenly in the selected fields. The study was started March 2007 and will end March 2008. The red date palm weevil, longhorn date palm stem borer and *Oryctes* sp adults were collected weekly for the study period by the traps and by dissecting the highly infested trees.

Results: Understanding the relationship is a critical component on integrated Pest Management (IPM) program.

Insect morphometrics: Trends and prospects in the postgenomic era

James S. Patterson[1], Casper J. Breuker[2], Christian Peter Klingenberg[3]

[1]University of Sussex, Brighton, United Kingdom, [2]Oxford Brookes University, Oxford, United Kingdom, [3]University of Manchester, Manchester, United Kingdom

Introduction: In addition to its traditional application in taxonomy and related areas, morphometrics has found new uses in many areas of entomology. In particular, morphometric studies of insects using genomic approaches have increased. Thanks to the availability of new resources such as collections of mutant stocks, microarrays, and new genotyping tools, considerable advances have been made in the understanding of the genetics of shape in insects. Moreover, the trend to high-throughput studies has made it necessary to consider automating steps in the data collection for morphometric studies.

Case study: We illustrate these trends with a study searching for genomic regions influencing wing shape in *Drosophila melanogaster*. We screened the Exelixis collection of *Drosophila melanogaster* stocks, each of which contains a different small chromosomal deficiency in an otherwise isogenic background. We found that many of the deficiencies have significant effects on wing shape, but that most of these effects are small. Furthermore, the magnitude of the effect is positively related to the size of the deleted genomic region and number of genes contained in it. Altogether, this analysis underscores that the genetic architecture of wing shape is highly polygenic, as there may be hundreds of loci that affect wing shape.

Perspective: This approach highlights the potential for linking the otherwise disparate disciplines of morphological variation and genomics. With the ascendance of more insect genomes on the horizon, and the potential for the subsequent development of comparative insect genomics it seems clear that morphometrics will have a key role to play.

Fighting ability in honeybee queens: Avoiding death and optimizing reproduction

Christian Pirk[1], Vincent Dietemann[1], Huo-Qing Zheng[2], Colleen Hepburn[3], Randall Hepburn[3], Sarah Radloff[4], Fu-Liang Hu[2], Robin Crewe[1]

[1]Department of Zoology and Entomology, University of Pretoria, Pretoria, South Africa, [2]College of Animal Sciences, Zhejiang University, Hangzhou, China, [3]Department of Zoology and Entomology, Rhodes University, Grahamstown, South Africa, [4]Department of Statistics, Rhodes University, Grahamstown, South Africa

Contests mediate access to reproductive opportunities in almost all species of animals. An important aspect of the evolution of contests is the reduction of the costs incurred during intra-specific encounters. Strategic decisions by individuals during contests are influenced by internal and external factors. Models based on game theory have considered the possibility that contestants gauge their own fighting ability (internal factor) and not that of their opponent (external factor), when assessing their behavioral options. Results from some species suggest that contestants indeed determine their fighting strategy solely based on self-assessment.

Although physical contests are widespread in social insects, they have rarely been used as model systems for the study of fighting strategies. Here we present a novel multi queen system to test the decision rules underlying the lethal fights between honeybee queens when competing for reproductive monopoly. By experimentally reducing their fighting abilities, we obtained evidence that queens without prior experience assess their own fighting ability and not that of their opponents. As a consequence, queens with reduced fighting ability refrain from engaging in fights. The presence of several of these queens in a colony results in their peaceful coexistence within the colony. Our results suggest that during contests for reproductive monopoly, honeybee queens make strategic decisions, based solely on the assessment of their own absolute fighting ability and that alternatives to lethal fighting can emerge.

Lethal and sublethal effects of endosulfan, imidacloprid and indoxacarb on green lacewing adults in laboratory

Mir Jalil Hejazi, Golamreza Golmohammadi, Shahzad Iranipour, Seyed Abolghassem Mohammadi

University of Tabriz, Tabriz, Islamic Republic of Iran

Introduction: Commonly, two types of toxicological assessments are made on natural enemies: Acute toxic and sublethal effects**.** In IPM programs, sublethal effects of insecticides are important in relation to the decrease in ability of entomophages in regulating their hosts or preys. Since *Chrysoperla carnea* is an important predatory insect in many crops that imidacloprid, indoxacarb and endosulfan are applied to, understanding the lethal and sublethal effects of these insecticides on it, would be very useful.

Methods: Glass petri dishes were sprayed with 2 ml of each concentration of the insecticides at a pressure of 0.5 bar using Potter tower**.** Fifteen adults (up to 24 h old) were transferred to each petri dish. Mortality was assessed 24 h after treatment**.** Each treatment was replicated at least four times at different days. To study the sublethal effects, adults were treated with LC_{25} of each of the insecticides. Twenty four hours after treatment, the surviving adults were kept separately as pairs of males and females; and the eggs were collected and counted daily.

Results: the LC_{50} values, for indoxacarb, imidacloprid and endosulfan were 11.2, 53.0, and 343.0 mg ai/L for males, and 19.2, 98.4 and 398.0 mg ai/L for females, respectively. All three insecticides tested produced significant adverse effects on fecundity, oviposition and longevity of both male and female adults ($p<0.01$).

Conclusion: the adult stage of *C. carnea* is very sensitive to indoxacarb, imidacloprid and endosulfan. Hence, these insecticides should not be applied when the density of adults is high in the field.

Lethal and sublethal effects of endosulfan, imidacloprid and indoxacarb on grren lacewing adults in laboratory

Mir Jalil Hejazi, Golamreza Golmohammadi, Shahzad Iranipour, Seyed Abolghassem Mohammadi

University of Tabriz, Tabriz, Islamic Republic of Iran

Introduction: Commonly, two types of toxicological assessments are made on natural enemies: Acute toxic and sublethal effects**.** In IPM programs, sublethal effects of insecticides are important in relation to the decrease in ability of entomophages in regulating their hosts or preys. Since *Chrysoperla carnea* is an important predatory insect in many crops that imidacloprid, indoxacarb and endosulfan are applied to, understanding the lethal and sublethal effects of these insecticides on it, would be very useful.

Methods: Glass petri dishes were sprayed with 2 ml of each concentration of the insecticides at a pressure of 0.5 bar using Potter tower**.** Fifteen adults (up to 24 h old) were transferred to each petri dish. Mortality was assessed 24 h after treatment**.** Each treatment was replicated at least four times at different days. To study the sublethal effects, adults were treated with LC_{25} of each of the insecticides. Twenty four hours after treatment, the surviving adults were kept separately as pairs of males and females; and the eggs were collected and counted daily.

Results: the LC_{50} values, for indoxacarb, imidacloprid and endosulfan were 11.2, 53.0, and 343.0 mg ai/L for males, and 19.2, 98.4 and 398.0 mg ai/L for females, respectively. All three insecticides tested produced significant adverse effects on fecundity, oviposition and longevity of both male and female adults ($p<0.01$).

Conclusion: the adult stage of *C. carnea* is very sensitive to indoxacarb, imidacloprid and endosulfan. Hence, these insecticides should not be applied when the density of adults is high in the field.

Patterns of integration of *Drosophila* wing shape at multiple levels: From mutational potential to evolutionary divergence

Christian Peter Klingenberg[1], Casper J. Breuker[2], Nelly A. Gidaszewski[3], James S. Patterson[4]

[1]University of Manchester, Manchester, United Kingdom, [2]Oxford Brookes University, Oxford, United Kingdom, [3]University of Sheffield, Sheffield, United Kingdom, [4]University of Sussex, Brighton, United Kingdom

Introduction: Development plays a key role in the evolutionary process because it determines how genetic variation is expressed as observable phenotypic variation. The patterns of developmental integration influence evolution at multiple levels, from the distribution of new mutations through the standing genetic variation in contemporary populations to the patterns of divergence among evolutionary lineages. We combine the methods of geometric morphometrics with different experimental and comparative approaches to compare integration at these different levels.

Methods: We use a Procrustes fit of a constant set of 15 landmarks digitized on all wings to extract shape information in a consistent way. To characterize the integration of spontaneous variation in the developmental system, we analyze the fluctuating asymmetry in *Drosophila melanogaster*. Mutational integration is estimated from the distribution of average shapes of approximately 370 stocks of *Drosophila melanogaster* that carry small deficiencies but are otherwise isogenic. Standing genetic variation is estimated in three populations each of *Drosophila melanogaster* and *Drosophila subobscura*. Finally, the patterns of evolutionary divergence are from an analysis of the nine species of the *Drosopgila melanogaster* subgroup.

Analysis:.We establish the correspondence between the different levels of variation by comparison of the covariance matrices at the different levels and by comparing the directions of 'lines of least resistance'.

Conclusion: This study demonstrates the potential for analyses that use shape as a 'common currency' for comparing the results from different genetic experiments and comparative studies. This approach is feasible and promising not only for *Drosophila*, but for many other insects as well.

Metabolic insecticide resistance in field populations of the African malaria vector *Anopheles gambiae*

Pie Müller, Emma Warr, Bradley Stevenson, Patricia Pignatelli, Hilary Ranson, Mark Paine, Martin J. Donnelly

Vector Group, Liverpool School of Tropical Medicien, Liverpool, Merseyside, United Kingdom

Introduction: Pyrethroid-treated bednets and indoor residual spraying with pyrethroid insecticides are the mainstays of malaria vector control programmes in sub-Saharan Africa. Resistance to these insecticides threatens the sustainability of control. An understanding of the mechanisms conferring resistance facilitates the development of simple monitoring tools and may eventually lead to novel strategies to restore the efficacy of the insecticide, or the development of new compounds. These mechanistic studies have already led to the identification of novel genes associated with pyrethroid resistance in laboratory-reared mosquito colonies. However, laboratory colonies may not show the true picture of metabolic insecticide resistance in field populations, and hence investigation of field collected specimens is required.

Methods: We collected specimens from malaria endemic areas in Africa where pyrethroid resistance has previously been reported and evaluate the relationship between insecticide resistance phenotypes and gene expression levels. To identify genes conferring metabolic resistance we used microarray-based and multiplexed quantitative RT-PCR techniques to measure differential expression profiles between insecticide resistant and control mosquitoes collected from the field.

Results: We have identified several candidate cytochrome P450s which are associated with increased tolerance to pyrethroids and which were found at more than one field site in sub-Saharan Africa. These P450s are being characterised and preliminary data suggests some have a role in detoxifying pyrethroids.

Conclusions: Our current approach to screen for candidate loci associated with metabolic insecticide resistance in *A. gambiae* has yielded several candidates which will lead to genetic markers for the early detection of insecticide resistance in field populations.

Lack of effect of Bt-corn on the non-target arthropods

Oxana Habuštová, Hany Mohamed Mohamed Hussein, Petr Dolezal, Lukas Spitzer, Vlastimil Ruzicka, František Sehnal

Biology Centre, ASCR, Institute of Entomology, Ceske Budejovice, Czech Republic

Introduction: Genetically modified Bt-corn expressing *Bacillus thuringiensis* toxin Cry1Ab provides protection against the European corn borer. We examined if it does not affect other arthropods living on the corn field.

Methods: Bt-corn YieldGard® (MON 810) and a related non-Bt hybrid were grown each on 5 plots of 0.5 ha that were distributed checker-wise in a 14 ha field. The same type of corn was grown on identical plots for three successive years. Plants of the first crop were shred at the waxy stage of grain ripening and ploughed into the soil. ELISA was used to quantify the amount of Cry1Ab in the plants. Arthropod communities were examined on the plants (10 per plot and date) and sampled in pitfall traps every 2-3 weeks. Results were evaluated with Canoco statistics. Grant support: 1M06030.

Results: Bt maize expressed around 1 ppm Cry1Ab in the leaves and stem and undetectable amounts in the flowers and ears. The toxin provided full protection against the corn borer caterpillars, whereas the abundance of aphids, thrips, ladybirds and lacewings was statistically identical on the Bt and Non-Bt plants. As many as 23 species of spiders, 40 of Carabidae beetles, and 36 of Staphylinidae beetles were found on the field. The Bt and Non-Bt plots differed neither in the biodiversity nor in the abundance of these groups.

Conclusions: The expression of Cry1Ab provides protection against the European corn borer. No adverse effect was detected on other species dwelling on the corn plants or living on the ground.

A new baculovirus isolate that doesn't cause the liquefaction of the integument in *Spodoptera frugiperda* dead larvae

Fernando Valicente[1], Corina Macedo[2], José Wolff[3]

[1]Embrapa Maize and Sorghum Research Center, Sete Lagoas, Brazil, [2]Univeristy of Mogi das Cruzes, Mogi das Cruzes, Brazil, [3]Private, São Paulo, Brazil

Introduction: The *Spodoptera fruigiperda* nucleopolyhedrovirus (SfMNPV) can be very effective in controlling *S. frugiperda*, and has shown potential to be used in Brazil as a biopesticide. However, an important difficulty results from the disruption of the larvae integument due to SfMNPV infection (isolate 19). The liquefaction of the integument makes large scale production laborious because all larvae must be frozen before being harvested for polyhedra extraction.

Methods: One dead larva was found not disrupting the integument (isolate 6) and was multiplied during 5 generations in laboratory. Detection and sequencing of chitinase and cathepsin genes were performed as well as PIB production comparing the two isolates.

Results: The new Brazilian isolate 6 of *S. frugiperda* that doesn't disrupt the integument was confirmed to harbour cathepsin and chitinase genes. Restriction fragment analysis with *Bam*HI and *Hind*III did not show differences between isolate 19 and 6. PCR amplification of the regions encompassing the chitinase and the cathepsin genes produced an amplicon whose size was the same for the two isolates. Alignment of the sequence (isolate 6) obtained with the sequence of isolate 19 revealed a deletion of one base located within the chitinase gene. The framesift caused by this deletion resulted in appearance of a stop codon 15 base pairs downstream the mutation.

Conclusions: Isolate 6 proved to be very efficient to be used in a large scale baculovirus production. Using this isolate, the larval equivalent/ha could be lowered to 80 to 120 larvae/ha, which is equivalent to 10.75 and 13.86 g/ha, respectively

The effect of agri-environmental schemes on bumble bee abundance and diversity

Marika Mand, Reet Karise, Eneli Viik

Institute of Agricultural and Environmental Sciences, Estonian University of Life Sciences, Tartu, Estonia

Introduction: Habitat loss and the intensification of farming practices have lead to a rapid decline in the species-richness of bumble bees in Europe. In order to reverse this process, it is mandatory for the European Union member states to operate agri-environment schemes as part of the common agricultural policy. In Estonia, this policy has been in effect since 1997. The aim of the present study was to find out the impact of agri-environmental schemes on bumble bee abundance and diversity in Estonian agricultural landscapes.

Methods: The study was conducted in two regions with markedly contrasting landscape structures and proportions of semi-natural habitats. The number of bumble bees and the abundance of flowers were monitored on 66 field margins of three different farming types: organic farming, environmentally friendly farming and conventional farming.

Results: In mosaic agricultural landscapes, there were no differences in the abundance and diversity of bumble bees or in the abundance of flowers between the three different farming types. However, in the intensively used agricultural region, there were significantly more bumble bee species and higher density of flowers in organic farms and in farms that have joined the agri-environmental schemes. The number of bumble bees was very low on intensively managed cereal field margins.

Conclusion: In intensively used agricultural regions the number of compensation areas for pollinators is not sufficient and in this case the adopted agri-environment schemes enhance the species richness and abundance of bumble bees as well as pollination services on neighbouring intensively-managed farmland.

Origins of the push-pull concept as applied to pest management

James Miller

Michigan State University, East Lansing, Michigan, United States

Control of insect pests by either attractants/arrestants or repellents/deterrents used singly is difficult because the effects of behavioral modifiers are rarely overwhelming. Furthermore, the impacts of repellents/deterrents often diminish as pests become increasingly hungry or gravid. This dynamic nature of resource acceptance by insects was encapsulated in the rolling-fulcrum model of Miller and Strickler (1984), based largely upon our studies of the interactions of onion flies (*Delia antiqua*) with onions (*Allium cepa*). An important inference from this conceptual model was the sensibility of structuring a pest's environment so that positive outlets for feeding or oviposition (pull) are offered so as to sustain the effects of negative factors (push) applied to the valued resource. This "stimulo-deterrent diversion" concept was tested with limited success on onion fly in the late 1980s and formally introduced into peer-reviewed literature in 1990 (Miller and Cowles; *J. Chem. Ecol.*). The suggestion that this pest management principle might be more applicable to agriculture in developing rather than highly developed countries has proven true. This talk will summarize how the push-pull concept developed independently several times within entomology, as well as in various other fields like engineering, marketing, and politics, where it also thrives.

A phylogeny of genera of the *Pedaliodes* complex (Lepidoptera: Satyrinae: Pronophilini) based on morphological and molecular analyses

Mónica Higuera[1], Giovanny Fagua[1], Luz Angela Galindo Leva[2]

[1]Pontificia Universidad Javeriana, Bogotá, D.C., Colombia, [2]Cenicafé, Chinchiná, Caldas, Colombia

Introduction: The complex Pedaliodes Butler 1867 is a neotropical group of butterflies containing a high number of species distributed along a wide altitudinal range. This group is an interesting taxon to study the effects of orography and historic climate changes on speciation. This study was aimed to elucidate the phylogenetic relationships within the group.

Methods: 44 species of 12 genus of the complex were analyzed in the in-group. 12 species from the tribes Pronophiliini and Erebiini were employed as out-group. 76 morphological characters were used join to a fragment of 630 bases pair of cytochrome-c oxidase subunit I (COI). The resulting data matrix was analyzed by total evidence using PAUP and TNT packages.

Results: The complex *Pedaliodes* was a monophyletic group. Inside to complex, only *Praepronophila* was a monophyletic group while *Protopedaliodes*, *Punapedaliodes*, *Redonda* and *Steromapedaliodes* can be monophyletic groups. Several inner genera were paraphyletic or polyphyletic, such as *Altopedaliodes*, *Neopedaliodes*, *Panyapedaliodes, Phereopedaliodes*, *Pedaliodes* and *Praepedaliodes* among others. Into *Pedaliodes* were observed other species groups.

Conclusions: The complex *Pedaliodes* is a monophyletic group, but several inner genera are paraphyletic or polyphyletic. New morphological characters were described and some characters traditionally employed in Lepidoptera and particularly in the complex *Pedaliodes* were redefined.

Above- and belowground direct and indirect defense mechanisms of transgenic Bt maize and implications for biological control

Claudia Zwahlen, Lechot Géraldine, Ted Turlings

University of Neuchâtel, Institute of Biology, Neuchâtel, Switzerland

Herbivore-induced direct and indirect defense mechanisms are important for the plant's ability to combat attacking herbivores. Transgenic *Bacillus thuringiensis* (Bt) maize produces one or two Cry endotoxins against various pests, such as the European corn borer (Cry1Ab) and the corn rootworm (Cry3Bb1), which provides a highly effective direct defense mechanism against the target pests, but it is unclear whether the continuous production of these Cry proteins affects the plants' ability to allocate resources to fend off other, non-target attackers. Here we present results from our laboratory and field studies that determine the capacity of Bt maize to defend themselves using direct defense compounds and inducible volatile emissions that attract natural enemies, such as entomopathogenic nematodes (EPN) against corn rootworm larvae. So far, we have found that when Cry1Ab Bt maize and its near isogenic control were artificially induced to produce volatiles in a similar manner as corn rootworm feeding, they were equally attractive to EPNs. This suggests that Cry1Ab Bt maize is able to recruit natural enemies to combat its non-target belowground attackers similarly as non-Bt maize. However, artificially induced Bt maize produced significantly less Cry1Ab in their leaves and roots than untreated Bt maize. In a next step we will determine whether this has an effect on the plants' ability to fend off its aboveground target pests. Our studies will contribute to a better understanding of the resource allocation of plants under herbivore attack. Moreover, they provide a first step towards comparing transgenic plants with biological control systems.

Climate change and biological control: A multitrophic perspective

Nick Mills

University of California, Berkeley, CA 94720-3114, United States

Classical biological control is one of the most effective approaches for the management of invasive species through which specialized natural enemies from the region of origin of the invader are purposefully introduced to provide sustained long-term control. Although this approach is not without controversy, due to the potential for non-target impacts, it has provided some spectacular examples of large scale ecological experiments of the suppression and regulation of invaders by natural enemies. While classical biological control has been practiced for more than 100 years, with historical examples continuing to provide effective control, there is increasing concern regarding the future vulnerability of such systems to disruption through global climate change. As introduced populations show reduced genetic heterogeneity in comparison to source populations, due to founder effects, they may consequently have a reduced capacity to adapt to global climate change. Whether the capacity for genetic adaptation varies among trophic levels and whether climate change could disrupt classical biological control remain open to question. To explore these questions I will examine the frequency of regional variation in the outcome of classical biological control due to climatic factors using the historical record of natural enemy introductions for both arthropod pests and weeds. To understand the reasons for such variation and the potential for disruption of biological control through climate change, I will compare temperature tolerance data across trophic levels and consider the importance of synchronization of life cycle stages among trophic levels to the success of pest population suppression.

Hormonal regulation of larval diapause in a noctuid moth

Frantisek Sehnal, Matilde Eizaguirre, Christa Schafellner

Biology Centre, ASCR, Institute of Entomology, Ceske Budejovice, Czech Republic

Introduction: *Sesamina nonagrioides* overwinters in diapause as fully grown caterpillar that undergoes supernumerary larval molts. Their hormonal control was examined.

Methods: Development under short-day (SD) and long-day (LD) conditions was correlated with titre changes of juvenile hormones (JH) and ecdysteroids and the activity of JH esterase (JHE). Causality of correlations was verified with hormone agonists and a specific JHE inhibitor. Grant support: 522/06/1591.

Results: Larval development under LD conditions occurred at about 7 ng JH /ml hemolymph and was associated with ecdysteroid rises to over 300 ng/ml two days after each ecdysis (data for 4^{th} and 5^{th} instars). SD larvae contained nearly 15 ng JH /ml in the 4^{th} and 5^{th} instar and 5 ng/ml during subsequent diapause; ecdysteroids peaked in long (> 14 days) and irregular intervals. The transformation to pupa in LD 6^{th} instar larvae occurred at undetectable JH, while ecdysteroids rose to 600 ng/ml. JHE activity was negatively correlated with the ecdysteroid titre. Administration of JH agonist methoprene to 6^{th} instar LD larvae induced extension of typical larval development (molts in short intervals plus body growth), whereas in SD larvae it did not affect the slow diapause molting rhythm without growth. Ecdysteroid agonist RH-2485 stimulated both JH and ecdysteroid titres and evoked larval development in either type of larvae.

Conclusions: Larval diapause is induced by moderate JH and low ecdysteroid titers; feedbacks between these hormones prevent failures in the specification of larval development, metamorphosis, and diapause, respectively. JHE does play a significant role in JH titer regulation.

Insect species, landscapes and climate change: A northern hemisphere perspective

Juergen Ott

[1]L.U.P.O.GmbH, 67705 Trippstadt, Germany, [2]Dep. of Environmental Sciences, University of Landau, Landau, Germany

Introduction: In the past decades Europe faced a strong change in the distribution pattern of many insect taxa. Here a review on existing data is given, as well as the consequences for ecosystems and nature conservation are described.

Methods: Field data from several long-term monitoring projects in reference areas were analyzed and the literature on the ecology and nature conservation of several taxa is reviewed.

Results: A few decades ago a process started, which is still ongoing with an even increasing velocity: the invasion of Central and Northern Europe by Mediterranean insects, whereas recently in the Mediterranean also more and more African species are documented. This is in particular true for some mobile and easy to determine taxa like the Odonata. In the short term these invasions from the south may lead to an increase of biodiversity, in particular as euryoecious Odonata species are increasing their range. But in the medium term stenoecious mooreland and alpine species will disappear. In other taxa, like in the Trichoptera, this seems to be different: here, beside the Alpine species, mainly the diversity in the Mediterranean is under threat, as this area has the highest degree of endemism. Consequences for aquatic and terrestrial systems can be foreseen and new problems in nature conservation (e.g. new pests, invasions of alien species, the functioning of the European NATURA 2000 network) will arise.

Conclusions: Insects can be used very well as indicators for climate change and many effects on the different taxa can be registered, as well as on the coenosis and ecosystems can be expected. This may lead to new nature conservation strategies.

Grasshoppers, locusts, crickets and katydids of Mexico: A new synthesis

Ricardo Mariño-Pérez[1], Paolo Fontana[2], Filippo M. Buzzetti[2]

[1]Laboratorio de Protozoología, Departamento de Biología Comparada, Facultad de Ciencias, Universidad Nacional Autónoma de México, C.P. 04510, Ciudad Universitaria, Distrito Federal, Mexico, [2]Dipartimento Agronomia Ambientale e Produzioni Vegetali, Università di Padova Agripolis, Viale dell'Università, 16, I-35020, Legnaro (Padova), Italy

Introduction: The current knowledge of the Orthoptera of Mexico is scattered throughout literature, and is only available for the most part in old monographs. Also, only few genera have been reviewed recently and, in a global sense, little is known about Mexican Orthoptera. All the available information was grouped adding our new data.

Methods: Six entomological field expeditions (2004-2007) were conducted, also an intensive revision of the material of Ann Arbour (Michigan, USA) and CNIN (UNAM, Mexico) collections and literature was made.

Results: An updated checklist revised and integrated with new data numbers 978 species of Orthoptera (425 Ensifera and 553 Caelifera) actually known from Mexico, representing the 5 % of the about 20,000 species of Orthoptera worldwide known. During field expeditions many photos were taken to living specimens to create a photographic guide.

Conclusions: Current knowledge about Orthoptera biodiversity is far to be complete. Recently however, many species have been identified; some still have not been described officially, and many others have not been adequately studied. This new synthesis is the first step to start future researches on this group.

Structure of Orthoptera communities in an altitudinal gradient with Andean forest and oak forest.

Andrés Felipe Sandoval Mojica[2], Giovanny Fagua[1]

[1]Pontificia Universidad Javeriana, Bogotá, D.C., Colombia, [2]University of Florida, Gainesville, Florida, United States

Introduction: The study of distribution of animals and plants on natural gradients is useful for the determination of patters and process that govern the diversity. An Andean altitudinal gradient on the west of Cordillera Oriental (Colombia) has an interesting transition between Andean forests to oak forest. The incidence of both, altitude and vegetation, over diversity of Orthoptera was studied

Methods: The variation in abundance, richness, diversity, dominance and composition of the Orthoptera was studied along an altitudinal gradient, between 2000 and 3000 m, in an Andean forest at Santander (Colombia). Surveys were conducted at five places every 250 m in altitude. In each altitude was included four quadrants for manual sampling.

Results: The analysis defined two communities (2000–2250 m and 2750-3000 m) due possible to the structural differences across the vegetation on altitudinal gradient: an heterogenean Andean forest to oak grove with higher dominance of *Quercus humboldtii*. All altitudinal stations showed that species richness and diversity decreased gradually with increasing altitude, due to the reduced plant resource at high elevations. There was a positive correlation between altitude and dominance of Orthoptera species by higher proportion of the generalist species. However, the analysis without the altitudinal stations with dominance of *Q. humboldtii* showed that oak grove increased the slope of the declination in species richness and diversity, and the increasing of the dominance.

Conclusions: We conclude that oak grove exacerbate, by their homogeny composition and lowest complexity, the pattern of declination associated to the altitudinal effect.

Differential foraging response to racially-derived blends of brood pheromone in the honey bee, *Apis mellifera*

Bradley Metz, Tanya Pankiw

Texas A&M University, College Station, TX, United States

Introduction: Brood pheromone is a blend of ten fatty-acid methyl and ethyl esters extractable from the larval cuticle that has been shown to affect individual age of first foraging and foraging choice, and colony-level foraging investment. Most studies of brood pheromone have been performed using a synthetic blend formulated from a single race of honey bee, *Apis mellifera ligustica.* Bees in the United States, however, are primarily crosses of several different European honey bee races. Also present are Africanized bees which are crosses between European bees and *Am scutellata*.

Methods and Results: Using gas chromatography, we characterized BP esters from larvae selected from 8 colonies of Africanized and 8 colonies of European bees. We found that two BP components, methyl oleate and methyl stearate, differ significantly by race. We then formulated racially-derived blends of synthetic BP and performed a colony-level foraging bioassay using European bees. We observed that European BP released pollen foraging behavior, increasing proportional pollen foraging relative to control, while Africanized BP elicited the opposite response and suppressed pollen foraging.

Conclusions: *Am scutellata* evolved in a tropical climate and Africanized hybrids exhibit a characteristic foraging pattern of collecting large amounts of pollen, while temperate evolved bees characteristically forage preferentially for nectar. The divergent effects elicited by Africanized and European blends of brood pheromone may have evolved as a response to racial differences in foraging behavior.

Interaction between baculoviruses and midgut cells

Basil Arif, Jeffrey Slack

Great Lakes Forestry Centre, Sault Ste. Marie, Canada

Baculoviruses are a family of insect viruses that have been used for decades in biocontrol. Insects become vulnerable to infection when they ingest foliage contaminated with viral occlusion bodies (OBs). Liberated occlusion-derived virions (ODVs) initiate infection in epithelial cells when OBs dissolve in the alkaline environment of the larval midgut. While lepidopteran baculoviruses have been shown to synthesize two viral phenotypes, the budded virus (BV) and the ODV, genomics evidence revealed that hymenopteran baculoviruses are not likely to synthesize BV and this phenotype may not play a role in the biology of sawfly viruses. This observation is consistent with the fact that viruses of sawflies are confined to infecting midgut cells. It has been shown that the P74, present on the surfaces of ODVs, was essential for infection. A soluble form of the protein was generated and it was observed that it is cleaved when incubated with insect midgut tissues under alkaline conditions and that cleavage was prevented by soybean trypsin inhibitor (SBTI). Biological assays were carried out and suggested that SBTI inhibited baculovirus infection and that trypsin enhanced infectivity. This may be due to trypsin cleavage and activation of P74. Analysis of the peptide sequences of P74 homologues identified a highly conserved trypsin cleavage site that could generate the observed cleavage product. Further more; mutagenesis of the trypsin cleavage sites in P74 had an effect on the oral infectivity. We link molecular biology with practical biocontrol improvements and present evidence that plant products may affect baculovirus efficacy.

Interactions between colour pattern, temperature and life history traits in three coccinellid species (*Harmonia axyridis, Adalia bipunctata* and *Adalia decempunctata*)

Laura Jane Michie, Michael Majerus

University of Cambridge, Cambridge, United Kingdom

Many coccinellid species show conspicuous colour pattern polymorphism. It has been demonstrated that within these polymorphisms, the major forms are genetically controlled. This is the case in *Harmonia axyridis, Adalia bipunctata* and *Adalia decempunctata*, but comparatively little research has been carried out on the effect of environment on the detailed colour pattern variations within forms. Similarly, the effect that colour pattern has on life history traits in different environments has not been examined comprehensively. While there is some evidence of genetically controlled mating preferences for specific colour forms in *H. axyridis* and *A. bipunctata*, the effect of colour pattern on other life history traits has received very little attention. Here we present investigations of the effects of temperature during development on adult colour pattern in these three polymorphic coccinellids, and the impact of different temperatures on a variety of life history traits (activity, mating success, oviposition rate, fecundity) for melanic and non-melanic morphs of each species. We show that the interaction between morph and temperature differ between species in respect of both the effect of temperature on phenotype and its impact on life history traits.

Insect outbreaks viewed through a nutritional physiology framework

Spencer T. Behmer[1], Anthony Joern[2]

[1]Texas A&M University, College Station, TX, United States, [2]Kansas State University, Manhattan, KS, United States

Introduction: Food quality has important implications for insect performance, but the extent to which food quality and the nutritional landscape facilitate insect outbreaks is poorly understood. This is particularly true among grasshoppers.

Methods: Here we employ an experimental framework grounded in nutritional physiology to show what ratios and amounts of protein and carbohydrate different species of grasshoppers (including a range of North American species and two African locust species) prefer to eat.

Results: We demonstrate that among North American species coexistence may be facilitated by the existence of species-specific nutritional niches. We also show that performance by grasshoppers allowed the opportunity to mix their diets and thus regulate their protein–carbohydrate intake matches optimal performance peaks generated from no-choice treatments. Our results indicate the active nature of diet selection to achieve balanced nutritional intake can provide buffering capacity in the face of variable food quality.

Conclusions: Our results and experimental approach can be extended to generate and test predictions concerning the intensity of biotic interactions between species, the relative abundance of species, yearly fluctuations in population size, as well as the nature of interactions with natural enemies in tritrophic niche space.

Phylogenetic analysis of the *Zanchius*-group (Heteroptera: Miridae: Orthotylinae)

Dimitri Forero

[1]Cornell University, Ithaca, NY, United States, [2]American Museum of Natural History, New York, NY, United States

Miridae is the most diverse family of Heteroptera with more than 10.000 species described. Eight subfamilies are recognized in Miridae. Among these, Phylinae and Orthotylinae, which are considered to be sister groups, are the focal taxa of the Plant Bug Planetary Biodiversity Inventory project. Currently, three tribes within Orthotylinae are recognized: Orthotylini, Nichomachini, and Halticini. Orthotylini is the largest, including more than 200 genera. Schuh (1974) divided the tribe in several generic groupings: the *Orthotylus*, the *Sericophanes*, the *Falconia*, and the *Zanchius* groups, thus providing the most current concept of suprageneric categories.

Schuh proposed the Pantropical *Zanchius*-group to include 11 genera, identified by a flattened appearance, delicate body structure, usually hyaline hemelytra, and vesica without spicules. Additional genera have been proposed to be part of the *Zanchius*-group but until now no phylogenetic analysis have been performed in order to evaluate the limits of the group. The monophyly and generic relationships of the group were studied using several morphological character complexes, in particular male and female genitalia. Species of the *Sericophanes*, *Falconia*, and *Orthotylus* groups served as outgroups. About eighty percent of the genera ascribed to the group were examined. In addition, species of the yet undescribed Australian fauna were included. As result of the analysis, the initial diagnosis of the group is modified to include members with vesical spicules, although usually delicate; phallotheca with lateral protuberances; embolium of hemelytra with apically enlarged area; and eyes usually removed from the anterior margin of the pronotum, with a particular caudal structure.

Post-disturbance recovery of apple orchard spider communities

Viktor Markó, Balázs Keresztes, Jerry V. Cross

[1]Department of Entomology, Corvinus University of Budapest, Budapest, Hungary, [2]Institute for Plant Protection, University of Pannonia, Keszthely, Hungary, [3]East Malling Research, East Malling, United Kingdom

Introduction and methods: In our 4-year study the effect of two pest management strategies (i) 'zero pesticide residue integrated pest management program', where pesticides moderately harmful to natural enemies are applied only up to petal fall, but during the fruit development period pest control based on biocontrol agents (ii) a conventional pest management system (based on broad-spectrum insecticides) on apple orchard spider communities were compared. Pesticide free apple orchard plots served as a control. Special attention was paid to prey availability and post disturbance development of spider communities in the second part of the growing season.

Results: The 'zero pesticide residue' integrated pest management strategy results in higher spider abundance compared to the conventional pest management strategy in the first part of the fruit growing season. However, if the application of toxic pesticides to spiders is restricted up to first part of July the abundance of spider communities become identical in one month because of intensive immigration.

Apple orchard spider communities restructure after July probably because of habitat change of the juveniles and between-species differences in offspring and mortality. This re-structuring occurs both in non-disturbed and pesticide treated orchard plots and can help the post-disturbance recovery of the spider communities. The post-disturbance increase rate of spiders (immigration, within orchard reproduction) is tightly regulated by prey availability. Therefore post disturbance spider abundances saturate quickly to a point where they are in balance with their prey supply.

Goldenrod's resistance against gall flies may cost more than it's worth

Michael Wise, Warren Abrahamson

Bucknell University, Lewisburg, Pennsylvania, United States

Introduction: Arthropod-induced galls can be very detrimental to plant fitness. Even so, plant populations often have apparently suboptimal levels of resistance, despite the presence of substantial genetic variation. One constraint on the evolution of resistance is that increased resistance may cost more than it is worth.

Methods: We investigated costs and benefits of resistance of the goldenrod *Solidago altissima* to the gall-inducing tephritid *Eurosta solidaginis*. Goldenrods are genetically variable for a resistance response in which meristem cells become necrotic and kill fly larvae before gall induction. In a greenhouse study, we exposed replicates of 26 goldenrod genets to oviposition by *E. solidaginis* and followed gall development and plant performance.

Results: The presence of a gall cost plants an average of 1743 seeds, but the cost varied ten-fold across three environmental treatments. There was no evidence that resistance to gall formation carried an allocation cost. However, resistance carried a risk of autotoxicity, as necrosis killed the apex of 37% of the ungalled plants, which cost them an average of 5015 seeds. The risk was lowest in the highest resource treatment, with the result that resisting gall formation was 1.7 times more profitable than tolerating their presence. In the nutrient-stressed treatment, in contrast, tolerance was 3.0 times more profitable than resistance.

Conclusions: The potential for autotoxicity may constrain *S. altissima*'s resistance to *E. solidaginis* to an intermediate level, and spatial or temporal variation in environmental conditions may alter the relative costs and benefits of resistance, thus maintaining genetic variation for resistance.

Exploiting natural variation in ecologically relevant traits to improve natural enemies for biocontrol

Suzanne Lommen[1], Kees Koops[1], Peter de Jong[2], Paul Brakefield[1]

[1]*Evolutionary Biology, Institute of Biology, Leiden University, Leiden, Netherlands,* [2]*Laboratory of Entomology, Wageningen University, Wageningen, Netherlands*

Natural enemies of pest species are potential biological control agents but they may possess traits that prevent successful implementation of biocontrol. If there is heritable natural variation for these traits, suitability for biocontrol may be improved through artificial selection. We report on an example of a ladybird beetle where we used the principles of evolutionary ecology to improve suitability for biocontrol.

Ladybird beetles are important predators of aphids, one of the major pests in greenhouse crops. Because of their tendency to fly away soon after release, using these predators in augmentative control is problematic. Natural populations of the two-spot ladybird beetle, *Adalia bipunctata*, show heritable variation in flight ability. Therefore, we were able to rear a pure flightless stock. When released on aphid-infested plants, flightless beetles had a longer residence time and therefore they better controlled aphid pests compared with conspecifics that were able to fly.

We used artificial selection on ecologically relevant traits to further improve two methods for augmentative control by flightless beetles. One experiment focused on inundative control (mass-release of natural enemies) and we increased survival of flightless beetles by selecting on variation in wing morphology ($h^2 = 0.74 \pm 0.09$). The second experiment aimed to improve inoculative control (the offspring of the released enemies control the pest) by increasing early fecundity. Offspring number did not respond over ten generations of selection but reproduction became earlier and fertility increased. We suggest that these flightless phenotypes that have been selected for ecologically relevant traits improve aphid biocontrol.

Effect of pollen diet and primer pheromones on worker honey bee mandibular glands

Lizette Peters, Tanya Pankiw

Texas A&M University, College Station, United States

Introduction: Only two social insect primer pheromones have been chemically characterized: honey bee queen mandibular (QMP) and brood (BP) pheromones, communicating queen and larva presence, respectively (Pankiw, 1996; Le Conte, 1990). Primers gradually change endocrine, reproductive, and neurosensory systems of workers. Previous studies have shown an increase in hypopharyngeal gland protein content of worker bees in response to brood pheromone and pollen diet rearing environment (Hrassnigg and Crailsheim, 1998). However, effects on the mandibular gland, also involved in the production of brood food and in royal jelly, have not been examined in relation to primer pheromones and pollen diet. Learning what factors influence the development of these glands could improve brood rearing or increase colony fecundity.

Methods: Newly emerged bees were placed in cages and reared 12d with the following pheromone treatments: no primer pheromone, QMP, BP, and QMP + BP. Each pheromone treatment was conducted both with and without pollen resulting in a total of 8 treatments. Subsamples of 20 bees per treatment were collected every 3 days. Mandibular gland size, and mandibular and hypopharyngeal gland protein content were measured.

Results: This study indicated that regardless of pheromone treatment, pollen was the most influential factor regarding gland protein content and size.

Conclusions: The results of this study suggest that BP and QMP may regulate feeding behavior for provisioning royal jelly and worker brood food rather than gland physiologies. Further studies are needed to determine the physiological roles, if any, BP and QMP play on mandibular gland protein biosynthesis.

Landscape composition modulates population genetic structure of *Eriosoma lanigerum* (Hausmann) on *Malus domestica* Borkh in Central Chile

Blas Lavandero[1], Marcelo Miranda[2], Claudio Ramirez[1], Eduardo Fuentes-Contreras[1]

[1]Universidad de Talca, Talca, Maule, Chile, [2]Universidad Catolica de Chile, Santiago, Metro, Chile

Introduction: The woolly apple aphid *Eriosoma lanigerum* is an important pest of apple orchards worldwide. In North America this aphid seems to be holocyclic, with sexual forms on elm trees and asexual forms on apple. In other regions of the world this aphid has all year round asexual forms occurring on apple trees. Since genetic variability and structure of insect pest populations, associated with life cycle characteristics can provide some insights into the dispersal mechanisms of these, in the present study we tested whether geographical parameters affected genetic diversity and gene flow of this pests.

Methods: The individuals were collected on apple trees from different locations in a 400 km north-south transect trough central Chile. In order to determine if there was population structure, diversity and flow were assessed.

Results: A total of 215 individuals from these locations were analysed using Inter Simple Sequence Repeats (ISSR) markers. The percentage of molecular variation among locations was 18 %. Individuals were assigned to groups through different Bayesian methods, due to isolation-by-distance relationships detected in the data set. We inferred the presence of four genetic clusters in the study region. Clustering of individuals followed a pattern explained by some geographical barriers. Using partial Mantel tests, we detected barriers to gene flow other than distance, created by a combination of main rivers and mountains.

Conclusions: Although landscape genetics are rarely used in pest management, our results suggest that these tools may be suitable for the design of area-wide pest management programs.

Semiochemical-mediated fire ant-phorid fly interactions: GC-EAD response of *Pseudacteon tricuspis* to *Solenopsis* fire ants

Henry Fadamiro, Li Chen

Auburn University, Auburn, Alabama, United States

The decapitating phorid fly, *Pseudacteon tricuspis* has been released since the mid 1990s for biocontrol of imported fire ants, *Solenopsis* spp. in southern U.S. Little is known about the cues used by *Pseudacteon* phorid flies to locate fire ant hosts. We recently provided the first direct evidence of semiochemical-mediated attraction of *Pseudacteon* species to imported fire ants: *P. tricuspis* showed significant behavioral and electroantennogram (EAG) responses to body extracts imported fire ants. In this paper, we present the results of a follow-up study to determine the identity of the chemicals mediating this observed response of *P. tricuspis* to imported fire ants. Conventional silicon gel chromatography was utilized to purify and separate crude body extracts of three fire ant species (*S. invicta* = red, *S. richteri* = black, and *S. invicta* × *S. richteri* hybrid) into different fractions (e.g., alkaloids, cuticular hydrocarbons, etc). The principal fractions were then analyzed by GC followed by testing of EAG responses of *P. tricuspis* to the different fractions. Female *P. tricuspis* did not show significant EAG response to the cuticular hydrocarbon fraction, but other fractions (including the alkaloid fraction) did elicit significant EAG responses. The most EAG-active fractions were then subjected to further analyses by coupled gas chromatography electroantennogram detection (GC-EAD) to determine biologically-active peaks. The same 2-3 unknown compounds (peaks) from extracts of all three fire ant species were shown to consistently elicit significant GC-EAD responses in *P. tricuspis*, suggesting that these unknown compounds may play a role in mediating fire ant-phorid fly interactions.

Vector potential of stable flies (*Stomoxys calcitrans*) for transmission of Porcine Reproductive and Respiratory Syndrome Virus (PRRSv)

Kateryn Rochon[1], D. Wes Watson[1], Adalberto A. Pérez de León[2], Isabel M. Gimeno[3], Monte B. Mccaw[3], Rodney B. Baker[4]

[1]Department of Entomology, College of Agriculture and Life Sciences, North Carolina State University, Raleigh, North Carolina, United States, [2]Environmental Science Division, Valent Biosciences Corporation, Libertyville, Illinois, United States, [3]Population Health and Pathobiology, College of Veterinary Medicine, North Carolina State University, Raleigh, North Carolina, United States, [4]Department of Veterinary Diagnostic and Production Animal Medicine, College of Veterinary Medicine, Iowa State University, Ames, Iowa, United States

Introduction: Porcine Reproductive and Respiratory Syndrome (PRRS) is a globally significant swine disease. The virus (PRRSv) replicates in macrophages of infected pigs resulting in pneumonia and late-term abortions in sows. The link between outbreaks in separate farms within an area despite biosecurity measures remains unclear. House flies and stable flies are a common occurrence around swine facilities. House flies can transmit the virus from pig to pig under laboratory conditions. We have investigated the vectorial potential of stable flies in the transmission of PRRSv under laboratory conditions.

Methods: Groups of stable flies fed blood containing PRRSv or intrathoracically inoculated with the virus were sacrificed at different time intervals to determine virus persistence in the gut and haemolymph. Regurgitation and defecation of virus-fed or virus-inoculated stable flies were also monitored. In transmission experiments, groups of virus-fed flies were placed on naïve pigs for four subsequent blood meals.

Results: Active virus was recovered from stable fly guts up to 24 h post feeding. Detectable virus decreased with time, suggesting no virus replication in fly tissues. Flies shed virus for at least 6 h post-feeding. Intrathoracically inoculated stable flies had ~1,500 times more PRRSv copies/ml 48 h post inoculation compared to virus-fed flies. Transmission of the virus to naïve healthy pigs was unsuccessful under the current experimental conditions although all fly groups tested positive with virus isolation.

Conclusions: The potential for stable flies to transmit PRRSv to pigs under conditions conducive to infection remains to be determined.

Use of proteomics to investigate the respective role of insect and bacterial endosymbionts in aphid - plant interactions

Frederic Francis[1], Edwin De Pauw[2], Eric Haubruge[1]

[1]Gembloux Agricultural University, Functional and Evolutionary Entomology, Gembloux, Belgium, [2]University of Liege, Mass Spectrometry Laboratory, Liege, Belgium

Introduction: Proteomics found recent developments due to significant improvement and availability of both protein separation and identification methods. Moreover, functional information's linked to the studied proteins was brought when compared to genomic approach. For these reasons, molecular entomologists have now a panel of tools to determine the proteome patterns related to differential adaptation of insects to cope with plant defence mechanisms. The aphid-plant relations will be used as a case study. Indeed, aphids represent a wonderful model in the study of plant adaptation.

Methods: The adaptation and metabolic changes of aphids in relation to host plants focusing on the role of the bacterial endosymbionts was investigated. Use of artificial diet including diverse antibiotics but also the comparison of proteomes related to whole aphid and respective purified bacterial symbionts were studied to identify the respective origin and function of proteins constituting the studied proteomes. Diverse methods including traditional two dimension electrophoresis, 2D-Differencial In Gel Expression, liquid chromatography (LC) coupled with mass spectrometry (ESI-MS-MS and Maldi-Tof-MS-MS) and data bank investigations were developed.

Results: From the proteome investigation and identification from aphid fed with particular antibiotics but also from proteomes of whole aphid and related extracted bacterial endosymbionts, particular proteins of interest were selected and accurately characterised with both fundamental but also applied views. This broad proteomic approach will be discussed as an interesting and reliable tool to study the biologically involved proteins from aphids in response to several environmental changes, and particularly the insect - host plant interactions.

The enticing odour of fungi: Partner feedback in a primitive fungus gardener of Lymexylidae (Coleoptera)

Gerrit Holighaus, Stefan Schuetz

Buesgen Institute, Dept. of Forest Zoology and Forest Conservation, University of Goettingen, Goettingen, Germany

Introduction: In woodboring beetles, insect-fungus associations range from dispersal to true "gardening". Both partners evolved complex adaptations assuring their benefit without imbalancing the relationship. In a member of the primordial beetle superfamily *Lymexyloidea*, including fungal gardeners, we found a remarkable semiochemical based interaction with its main cultivar.

Methods: Chemoecological studies have been carried out for the Large Timberworm (*Hylecoetus dermestoides* L.; Col., *Lymexylidae*). Larvae feed mainly on an ascomycetous yeast within a fungus assemblage found in galleries of various tree species. We investigated host plant and fungal odours, their perception by the insect antenna by means of coupled gaschromatography and electroantennography (GC/MS-EAD).

Results: Behavioural field studies with thus identified chemicals showed effects of fungal volatiles on beetle behaviour. Fungus transfer to the beetles offspring is assured by genitalian mycetome and exploring uncolonized wood is regular. Thus, to our surprise, a single isoprenoid compound released exclusively by the main cultivar *Ascoidea hylecoeti* (Batra & Francke-Grosmann) strongly attracts female *H. dermestoides* on host search flight. The attraction of ovipositing females to volatiles of its cultivar inside conspecific galleries is remarkable.

Conclusions: The observed mechanism can be hypothesized as follows: The fungal odour compound acts like aggregation pheromones. Larval development benefits from reinfestation or vertical fungus transfer fails in some cases. Furthermore, horizontal cultivar transmission could be influenced to either benefit. Last, it is a persisting relict maintained during evolution of beetles adaptations as the mycetome. Chemoecological methods can enlighten the function of insect-fungal associations. Further insights might be identified by this chemotaxonomic data. Evolutionary studies on the interactions within *Lymexyloidea* seems promising.

Differences among populations in susceptibility of the grasshopper *Melanoplus sanguinipes* to a generalist fungal pathogen

Stefan Jaronski, Rob Schlothauer

USDA ARS NPARL, Sidney MT, United States

Introduction: While generalist entomopathogenic fungi such as *Beauveria bassiana* are understood to have broad host specificity, little is known about variations in the susceptibility of a host species, specifically among different, geographically separate, populations.

Methods: The model system consisted of the fungus *Beauveria bassiana* Strain GHA, five geographically separate populations and two different laboratory colonies of the Migratory Grasshopper, *Melanoplus sanguinipes*. Relative susceptibility of each population to the fungus was based on replicated, multiple dose, topical bioassays to yield a mean fungal LD50 and associated statistics for each population. Each population was tested 3-5 times over a three year period.

Results: The mean LD50 values for two Montanan, one Idahoan, one Alaskan population and the USDA colony were not significantly different from each other. The LD50 values ranged from 53,000 – 81,000 conidia per insect. A North Dakotan population was significantly less susceptible by a factor of 5-8, and a colony from Agriculture Agrifood Canada was significantly more susceptible by a factor of 5-7.5. This is first evidence for significant differences among host insect populations in their susceptibility to a generalist fungal pathogen.

Field response of *Steirastoma breve* (Sulzer, 1776) (Coleoptera: Cerambycidae) to odors of *Theobroma cacao* L.

Carmen V. Liendo-Barandiaran[1], Beatriz Herrera-Malaver[1], Franklin Morillo[2], Pedro Sanchez[2], José Vicente Hernández[1]

[1]Universidad Simón Bolívar, Caracas, Estado Miranda, Venezuela, [2]Instituto Nacional de Investigaciones Agrícolas, Caucagua, Estado Miranda, Venezuela

Introduction: *Steirastoma breve* is the most important insect pests in Neotropical cocoa plantations. Larvae and adults cause severe damage in stems and branches of infested plants. In the present work, field responses and olfactory behavior of *S. breve* to its host plant odors were evaluated.

Methods: Olfactory response of adults *S. breve* was evaluated using *Theobroma cacao* L. and *Bauhinia* sp. branches piles as odor source. In both cases, 60 kg of branches were placed under sunny and shade conditions in an experimental cocoa plantation. During 23 consecutively days, from 9:00 to 15:00 h, the sex and adults number of *S. breve* observed in the piles were recorded each hour. Approach behavior and other behavioral activities of *S. breve* towards *T. cacao* piles were recorded and described.

Results: Adults of *S. breve* are attracted towards *T. cacao* branches piles under sunny and shade conditions, contrary as occur with *Bauhinia* sp. Adults beetle average value to both sexes was higher in shade than in sunny conditions. In both conditions, males average value was higher than females one. Behaviors performed by this beetle on piles were classified as follow: resting, mating, flying, exploring and feeding. Three types of approach flight were observed towards the branches piles: zig-zag, direct and turns around branches pile.

Conclusions: All those results confirm kairomones presence emitted by *T. cacao*, they are involved in the chemical communication system of *S. breve*.

Transitions between respiratory patterns in sedentary insects is dependent on metabolic rates: A look into the respiratory patterns of *Rhodnius prolixus* and *Gromphadorhina portentosa*

Heidy Contreras

University of California, Irvine, Irvine, CA, United States

Relatively little is known about the response of insect respiratory pattern to changes in metabolism (i.e. aerobic demand) despite the fact that respiratory patterns of insects have been the subject of intense study. The reason for this is that any locomotory activity, which may accompany an increase in metabolic rate, tends to disrupt the observed respiratory pattern. We have sought to get around this problem by using insects that are highly sedentary and by adjusting metabolic rate in these poikilothermic animals using temperature. *Rhodnius prolixus,* a sit and wait bloodsucking insect, has a classic discontinuous respiratory pattern (closed, flutter and open phase). The hissing cockroach, *Gromphadorhina portentosa*, a relatively sedentary detritus feeder exhibits the classic active ventilatory pattern typical of cockroaches. We found that at low temperatures, both insects exhibit lengthy periods of spiracular closure reflecting a discontinuous pattern of respiration. As the temperature and metabolic rate increase, the insects show shortened closed periods, transitioning to the cyclical respiratory pattern. Finally, at the highest temperatures, the insects exhibit a continuous respiratory pattern. Our results suggest that the three described respiratory patterns in insects are not distinct but are instead a continuum of respiratory responses driven by the metabolic demand experienced by the insect.

A tritrophic view of diversity

Lee Dyer

Tulane University, New Orleans, LA, United States

Diversity is usually examined at single trophic levels, and many prominent diversity hypotheses, such as neutrality and intermediate disturbance, focus on primary producers. The focus of these diversity studies is also on species richness or a diversity index that utilizes species as the unit of interest. It is equally useful to view trophic chains as units of diversity and to focus on how the number of n-link chains varies across biotic or abiotic gradients. Utilizing collaborative data sets from large caterpillar rearing projects around the world and meta analyses from published studies, I tested the following assumptions about tritrophic (1 to 3-chain) diversity across a latitudinal gradient: 1) tritrophic diversity decreases with latitude, altitude, and disturbance, 2) consumer specialization decreases with latitude, and 3) pressure from natural enemies is more intense in the tropics and in predictable habitats. Tritrophic diversity, dietary specialization, and strength of trophic cascades all decreased significantly with increasing latitude. Gradients in disturbance and climatic variability were the best predictors of pressure from natural enemies, and this pressure did not vary consistently with latitude. Understanding mechanisms underlying these gradients in tritrophic diversity will contribute to clarifying issues about climate change, resiliency of tropical ecosystems, and the origin and maintenance of high tropical diversity.

Impact of invasive insect pests on eastern hemlock in the southern Appalachians, USA: Novel approaches to evaluating biological control agents for forest health management

Jerome Grant[1], Paris Lambdin[1], Gregory Wiggins[1], James Rhea[2]

[1]University of Tennessee, Knoxville, Tennessee, United States, [2]United States Department of Agriculture Forest Service, Southern Region, Asheville, North Carolina, United States

Introduction: Forest health in the southeastern USA is affected by numerous exotic insects, weeds, and plant diseases. Two invasive insect pests, elongate hemlock scale (EHS), *Fiorinia externa*, and hemlock woolly adelgid (HWA), *Adelges tsugae*, currently threaten forest health in the southern Appalachians, where HWA has caused high mortality of eastern hemlock (*Tsuga canadensis*). As part of a forest health management program, the feasible use of biological control agents against both invasive pests is underway. Large canopy enclosures (i.e., tree cages) were designed to evaluate their feasibility as tools to assess effectiveness and impact of introduced biological control agents in forest systems.

Methods: The impact of several established natural enemies of EHS was assessed; however, densities of HWA were not reduced by established natural enemies, emphasizing the need for the introduction and release of suitable biological control agents. Novel approaches to evaluating these introduced natural enemies were developed. Large screened cages (ca. 8 m tall x 24 m at base) were designed and placed over HWA-infested eastern hemlock trees in a forest setting. Densities of HWA were determined on each tree, and tree and HWA parameters were measured. One of three species of predatory beetles was placed in each cage. Predator and HWA densities were monitored to assess survival, establishment, reproduction, and impact on HWA.

Results: Impact of EHS on eastern hemlock was minimal in forest settings, due to the presence of numerous parasitoid and predator species. One parasitoid, *Encarsia citrina*, caused 20% mortality of EHS. Through trial and error, and resulting modification of cage strategy, a large tree cage that can withstand the various pressures placed upon it under field conditions was developed to better evaluate introduced natural enemies of HWA. These large cages have withstood rain, snow, and winds (some as high as 72 km/hr), with minimal damage. Results on the survival of each introduced biological control agent and its impact on HWA, as well as tree growth parameters, will be presented and discussed.

Conclusions: Large canopy enclosures provide a unique opportunity to assess introduced natural enemies of exotic pests of native trees in forest ecosystems. These cages have applicability to assessing the practicality of other forest pest/natural enemy systems.

Evolving out of conflict: Imperialism and altruism in gall-forming eusocial aphids

Patrick Abbot

Vanderbilt University, Nashville, TN, United States

The precise role of conflict in evolution of cooperation remains contentious. At debate are the conditions under which biological organization at more inclusive levels is promoted or inhibited by conflict and competition at lower levels. Eusocial, soldier producing aphids provide an interesting perspective, because they exhibit complex social organization in clonal societies. While admixture between clones occurs in some social species, clonality has been thought to be a necessary condition of social evolution in aphids. What is not known, however, is what role competition and conflict have played in these clonal societies. Here, we show that non-unitary relatedness evolved early in the radiation of the gall-forming North American genus *Pemphigus*, prior to the evolution of social behavior. Thus, social behavior evolved out of a more complex genetic group structure than previously known. These results update our understanding of social evolution in aphids, and provide a nuanced view of the evolution of conflict and cooperation in these insects. Namely, the function of aphid soldiers may not only be to ensure the survival of their resident kin group, but also the capacity of their clone to successfully exploit other clones. Because of their impressive dispersal abilities, all gallforming aphids - social or not - are probably clone-invading 'imperialists'. Eusocial aphids may not be so much 'fortress defenders' as they are 'fortified imperialists'.

Transdisciplinary approaches in documentation of biodiversity

Karl-Heinz Lampe

Zoologisches Forschungsmuseum Alexander Koenig (ZFMK), Bonn, Germany

Introduction: The traditional 'analogous' practice of documentation in Natural History museums is mainly based on more or less atomized entities which are often simple field names such as locality, collector or author. With modern approaches the documentation becomes more focused on processes and events. Thus the above mentioned entities what, who, where and when or respectively object/concept, person, place, time and activity have to be related to each other.

Methods: Information is modelled here with an ontology based on the CIDOC-Conceptual Reference Model (ISO 21127). In informatics, ontology is a formal specification of semantic concepts.

Results: As to be specified with some realistic examples taken from the field of biodiversity (collecting-, determination-, type creation-, expedition-, observation and painting events) the formal specification of semantic concepts makes scientific activities commonly understandable. In scientific (as well as scholarly) disciplines that should be an efficient way to document information in their full scientific depth rather than simply administering it. Thereby information content and handling can be improved by multiple instantiation, mutual verification and semantic enrichment.

Conclusions: A documentation of processes and events seems to be a prerequisite for trans-disciplinary information integration which is needed for developing knowledge networks and knowledge representation tools on the internet.

Neuronal organization of the trail pheromone pathway in Attine ants

Christoph J. Kleineidam, Christina Kelber

University of Wuerzburg, Wuerzburg, Germany

Leaf-cutting ants (genus *Atta*) are evolutionary-derived Attine ants with an extreme size polymorphism among workers and the most complex social organization. Body size is related to the behavior of workers and their assessment of the trail pheromone. Our behavioral experiments with *Atta vollenweideri* suggest that large workers primarily respond to the releaser component of the multi-component trail pheromone, whereas small workers rely more on blend-specific traits. We asked why the individuals behave differently and how neuronal information processing generates the inter-individual variance found in behavior. Using functional imaging, we found that the releaser component of the trail pheromone is represented in a substantially enlarged glomerulus (macroglomerulus) located in the antennal lobe. Only the antennal lobe of large workers contains a macroglomerulus, and correlating body size with glomerular volumes revealed two neuroanatomical sub-castes of workers (with or without macroglomerulus). The phenotypic plasticity found in the antennal lobe is probably the neuronal basis for the described differences in olfactory guided behavior.

In a comparative study across 24 species, we found a macroglomerulus only in the higher Attini (*Atta* and *Acromyrmex*) but not in any of the 10 investigated basal and intermediate Attini. This indicates that the macroglomerulus in the olfactory pathway of leaf-cutting ant workers is a derived trait. The neuroanatomical sub-castes of the polymorphic species lead to specialization and contribute to their complex social organization, whereas behavioral flexibility alone promotes division of labor in the species with less pronounced polymorphism and smaller colonies.

In addition to the genus-specific variation of glomerular volumes, we found an enormous variation in the number of glomeruli (288-630) indicating a strong selective pressure on the organization of the olfactory pathway.

Funding: DFG SFB 554/A6

Mass spectrometric analysis of neuropeptide-synthesizing neurons in the CNS of insects

Reinhard Predel, Susanne Neupert

Institute of Zoology, University of Jena, Jena, Germany

Neuropeptides are widespread signal molecules that display a great chemical and functional diversity. The predictions of neuropeptide cleavage from precursor proteins are not always correct and thus biochemical identification is essential. Particularly single cell analysis can be prerequisite for a better understanding of the complex functions of neuronal circuits. Currently, MALDI-TOF mass spectrometry is the method of choice to deal with that problem.

We present an overview of the methods that are used for cell identification and subsequent mass spectrometric analysis of peptidergic neurons in insects.

Supported by the Deutsche Forschungsgemeinschaft (Predel 595/6-3,4)

Insects with blue blood: On the occurrence of respiratory hemocyanins

Thorsten Burmester, Christian Pick

University of Hamburg, Hamburg, Germany

For a long time, respiratory proteins have been considered unnecessary in most insects because the tracheal system was thought to be sufficient for oxygen supply. Only a few species that dwell under hypoxic conditions were known exceptions and have hemoglobins. Other arthropods (crustaceans and chelicerates) harbour copper-containing hemocyanins in their hemolymph for transport of oxygen. No hemocyanins had been known from Hexapoda. However, recently we discovered a functional hemocyanin in the stonefly *Perla marginata*, which is present at high concentrations the hemolymph of nymphs and adults. *P. marginata* hemocyanin is a hexamer with two distinct subunit types of 659 and 655 amino acids, respectively. It has a moderate oxygen affinity (P_{50} ~ 8 torr) and displays cooperative oxygen binding. We further identified and cloned hemocyanin sequences from Collembola, Archaeognatha, Zygentoma, Phasmida, Dermaptera, Mantodea, Isoptera, Blattodea and Orthoptera. No hemocyanins could be identified by molecular or biochemical means in various representatives of Odonata and Ephemeroptera, suggesting its loss in these orders. Apparently, hemocyanin is also absent in Eumetabola (Hemiptera + Holometabola). Phylogenetic analyses show that there are two distinct hemocyanin subunit types (Hc1 and Hc2) in Hexapoda. While Hc1 groups with the copper-less, insect storage hexamerins, Hc2 is of more ancient evolutionary origin. The Pancrustacea hypothesis is supported by the hemocyanins. While the occurrence of hemocyanins adds further complexity to our view on insect respiration, there is currently no physiological or morphological character that could explain the presence or loss of hemocyanins in distinct taxa.

INOTAXA: open access, easy navigation and data mining of taxonomic literature on the web

Christopher Lyal[1], Anna Weitzman[2]

[1]The Natural History Museum, London, United Kingdom, [2]National Museum of Natural History, Washington, D.C., United States

Taxonomic literature produced over the past 250 years is required by all taxonomists, and contains a vast amount of information that is both of immense potential value and virtually inaccessible outside a few large libraries and collections. While progress has been made in producing digital versions of literature in formats such as PDF or JPEG and placing them on the web, these have drawbacks in terms of navigation, finding specific content or even finding the publication. The Biodiversity Heritage Library addresses some of these issues, but the content remains presented in a publication-centred manner rather than a user-centred way. INOTAXA (INtegrated Open TAXonomic Access) is a new way of making taxonomic literature and data available on the web. Using a purpose-designed XML schema interoperable with other TDWG standard schemas, and a purpose-built portal, a corpus of taxonomic literature can be searched using any term or set of terms, the search narrowed by restrictions such as geography, publication or higher taxon, or browsed by taxonomic classification, geography, person or publication. In addition to retrieving taxonomic treatments and keys, the content can be mined for specimen data, biological associations, classifications, people and much more. In addition to dealing with legacy literature, INOTAXA opens the door to much faster publication of new taxonomic information. Because of the use of standards data can be exchanged with resources such as GBIF, Catalogue of Life and the Encyclopedia of Life. A prototype of INOTAXA will be briefly shown and some of its functionality will be displayed.

Syngenta's approach to deploying transgenic insect resistance traits

Ryan Kurtz

Syngenta Biotechnology, Inc, Research Triangle Park, NC, United States

Syngenta currently has insect resistant transgenic maize and cotton products which are or are nearing commercialization in North and South America. Each of these products expresses one or more of three *Bacillus thuringiensis*-derived insecticidal proteins, Cry1Ab, Vip3A or mCry3A. The Cry1Ab protein provides protection against certain lepidopteran insect pests including *Ostrinia nubilalis, Diatraea grandiosella, Diatraea saccharalis, Heliothis virescens* and *Helicoverpa spp.* The Vip3A protein provides protection and a second mode of action against economically important lepidopteran pests including *D. grandiosella, D. saccharalis, Spodoptera frugiperda, Heliothis virescens* and *Helicoverpa spp.* The mCry3A protein provides protection against economically important corn rootworm pests such *Diabrotica virgifera virgifera* and *Diabrotica longicornis barberi*.

These proteins' high degree of specificity and demonstrated safety are the basis for their utility as plant incorporated protectants. The successful deployment of these products will provide substantial benefits to growers and to society. Consequently, it is essential that we foster the continued utility of this technology through the implementation of appropriate insect resistance management tactics. Syngenta's Vip3A toxin offers a distinct mode of action compared to Cry toxins. Pyramiding these two modes of action will reduce the risk of resistance in insects controlled by both events. In North America, Vip3A will only be offered as a pyramid with Cry1Ab in both maize (Bt11 x MIR162) and cotton (VipCot™). Vip3A and Cry1Ab will initially be offered singly in South America followed soon as pyramided in Bt11 x MIR162.

Taxonomic needs in managing invasive species: A global assessment

Christopher Lyal[1], Richard Smith[2]

[1]The Natural History Museum, London, United Kingdom, [2]BioNET-INTERNATIONAL, Egham, United Kingdom

Although taxonomy is recognized as important in managing invasive species there is little clarity on the overall priorities at a global policy level. The lack of explicit statements hinders access to taxonomic expertise and the development of protocols and practices to ensure taxonomic information and expertise are available when and where they are needed. An assessment of taxonomic needs in the context of Invasive Alien Species management at a global level showed that high prioritization was given by members of the IAS community to provision of names, their synonyms and their vernacular equivalents, to identification tools, and to the availability of expert taxonomists to provide identifications. The assessment provides recommendations to address the taxonomic impediment in IAS, and these are being made available both publically and to relevant policy and implanting bodies, such as the Convention on Biological Diversity and the Global Invasive Species Programme.

Vegetation management for biological control in annual crops: Spatial scale and meta-communities

Deborah Letourneau, Carol Shennan, Sara Bothwell, Tara Pisani-Gareau

University of California, Santa Cruz, CA, United States

Perennial vegetation in agricultural landscapes may contribute to ecological pest management by provision of critical habitat and food resources for arthropod parasitoids and predators of crop pests, especially in frequently disturbed, annual cropping systems. We determined the extent to which natural enemy abundance or diversity is predicted by the presence or relative cover of perennial vegetation at the field-level (vacuum samples on hedgerows adjacent to vegetable crops) and the landscape-level (Malaise trap samples in vegetable fields embedded in a range of vegetation and land-use mosaics). Landscape factors, within a 1.5km radius of each Malaise trap, were measured using manual aerial photo interpretation with GPS field-verification. We also measured parasitism rates of sentinel moth larvae (*Trichoplusia ni*) and aphids (*Brevicoryne brassicae*) to determine if diversity, abundance, or movement rates of natural enemies predict conservation biological control potential on farms. Robust results include: (1) a positive association between the amount of perennial vegetation cover and the richness of ichneumonid wasp species versus a negative association between annual cropland cover and species richness of ichneumonid wasps, (2) a positive association between parasitoid abundance and *Baccharis pilularis* shrubs in hedgerows versus a negative association between these factors on the landscape-scale, (3) differential hedgerow shrub usage by pests and natural enemies, and (4) a tenuous association between biodiversity and parasitism rates. We will discuss current evidence and experimental methodologies in the context of theoretical expectations regarding biodiversity and pest control as an ecosystem service.

Rapid and gradual shifts in tropical and temperate styles of herbivory from the North American Paleogene

Conrad Labandeira[1], Ellen Currano[3], Peter Wilf[3], Scott Wing[1]

[1]Smithsonian Institution, Washington, DC, United States, [2]University of Maryland, College Park, MD, United States, [3]Pennsylvania State University, University Park, PA, United States

Introduction: Comparisons of the intensity of tropical and temperate insect herbivory in the modern world show strong latitudinal patterns. These geographic patterns are mirrored in the paleontological record, such as the ~10^5 yr-long Paleocene-Eocene Thermal Maximum (PETM) occurring 55.8 million years ago.

Methods: Herbivore intensity and diversity are estimated from characteristic modes of insect feeding on fossil leaves. The units of analysis are damage types (DTs), which are diagnosable, stereotyped patterns of insect damage on fossil plants. Indices include the frequency and diversity of attack on bulk floras and specific, taxonomically identified plant groups.

Results: Pre-PETM floras from northern Wyoming, which were dominated by deciduous plants, had low levels of herbivory. During the PETM, a transient global temperature increase of ~5°C and tripling of atmospheric CO_2 was associated with a rapid increase in abundance and diversity of subtropical plant taxa and a major increase in total and specialized herbivory. Post-PETM climate and floras reverted to the previous state, as did levels of herbivory. Several million years later, as climates in northern Rocky Mountains became warmer and locally drier, the amount and character of herbivory changed again. During this interval there was a separation in herbivory style between more palatable deciduous taxa in wetter habitats versus highly defended, evergreen taxa in better drained and elevated areas.

Conclusion: The PETM is analogous to the modern rise of global anthropogenic in CO_2 and temperature. The PETM increase in insect herbivory is a preview for current managed and natural ecosystems.

Longitudinal studies on the emergence of dengue virus in Iquitos, Peru

Amy Morrison[1], Tadeusz Kochel[2], Gregor Devine[3], Moisés Sihuincha[4], Thomas Scott[5]

[1]University of California Davis, Davis, California, United States, [2]U.S. Naval Medical Research Center, Lima, Peru, [3]Rothamsted Research, Harpenden, United Kingdom, [4]Laboratorio Referencial, Iquitos, Peru, [5]University of California, Davis, California, United States

Dengue virus seroconversions were monitored among study populations of 2,000-3,000 residents in 3 prospective cohort studies carried out since 1999 in the Amazonian city of Iquitos, Peru. Study participants were tested by plaque reduction neutralization at 6 month intervals. Their homes and neighborhoods were also monitored regularly for *Aedes aegypti* vectors. In 1999, seroprevalence rates to dengue ranged from 65-89% and were correlated with vector densities ($r>0.5$). Under conditions of endemic transmission (prior to 2002) overall seroconversion rates ranged from 2-3 conversions/100 person-years at risk. In contrast, since the introduction of dengue-3, Iquitos has experienced 4 significant dengue outbreaks in which incidence rates ranged from 12 to 44 conversions per 100 person-years at risk. Dengue Hemorrhagic Fever cases were confirmed for the first time in 2004 and have occurred only when transmission rates were high over all. Only adult, not immature *Aedes aegypti* indices correlate with seroincidence rates; correlation rates were < 0.25 during inter-epidemic periods and 0.38-0.41 during periods of epidemic transmission.

House to house ULV pyrethroid spray applications consistently lowered vector populations to negligible levels and decreased dengue virus transmission significantly, whereas in a variety of controlled trials of larviciding strategies had minimal impact on vector populations. We will discuss the implications of these observations on dengue prevention and control strategies world-wide including the merits of strategies focused on preventing severe disease rather than complete suppression of virus transmission.

Spatially and temporally targeted vector-borne disease interventions

Thomas Scott, Amy Morrison

University of California, Davis, California, United States

Contemporary dengue prevention is based on the unvalidated assumption that a reduction in adult *Aedes aegypti* population densities will decrease risk of virus transmission. *Ae. aegypti* eradication is not considered feasible and there are no commercially available dengue vaccines or clinical cures. Mosquito vector control is the only currently available dengue prevention strategy. We will discuss the theoretical underpinnings and implications of temporally and spatially targeted vector control for dengue prevention in the context of four interrelated questions. What is an acceptable level of dengue risk? What are the mosquito densities necessary to achieve that goal? What is the best way to measure entomological risk? Because most dengue risk factors are likely to exhibit spatial dependence, at what geographic scale are the components of dengue transmission important?

Two important outcomes are necessary for meaningful improvement in dengue surveillance and control. First, there is an urgent need for field-based prospective longitudinal cohort studies on the relationships among measures of entomological risk (i.e. *Ae. aegypti* density), dengue incidence, and severity of disease. Second, new rapid, inexpensive, and operationally amenable methodologies are needed to evaluate and monitor the impact of vector control strategies on disease reduction. Unless mosquito vectors are eliminated entirely, predicting and evaluating success of dengue prevention programs will continue to require a more thorough understanding of the site specific relationships among effective disease prevention strategies, risk of human disease, and application of intervention strategies through time and space.

Different seasons, different reasons: Behavioral plasticity of the discriminating sex in mate choice

Kathleen Prudic, Antonia Monteiro

Yale University, New Haven, CT, United States

Introduction: *Bicyclus anynana* (Lepidoptera: Nymphalidae) displays seasonal variation in the size of its ventral eyespot patterns, a likely defensive adaptation against predators. This species also has dorsal eyespots that are stable in size across seasons, but little is still known about their function. Here we evaluate the role of dorsal eyespots in mate choice to understand why this character does not display the seasonal variation characteristic of other eyespots.

Methods: We designed experiments to evaluate mate preference of each sex from each season. We manipulated wing pattern by either applying opaque paint on top of UV-reflective scales in the center of the eyespots or away from the UV-reflective center. We observed the effect of eyespot treatment on first mating. We also recorded butterfly longevity as it related to mate seasonal form.

Results: Dry season males preferred females with intact dorsal eyespots while wet season males did not show a preference. Conversely, wet season females preferred males with intact dorsal while dry season females did not show a preference. Mating with a dry season male increased the longevity of both dry and wet season females, but mating with a wet season male did not affect female longevity.

Conclusions: Dorsal eyespots are vital for sexual signaling in *B. anynana*; however, the signaling sex changes between dry and wet season. This pattern can be explained by both species recognition mechanisms and seasonal resource availability. Behavioral plasticity appears to constrain morphological plasticity in the eyespots important for mate signaling.

Indirect host-related chemical kairomones for improving egg parasitoid efficacy in IPM

Stefano Colazza[1], Ezio Peri[1], Eric Conti[2], Gianandrea Salerno[2], Ferdinando Bin[2]

[1]Department of SENFIMIZO – Section of Entomology, Università di Palermo, Palermo Sicilia, Italy, [2]Department of DSAA – Section of Entomology, Università di Perugia, Perugia Umbria, Italy

Successful parasitism by Hymenoptera parasitoids of herbivores is arisen trough several phases of host searching behaviour, which eventually lead the wasp females close to, or in contact with their potential hosts. During the host location process, wasp females encounter and explore a great variety of stimuli, mainly chemical cues, named semiochemicals, that play a major role. In the last decades, semiochemicals have become a valuable tool for developing Integrated Pest Management (IPM) programs. However, applied approaches towards field use of semiochemicals as a mean for behavioural manipulation of insect parasitoids have rarely been considered. Attempts of kairomone employment in the field have been carried out with egg parasitoids, with the aim of retaining the parasitoids in the target area. Laboratory experiments on egg parasitoids belonging to the families *Trichogrammatidae* and *Scelionidae*, showed that scales shed by adults of lepidopterans, and chemical residues left on a substrate by true bugs while moving, represent a set of indirect host-related contact kairomones that induce arrestment and motivated searching behaviour. A comparative analysis of these results suggest that the active compounds of these contact kairomones can be sprayed over the plants to increase the probability of egg parasitoid encounters with the hosts, thus increasing parasitism rate. However a better understanding of plant surface - kairomone interactions is necessary to define how to apply these chemicals in the field and predict impact on natural enemies and biological control efficacy.

Ecology of fungi from Ascospherales and their association with social and solitary bees

Annette Bruun Jensen[1], Jørgen Eilenberg[1], Rosalind James[2]

[1]University of Copenhagen, Copenhagen, Denmark, [2]USDA-ARS, Logan, UT, United States

All known species of Ascosphaerales are associated with bees (Apoidea), social as well as solitary soil and twig nesting bees. Different fungal life cycle strategies can be found, some species are obligate pathogens of bee larvae/pupae and some are secondary pathogens, while others live as saprophytes on pollen, pollen provision or feces. The insect pathogenic Ascospharales differ significantly from most other insect pathogenic fungi with respect to their primary infection route – these fungi infect bee larvae through the gut upon ingestion of ascospores. We will discuss the biological significance of this exemplified by recent studies performed on the two most well known species *Ascosphara aggregate* and *Asco. apis*. These two species represent pathogens of important pollinators, *Asco. aggregate* infects the alfalfa leafcutting bee *Megachile rotundata*, *Asco. apis* infects the honey bee *Apis mellifera*, thus representing pathogens of a solitary and social bee, respectively.

Hygienic behaviour, removal of diseased larvae by worker bees is an important defence mechanism seen in social insects, and to eliminate this factor bioassays can be performed on *in vitro* reared larvae. We performed such bioassays to investigate susceptibility of different honey bee races to *A. apis*. *Megachile rotundata* is not known to have different races, but we have found the susceptibility of this bee to be affected by environmental temperature conditions, where cooler temperatures increase infection levels. Cool temperatures have previously been found to increase chalkbrood infection levels in honey bees and the blue orchard bee (*Osmia lignaria),* as well.

Current status of oak wilt disease in Korea

Kyung Hee Kim, Seung-Kyu Lee, Sang Tae Seo, Eunsung Oh, Won Il Choi

Korea Forest Research Institute, Seoul, Republic of Korea

Oak wilt disease in Korea was first reported in 2004. The causal agent was identified as *Raffaele*a sp. associated with an ambrosia beetle, *Platypus koryoensis*. There are six oak species in forests, and *Quercus mongolica* is the most susceptible. It shows the dying or dead symptom from July to October after infection. The trees attacked by the beetles resulted in 17~21% of mortality. The study sites were selected to observe the progress of disease on naturally damaged trees. There were no dead trees found in 2^{nd}~3^{rd} year after penetration of beetles in the sites. Also, the sites that were located over 600m elevation had less death of trees and slow spread of the disease. The damage was limited to central region between 2004 and 2005. However, it was widely distributed over the country in 2006. The oak forests with mainly *Q. mongolica* in the central region have been cut down once and grown from the sprouts. Because the oak wilt disease was predisposed to the central area, the area has been mostly damaged compare to other regions. Also, the sunny area had more infected trees than shade area. Overwintering adult beetles of *P. koryoensis* emerged from bark in early May and even early October. It was analyzed that the high peak of the emergence was dependent on environment conditions in different locations over year.

Non-target risk assessment of insect-resistant GM crops: an international, multi-stakeholder approach

Jörg Romeis[1], Detlef Bartsch[2], Franz Bigler[1], Marco P. Candolfi[3], Marco M.C. Gielkens[4], Susan E. Hartley[5], Richard L. Hellmich[6], Joseph E. Huesing[7], Paul C. Jepson[8], Raymond Layton[9], Hector Quemada[10], Alan Raybould[11], Roby I. Rose[12], Joachim Schiemann[13], Mark K. Sears[14], Anthony M. Shelton[15], Jeremy Sweet[16], Zigfridas Vaituzis[17], Jeffrey D. Wolt[18]

[1]Agroscope Reckenholz-Tänikon Research Station ART, Zurich, Switzerland, [2]Federal Office of Consumer Protection and Food Safety (BVL), Berlin, Germany, [3]BASF SE, Limburgerhof, Germany, [4]National Institute for Public Health and the Environment, Bilthoven, Netherlands, [5]University of Sussex, Falmer, Brighton, United Kingdom, [6]USDA–ARS, Corn Insects and Crop Genetics Research Unit and Department of Entomology, Iowa State University, Ames, IA, United States, [7]Monsanto Company, St. Louis, MO, United States, [8]IPPC, Cordley Hall, Oregon State University, Corvallis, OR, United States, [9]DuPont Crop Genetics, Johnston, IA, United States, [10]Program for Biosafety Systems, Calvin College, Grand Rapids, MI, United States, [11]Syngenta, Jealott's Hill International Research Centre, Bracknell, Berkshire, United Kingdom, [12]USDA–APHIS Biotechnology Regulatory Services, Riverdale, MD, United States, [13]Julius Kuehn Institute, Federal Research Centre for Cultivated Plants (JKI), Institute for Biosafety of Genetically Modified Plants, Braunschweig, Germany, [14]Department of Environmental Biology, University of Guelph, Guelph, Ontario, Canada, [15]Department of Entomology, Cornell University/NYSAES, Geneva, NY, United States, [16]Environmental Consultant, Willingham, Cambridge, United Kingdom, [17]Biopesticides and Pollution Prevention Division, USEPA, Washington, DC, United States, [18]Biosafety Institute for Genetically Modified Agricultural Products and Department of Agronomy, Iowa State University, Ames, IA, United States

An international initiative is developing a scientifically rigorous approach to evaluate the potential risks to non-target arthropods (NTA) posed by insect-resistant, genetically modified (IRGM) crops. It adapts the tiered approach to risk assessment that is used internationally within regulatory toxicology and environmental sciences. The basic principles and rationale of this approach are outlined, and ways in which it has been refined by scientists from public, industrial and regulatory sectors, who have extensive experience with IRGM crops, are reported. The approach focuses on the formulation and testing of clearly stated risk hypotheses, making maximum use of available data and using formal decision guidelines to progress between testing stages (or tiers). It is intended to provide guidance to regulatory agencies that are currently developing their own NTA risk assessment guidelines for IRGM crops and to help harmonize regulatory requirements between different countries and different regions of the world. The approach will thus be of great benefit for regions that lack the capacities to conduct all the regulatory risk assessment studies themselves. It will also aid researchers developing IRGM crops as well as the funding agencies supporting their work by providing them a framework for organizing and planning regulatory studies in support of their products.

Edaphic factors influencing the performance of a root-feeding flea beetle, *Longitarsus bethae* (Coleoptera: Chrysomelidae), a biological control agent for *Lantana camara* (Verbenaceae)

David Simelane

Agricultural Research Council, Pretoria, Gauteng, South Africa

Adult preference and survival of the immature stages of the root-feeding flea beetle, *Longitarsus bethae* Savini and Escalona (Coleoptera: Chrysomelidae), a natural enemy of the weed, *Lantana camara* L. (Verbenaceae), were examined at four soil textures, three soil moisture levels, two soil surface conditions and at five levels of organic matter content under laboratory conditions. Both soil texture and moisture had no influence on leaf feeding and colonisation by adult *L. bethae*. Soil texture had a significant influence on oviposition, with adults preferring to lay on clayey and sandy soils to silty or sandy loam soils. However, survival to adulthood in clayey soils was significantly higher than in other soil textures. Although oviposition preference and depth of oviposition were not influenced by soil moisture, survival in moderately moist soils was significantly higher than in other moisture treatments. Development of immature stages in high soil moisture treatments was significantly slower than in low and moderate soil moisture treatments. There was a strong negative relationship between the percentage of organic matter in the soil and the number of eggs laid. There were no variations in the body size of beetles that emerged from different soil textures and moisture levels. Females laid almost three times more eggs on cracked than on non-cracked soils. It is predicted that clayey and moderately moist soils will favour the survival of *L. bethae*, and under these conditions, damage to the roots is likely to be high. This information will aid in the selection of suitable release sites where *L. bethae* would be most likely to become established.

The use of oil soluble dyes to mark *Eldana saccharina* Walker (Lepidoptera: Pyralidae) adults

Angela Walton, Des Conlong

[1]SASRI, Mount Edgecombe KZN, South Africa, [2]Stellenbosch University, Stellenbosch WC, South Africa

Two oil soluble dyes (Sudan red and Calco red) were incorporated into the diet used to rear *Eldana saccharina* at the SASRI Insect Rearing Unit. These dyes are taken up in the fat bodies of the target insect, which allow, upon dissection of these, the identification of laboratory-reared adults from wild counterparts caught in traps. However, the use of dyes such as these can have detrimental effects on the developmental biology, fecundity and fertility of *E. saccharina*. It was found that Sudan red reduced adult emergence by 38% and fecundity by 70% and prolonged development time. Development time was measured as % Pupation at the time of sampling. Pupation was reduced by 46% in the Sudan red treatment compared to the control. Calco red did not impact on the developmental and reproductive biology of this insect in any way.

This breakthrough allows these marked adults to be used in mating, field dispersion and population estimation studies. This information is important for the formulation of sterile insect technology and mating disruption control options for *E. saccharina*. The results will be discussed in the context of these area-wide management programmes.

Invertebrate conservation in Gauteng Province, South Africa: A retrospective overview

Ian Engelbrecht

Gauteng Dept. of Agriculture, Conservation and Environment, Johannesburg, Gauteng, South Africa

Gauteng Province has been championed as the economic development hub of South Africa, and the economic powerhouse of Africa. With this economic development has come extensive land transformation in the province, primarily for residential, industrial, and infrastructural purposes. This context provides significant challenges for biodiversity conservation. A systematic conservation plan, developed by the Department of Agriculture, Conservation and Environment, has provided the primary government regulatory tool for biodiversity conservation in the province. The invertebrates have featured significantly in the development of this conservation plan with six butterfly species, two beetle species, one scorpion species and twelve mygalomorph spider species included. These species were originally identified as conservation priorities through an expert consultation process, but evidence gathered subsequently indicated that their inclusion might not have been justified. As a result the decision was taken to apply the IUCN red list assessment criteria to these species in order to more objectively determine their likelihood of extinction, and hence more appropriately represent them in the conservation plan. This presentation will outline the mechanism by which the conservation plan is used as a regulatory tool in the province, the results of the Red List assessments and the implications for invertebrate conservation in Gauteng Province and elsewhere will be discussed.

Phenology modelling of major fruit tree pests: From biological basics to decision support

Jörg Samietz, Benno Graf, Heinrich Höhn, Hans Ulrich Höpli

Swiss Federal Research Station Agroscope Changins-Wädenswil ACW, Wädenswil, Switzerland

Introduction: Modern plant protection relies on precise timing of pest management. Forecasting tool are needed in order to optimize timing of monitoring and control of insect pests and growers or consultants have to be provided with according information. The system SOPRA has been developed to facilitate these needs by combining pest biology and behaviour, modelling, and modern internet technology.

Methods: Applying time-varying distributed delay approaches, phenology-models were developed driven by solar radiation, air temperature and soil temperature on hourly basis. Relationships between temperature and stage specific development rates for the relevant stages of the life cycles were established under controlled conditions for *Cydia pomonella*, *Grapholita lobarzewskii*, *Adoxophyes orana*, *Dysaphis plantaginea*, *Hoplocampa testudinea*, *Anthonomus pomorum*, *Cacopsylla pyri*, *Rhagoletis cerasi*.

Results: Validation of model predictions with independent field observations showed that, besides temperature-dependent processes, habitat choice of key stages needs to be regarded in order to achieve reliable results. On base of local weather data, age structure of the pest populations is simulated and crucial events for management activities are predicted. Simulation results are made available through the web-interface www.sopra.info covering all fruit growing regions of Switzerland. Phenology is directly linked to detailed decision support plus extended information about the pest insects, management strategies and plant protection products.

Conclusions: SOPRA is successfully applied as a simple to use decision support system in Switzerland, Southern Germany and beyond. It can serve as example for combining a wide range of information to establish a reliable and readily available information tool for growers and consultants.

Phenology modelling of major fruit tree pests: From biological basics to decision support

Jörg Samietz, Benno Graf, Heinrich Höhn, Hans Ulrich Höpli

Swiss Federal Research Station Agroscope Changins-Wädenswil ACW, Wädenswil, Switzerland

Introduction: Modern plant protection relies on precise timing of pest management. Forecasting tool are needed in order to optimize timing of monitoring and control of insect pests and growers or consultants have to be provided with according information. The system SOPRA has been developed to facilitate these needs by combining pest biology and behaviour, modelling, and modern internet technology.

Methods: Applying time-varying distributed delay approaches, phenology-models were developed driven by solar radiation, air temperature and soil temperature on hourly basis. Relationships between temperature and stage specific development rates for the relevant stages of the life cycles were established under controlled conditions for *Cydia pomonella*, *Grapholita lobarzewskii*, *Adoxophyes orana*, *Dysaphis plantaginea*, *Hoplocampa testudinea*, *Anthonomus pomorum*, *Cacopsylla pyri*, *Rhagoletis cerasi*.

Results: Validation of model predictions with independent field observations showed that, besides temperature-dependent processes, habitat choice of key stages needs to be regarded in order to achieve reliable results. On base of local weather data, age structure of the pest populations is simulated and crucial events for management activities are predicted. Simulation results are made available through the web-interface www.sopra.info covering all fruit growing regions of Switzerland. Phenology is directly linked to detailed decision support plus extended information about the pest insects, management strategies and plant protection products.

Connclusions: SOPRA is successfully applied as a simple to use decision support system in Switzerland, Southern Germany and beyond. It can serve as example for combining a wide range of information to establish a reliable and readily available information tool for growers and consultants.

Population management of cone- and seed insects in Norway spruce (*Picea abies* L. Karst.) seed orchards in Sweden

Olle Rosenberg, Jan Weslien

Skogforsk, UPPSALA, Sweden

Introduction: Seed orchards produce high-quality seeds for reforestation. Trees derived from these seeds have up to 20 % higher growth rate compared to trees derived from forest seeds, resulting in a high market value for orchard seeds. Several insect species have cones and seeds as their only/main food source. Different species have different flight periods which makes it difficult to decide when and for how long it is necessary to protect cones using e.g. insecticides.

Methods: By protecting branches during different development stages of flowers/cones, we studied at which time flowers/cones were susceptible to different insect species. We also monitored the flight time of one of the more serious pest insects, the lepidopterous species *Dioryctria abietella* using pheromone bated traps.

Results: Cones on branches protected during the whole season were undamaged. Protection during flowering to young cones (May-mid June) resulted in cones with very small damages, despite the fact that the monitoring of *D. abietella* showed that this pest species still were flying in August. Protection of young cones to mature cones (early June-October) resulted in heavily attacked cones from two lepidopterous species *Cydia strobilella* and *D. abietella* and the diptera *Strobilomyia anthracina*. Cones on branches that not were protected at all were damaged, although they had less damage compared to cones on branches protected during early June-October.

Conclusions: The infestation mainly occurs on flowers to young cones, a period of about one month. If cones are protected during this period they may remain healthy and thus produce viable seeds.

Invasive Hymenoptera: a global perspective

Michael Gates[1] and Michael Schauff[2]

[1]Systematic Entomology Laboratory, USDA, ARS, PSI, c/o National Museum of Natural History, Washington, D. C. 20013-7012, USA, [2]Plant Sciences Institute, USDA, ARS, 10300 Baltimore Ave., Beltsville, MD, USA

Introduction: Invasive arthropods cost governments and regulatory agencies billions of dollars annually in economic losses worldwide. Hymenoptera are an important component of many costly invasions requiring remediation by humans.

Methods: We intend to provide an introduction and brief overview of the role of Hymenoptera as invasive species, focusing especially on economic and ecological impacts. We evaluated published—electronic and paper based—records of Hymenoptera as invasive organisms worldwide during the past 25+ years in order to compose this overview, plus a short case study of a "beneficial invasive".

Results: While there are certainly numerous instances documenting the deleterious effects of invasions, there is also evidence that certain invasions have minimal or potentially beneficial effects. Larger aculeate Hymenoptera often capture the attention of the public and regulators, while smaller taxa may remain unnoticed initially. However, smaller taxa may cause plant damage through galling plant tissue, which serves to increase their apparency. We report on a case study in North America where previously undocumented parasitic Hymenoptera were detected during surveys of the emerald ash borer, an invasive buprestid from Southeast Asia.

Conclusions: Invasive Hymenoptera, in many cases, are here to stay. However, there are notable success stories in managing deleterious invasion events, ranging from active programs including eradication or partial mitigation via an integrated approach to passive "beneficial invasives" resulting from co-introductions with other arthropod invasives.

Population genetics of the eucalypt weevil; diversity and origin of Western Australian introductions

Tendai Mapondera, Mamoru Matsuki, Treena Burgess

School of Biological Sciences, Murdoch University, Perth, 6150, Australia

Gonipterus scutellatus is wide-spread in southeast Australia where it has limited impact. World-wide it has been introduced to most countries where eucalypts are grown and has become a significant defoliator of eucalypts. There are no early records of *G. scutellatus* occurring in Western Australia (WA). However, by 2002 it was the most abundant insect species collected in eucalypt plantations in WA. Unlike other regions of Australia where the pest is endemic, *G. scutellatus* causes significant damage to Western Australian plantations and in the absence of an effective biological control, chemical control has been routinely used in heavily impacted plantations. *G. scutellatus* was collected from 25 locations in eastern Australia (Tasmania, Victroia, New South Wales and South Australia) and several locations in WA. A 474 bp fragment of the mtDNA gene Cytochrome oxidase 1 was sequenced for 134 isolates, all sequences were converted to amino acid sequences to confirm they code for cytochrome oxidase 1. From the sequence data 46 haplotypes were revealed. Only one haplotype was found in WA, whilst collections from EA were very diverse, especially Tasmania. In the phylogenetic analysis, insects identified as *G. scutellatus* resided in five distinct and highly supported lineages strongly suggesting that this is a species complex rather than an individual species. Only one of these lineages have been introduced to WA. The distribution and biology of the different lineages needs to be determined. This data set will allow researchers world-wide to determine the identity and potentially origin of insects introduced into their countries.

Population genetics of the eucalypt weevil; diversity and origin of Western Australian introductions

Tendai Mapondera, Mamoru Matsuki, Treena Burgess

School of Biological Sciences, Murdoch University, Perth, Australia

Introduction: The stingless bees present large distribution, great diversity, very significant contribution as pollinator agents, and economic and medical value. Despite their biological and economic importance, basic aspects about their biology and evolution are still not elucidated. The multiple mate in Hymenoptera is relatively common, however in stingless bees only few studies on this subject have been published. To increase our understanding on this behavior the species *Plebeia remota* was choosen as experimental model. This species has a small body size and small number of individuals per nest. The literature has postulated that queens of *P. remota* mate once, however all these studies are based on just one temporal sample and one nest. The knowledge of queen mate number and the relationship degree among workers allows inferences on social evolution and conflict between queen and workers in the male production.

Methods: Workers and males from two colonies were collected monthly during one year, totalizing 123 individuals. Total DNA was extracted and used to PCR amplify microsatellite loci. Four loci were screening by using heterologous primers derived from *Melipona bicolor* (Mbi33, Mbi 215, Mbi 259 and Mbi278).

Results: The loci Mbi215, Mbi259 and Mbi278 presented two alleles each. By analyzing the males we could infer the queens genotypes, which were heterozygous for the three loci. Also most of the workers were heterozygous, however in different temporal samples we found workers homozygous for either alleles.

Conclusion: The data indicated that the queens likely were mated by at least two males.

Adaptive accuracy and evolution of morphological fit between flowers and insect pollinators

W Scott Armbruster[1], Thomas Hansen[2], Christophe Pelabon[3]

[1]University of Portsmouth, Portsmouth, United Kingdom, [2]University of Oslo, Oslo, Norway, [3]Norw Univ Sci Tech, Trondheim, Norway

Insects and their flowers participate in complex mutualisms based on four features: attraction, reward, fit, and pollination. Both reward and flower-pollinator fit depend on the interaction between morphological characteristics of plant and insect phenotypes, and in particular on genotype-phenotype mapping and adaptive accuracy. Insects collect nectar, pollen, oils, fragrances, or resins from flowers and must have appendages of appropriate length and shape to do so. Flowers, in turn, get pollinated by some of these floral visitors and must have the appropriate size and shape to benefit from their visitation. We can analyse these relationship in terms of visitation rate and pollination efficiency, employing the concept of adaptive accuracy. In this way we can consider simultaneously all sources of variance in how development translates genes into phenotype and how phenotype influences fitness. The two components of adaptive accuracy, precision and optimality (target deviance), are generated by different biological process and have different evolutionary dynamics in the context of plant-pollinator mutualisms.

Introduction of integrated pest management in hardy ornamentals: A good bug alone is not enough

Rob van Tol

Plant Research International, Wageningen, Netherlands

Introduction of IPM in hardy ornamentals in the Netherlands was initiated and intensively supported on several nurseries in the years 1991 to 1994 followed by an implementation project trying to extend IPM to larger areas within nursery industry. While the initial project was very successful in accomplishing the goal of reducing pesticide use the extension to other nurseries was much less successful. At best some single alternative pest control means were incorporated. The success of IPM depends, however, on the total concept of integrating all means (e.g. monitoring tools, pesticides, biologicals, labour, cultural means, planting schedule, etc.). The human factor as a key factor in success or failure of IPM is usually underestimated and may have limited successful spread of IPM. Complexity of management, knowledge support and risk assessment are only some of the factors involved in decision making of growers. In this presentation several key factors in decision making of growers are discussed.

The evolution of dorsoventral axis formation in insects

Siegfried Roth

University of Cologne, Cologne, Germany

The dorsoventral polarity in *Drosophila* is established during oogenesis when the asymmetric movement of the oocyte nucleus determines the dorsal side of the egg chamber. The mRNA of a TGFalpha-like ligand becomes restricted to the oocyte nucleus. From there the ligand is secreted and activates the EGF receptor in the overlaying follicle cells. This leads to dorsoventrally asymmetric gene expression within the follicular epithelium and subsequently to asymmetric spatial cues in the egg shell which are used to orient the embryonic dorsoventral axis. The embryonic dorsoventral axis depends on two major signalling cascades, the Toll/NF-kappaB and the BMP signaling cascade. This talk will review results form classical embryological and modern molecular-genetic studies which provide insights on how ovarian and embryonic dorsoventral axis formation have evolved in insects.

Juvenile hormone regulation of metamorphosis in the beetle *Tribolium castaneum*

Barbora Konopova, Marek Jindra

Biology Center ASCR, Institute of Entomology, Ceske Budejovice, Czech Republic

All recent winged insects undergo metamorphosis. Completion of wing development, besides sexual maturation, is the main metamorphic change. In holometabolan insects, metamorphosis transforms larval stages, which possess no external wings, into flying adults. A major part of wing development takes place during the pupal stage. Metamorphosis depends on the morphogenesis-promoting ecdysteroids and the morphostatic juvenile hormone (JH), whose presence precludes the metamorphic changes until the final larval instar. However, the mechanism of JH action remains poorly understood, mainly because JH signal transducers are unknown. Since JH has no robust effect on *Drosophila* larval-pupal transition, we chose to study JH regulation of metamorphosis in the red flour beetle *Tribolium castaneum*. Using systemic RNAi in *Tribolium*, we show that JH controls the entry into metamorphosis through the Methoprene-tolerant protein (Met). In contrast to *Drosophila*, where loss of *Met* causes resistance to ectopic JH but no developmental defects, *Tribolium* larvae lacking *Met* function enter the pupal program prematurely, developing wings and other pupal characters before reaching their final instar. Thus, Met is an essential transducer of the anti-metamorphic JH signal. We further show that in response to JH, Met regulates expression of the *Tribolium Broad-Complex* gene (*BR-C*), which is required for pupal development. Impaired function of *BR-C* blocks pupation and although it does not prevent cell proliferation within the wing primordia of the arresting *Tribolium* prepupae, it prevents their proper morphogenesis and elongation. Thus, Met and its downstream target *BR-C* play critical roles in the JH-dependent regulation of insect metamorphosis.

Red oak borer: History and population dynamics in Arkansas forests

Fred M. Stephen, Melissa K. Fierke, Laurel J. Haavik, John J. Riggins

University of Arkansas, Fayetteville, AR 72710, United States

In 2000, tens of thousands of dead and dying red oaks (*Quercus rubra* L.) were discovered in oak-hickory forests of northern and western Arkansas. A significant cause of tree mortality in this "oak decline event" was a population explosion of a previously innocuous, native wood-boring beetle, the red oak borer *Enaphalodes rufulus* (Haldeman) (Coleoptera: Cerambycidae). To obtain knowledge on population dynamics of this beetle and causes for this outbreak we have developed sampling methods for beetles within trees, stands and forests. We have shown, using dendrochonological methods, that from about 1940 until 1992 red oak borers were present in oaks but at consistently low levels. The recent outbreak on the Ozark National Forest appears to have begun in 1994 and peaked in 2000 and 2002, with population levels more than 100 times higher than at the beginning of the outbreak. Populations began to crash in 2004 and are now nearly as low as before the outbreak began. Hazard models predict that, of the different oak species, *Q. rubra* experiences the greatest mortality and that mortality is higher in dense stands on ridges than on north, east, west and south-facing benches or in forests with lower *Q. rubra* densities. Red oak borer populations are also highest on ridges. Preliminary studies of radial growth suggest that this oak decline event as well as the rise in red oak borer numbers is closely associated with reduced radial growth. Tree defense mechanisms and other factors affecting red oak borer mortality are discussed.

Effects of light intensity on pine engraver reproduction in ponderosa pine slash in northern Arizona

Christopher Hayes[1], Richard Hofstetter[2], Tom DeGomez[1], Michael Wagner[2]

[1]University of Arizona, Flagstaff, Arizona, United States, [2]Northern Arizona University, Flagstaff, Arizona, United States

Introduction: Within log abiotic conditions can affect pine engraver, *Ips pini* (Say), reproductive success, and slash management techniques often aim at reducing abiotic conditions. In this study, I investigate the affect of light intensity on phloem temperature and moisture in logs of two diameters and subsequent effects on pine engraver reproduction.

Methods: Thirty cm length logs with diameters of 10 and 15 cm were cut, left in the field for natural colonization by *I pini*, and then placed in an open meadow and under shade clothes of two densities. Phloem temperature and moisture were recorded over the duration of the experiment and, at the end of the field experiment logs were dissected and galleries were measured to gauge reproductive success.

Results: As sunlight exposure increased phloem temperatures increased and potentially lethal temperatures were often reached in the high light exposure but seldom in the low light. Smaller diameter logs were drier than larger diameter logs. All logs dried due to time in the field but sunlight level did not affect desiccation rates. *Ips pini* preferred attacking larger logs and on the bottom aspect of logs.

Conclusions: Sunlight exposure had a significant effect on net reproductive success in smaller diameter logs, with very little net reproductive success in high sunlight logs, and the highest reproductive success found in low and medium sunlight smaller diameter logs. Management implications of these results are discussed.

Effects of light intensity on pine engraver reproduction in ponderosa pine slash in northern Arizona

Christopher Hayes[1], Richard Hofstetter[2], Tom DeGomez[1], Michael Wagner[2]

[1]Univesity of Arizona, Flagstaff, Arizona, United States, [2]Northern Arizona University, Flagstaff, Arizona, United States

Introduction: Within log abiotic conditions can affect pine engraver, *Ips pini* (Say), reproductive success, and slash management techniques often aim at reducing abiotic conditions. In this study, I investigate the affect of light intensity on phloem temperature and moisture in logs of two diameters and subsequent effects on pine engraver reproduction.

Methods: Thirty cm length logs with diameters of 10 and 15 cm were cut, left in the field for natural colonization by *I pini*, and then placed in an open meadow and under shade clothes of two densities. Phloem temperature and moisture were recorded over the duration of the experiment and, at the end of the field experiment logs were dissected and galleries were measured to gauge reproductive success.

Results: As sunlight exposure increased phloem temperatures increased and potentially lethal temperatures were often reached in the high light exposure but seldom in the low light. Smaller diameter logs were drier than larger diameter logs. All logs dried due to time in the field but sunlight level did not affect desiccation rates. *Ips pini* preferred attacking larger logs and on the bottom aspect of logs.

Conclusions: Sunlight exposure had a significant effect on net reproductive success in smaller diameter logs, with very little net reproductive success in high sunlight logs, and the highest reproductive success found in low and medium sunlight smaller diameter logs. Management implications of these results are discussed.

Species, morphology, and relationships of the African genus *Oreiscelio* Kieffer (Hymenoptera: Scelionidae)

Elijah Talamas, Norman Johnson

Ohio State University, Columbus, Ohio, United States

Oreiscelio Kieffer is a small group of egg parasitoids endemic to Africa and Madagascar. The genus is classified within the tribe Scelionini, the members of which, as far as is known, all attack the eggs of grasshoppers and locusts (Orthoptera: Acrididae). The generic and species concepts are reviewed and revised. The relationship of *Oreiscelio* with the closely related genera *Heptascelio*, from the Afrotropical and Oriental regions, and the Neotropical *Acanthoscelio* are analyzed. Additionally, morphological structures not previously known to exist within the Scelioninae are discussed. This work is part of the Platygastroidea Planetary Biodiversity Initiative, and the collaborative taxonomic methods developed for this international project are outlined.

Harmonia axyridis – top predator or invader? A critical examination

Pavel Kindlmann[1], Hironori Yasuda[2]

[1]Biodiversity Research Centre, Institute of Systems Biology and Ecology AS CR, Ceske Budejovice, Czech Republic, [2]Department of Agriculture, Yamagata University, Tsuruoka, Japan

Introduction: There is no doubt that *Harmonia axyridis* has recently been successful in suppressing many native species in North America and subsequently in Europe. It is not quite clear, however, what are the ecological traits that enabled it to be so successful. Critical studies are needed to evaluate, whether these traits include its ability to invade the aphid colony very quickly and efficiently, its competitive superiority, or something else.

Methods: Using published and some yet unpublished data, we critically examine all the above-mentioned possibilities. We assess the relative impacts of the interactions of *Coccinella septempunctata* (CS) and *Harmonia axyridis* (HA) on their larval survival, in particular cannibalism and intraguild predation (IGP) throughout larval development in relation to prey abundance. Then we compare incidences of cannibalism and IGP between HA and CS, and quantify attack and escape rates as the mechanisms, which possibly account for the difference in incidences of these interactions. Finally, we use key factor analysis to determine the critical life stages for CS and HA.

Results: HA is a strong competitor, which usually wins heterospecific contests. It arrives to the aphid colonies later than the other ladybird species, but is able to suppress larvae of other species. Its efficiency in conversion ladybird biomass in its own biomass is better than its efficiency in conversion aphids into its own biomass.

Conclusions: It seems that the most important factor that enabled the success HA in suppressing its intraguild competitors might be is evolutionary orientation into becoming a top predator.

Genetic based multi-species herbivore interactions in a eucalypt system

Julianne O'Reilly-Wapstra, Matthew Hamilton, Brad Potts

University of Tasmania, Hobart, Australia

Introduction: Plants are faced with attack from multiple herbivores during all life stages. The presence of multiple herbivore species may influence the direction and rate of evolutionary change in a plant species as a result of interacting selection pressures and in these instances, any evolutionary relationships that exist could do so in a diffuse rather than a pair-wise manner. *Eucalyptus globulus* is a dominant tree species in south eastern Australian forests and an important commercial species world-wide. It is browsed by multiple invertebrate and mammalian herbivores and in this paper we investigate the genetic correlations between *E. globulus* resistances to multiple herbivores.

Methods: Using a series of randomised common garden trials we assessed browsing damage by several invertebrate and mammalian herbivore species on up to 600 *E. globulus* families, comprising numerous provenances and geographically distinct races. We determined the genetic correlations between resistances to this array of herbivores.

Results: Results indicate clear genetic based resistance of *E. globulus* to numerous enemies, however, the genetic relationships in preference between these herbivores is varied. These complex genetic correlations match the display of defensive mechanisms used by *E. globulus* to deter its herbivores.

Conclusions: This paper provides insight into the complex evolutionary relationships that exist between a foundation species and its community of herbivores.

Genetic based multi-species herbivore interactions in a eucalypt system

Julianne O'Reilly-Wapstra, Matthew Hamilton, Brad Potts

University of Tasmania, Hobart, Australia

Introduction: Plants are faced with attack from multiple herbivores during all life stages. The presence of multiple herbivore species may influence the direction and rate of evolutionary change in a plant species as a result of interacting selection pressures and in these instances, any evolutionary relationships that exist could do so in a diffuse rather than a pair-wise manner. *Eucalyptus globulus* is a dominant tree species in south eastern Australian forests and an important commercial species world-wide. It is browsed by multiple invertebrate and mammalian herbivores and in this paper we investigate the genetic correlations between *E. globulus* resistances to multiple herbivores.

Methods: Using a series of randomised common garden trials we assessed browsing damage by several invertebrate and mammalian herbivore species on up to 600 *E. globulus* families, comprising numerous provenances and geographically distinct races. We determined the genetic correlations between resistances to this array of herbivores.

Results: Results indicate clear genetic based resistance of *E. globulus* to numerous enemies, however, the genetic relationships in preference between these herbivores is varied. These complex genetic correlations match the display of defensive mechanisms used by *E. globulus* to deter its herbivores.

Conclusions: This paper provides insight into the complex evolutionary relationships that exist between a foundation species and its community of herbivores.

Effectiveness of different *Bacillus thuringiensis* additives on the greater wax moth *Galleria mellonella* L. (Lepidoptera: Pyralidae) larval feeding

Rasool Zareie, Ali Asghar Pourmirza, Nouradin Shayesteh, Shahram Aramideh

Urmia University, Urmia, Islamic Republic of Iran

Introduction: *Bacillus thuringiensis* Berline is a highly efficacious bioinsecticide that use to control of lepidopteran larvae in the field conditions. Nowadays different additives use in the B.t preparations to increase its effectiveness.

Methods: In this experiment, feeding effect of pre-gelatinized corn starch as an encapsulation matrix, sugar beet molasses as a phagostimulant, henna as a synergist, and congo red as a UV screener were indicated on the fifth instars of the greater wax moth *Galleria mellonella* L**.** For this purpose, each additive was mixed with artificial diet.

Results: The means of larval weight increasing were 122, 102, 98, 48, and 14 mg (after a week) for molasses, pre- gelatinized corn starch, control (artificial diet), congo red, and henna respectively. The larval weight increasing was analyzed by randomized complete block design.

Conclusions: The results were significant and indicated that sugar beet molasses by increasing preparations palatability, acted as a feeding stimulant, while henna and congo red were anti-feedants

Effectiveness of different *Bacillus thuringiensis* additives on the greater wax moth *Galleria mellonella* L. (Lepidoptera: Pyralidae) larval feeding

Rasool Zareie, Ali Asghar Pourmirza, Nouradin Shayesteh, Shahram Aramideh

Urmia University, Urmia, Islamic Republic of Iran

Introduction: *Bacillus thuringiensis* Berline is a highly efficacious bioinsecticide that use to control of lepidopteran larvae in the field conditions. Nowadays different additives use in the B.t preparations to increase its effectiveness.

Methods: In this experiment, feeding effect of pre-gelatinized corn starch as an encapsulation matrix, sugar beet molasses as a phagostimulant, henna as a synergist, and congo red as a UV screener were indicated on the fifth instars of the greater wax moth *Galleria mellonella* L**.** For this purpose, each additive was mixed with artificial diet.

Results: The means of larval weight increasing were 122, 102, 98, 48, and 14 mg (after a week) for molasses, pre- gelatinized corn starch, control (artificial diet), congo red, and henna respectively. The larval weight increasing was analyzed by randomized complete block design.

Conclusions: The results were significant and indicated that sugar beet molasses by increasing preparations palatability, acted as a feeding stimulant, while henna and congo red were anti-feedants

Electron beam treatment as a phytosanitary measure for stored product pests

Nouraddin Shayesteh, Abbas Hosseinzadeh, Mohammad Reza Ardakani, Hamid Reza Zolfagharieh, Mohammad Babaii, Hadi Fatollahi, Hasan Zareshahi, Shahram Aramideh

Islamic Azad University, Mahabad, Israel

Introduction: Grains and pulses infested with insects such as *Tribolum castaneum* and *Plodia interponctella* may be disinfested with methyl bromide. Despite low residues, however, fumigation with MeBr may not to be desirable from the viewpoint of human health. More importantly, MeBr can deplet the ozon layer and on this basis it will be phased out for most uses. Development of an alternative treatment is urgently needed.

Methods: Developmental stages of two stored-product insect pests **viz.** *Tribolum castaneum* and *Plodia interponctella* were exposed directly to electrons using Rhodetron accelerator(tt200). Exposure doses on all stages were 0, 270, 380, 520, 700, 840, 1640, 2020, 2400, 2750 and 3130 Gy.

Results: The results of these studies indicate that inhibiting doses for eggs, larval, pupal and adults of *Tribolum castaneum* were 840, 380, 2020 and 3130Gy respectively. These criteria for *Plodia interponctella* were 840, 520, 1640 and 3130 respectively. Due to results eggs, larval and adults of *Tribolum castaneum* were sensitive than *Plodia interponctella*.

Conclusions: We suggest that it is possible to disinfest grains contaminated with these insects using high energy electrons at 3130Gy.

Lower herbivory in diverse forests due to semiochemical diversity? Tests in an artificially mixed forest

Hervé Jactel[2], Göran Birgersson[1], Fredrik Schlyter[1]

[1]Chemical Ecology, Dept. Plant Prot., SLU, Alnarp, Sweden, [2]Laboratory of Forest Entomology & Biodiversity, INRA, Cestas, Bordeaux, France

Introduction: The *semiochemical diversity hypothesis* (SDH), a new dimension and functional aspect of biodiversity, postulates a reduced searching efficiency of specialist herbivores in the face of non-host plant volatiles. A prediction from the SDH is that conifer specialists should avoid mixed habitats with non-host volatiles (NHV) from angiosperms like *Betula*.

Experimentally, however, tests have only shown modulation (inhibition) of attraction behaviour to point sources (traps) or their vicinity (2 –4m), mainly in conifer bark beetles.

Methods and Results: We show a population effect of density reduction in a moth on habitat scale by the EAD-active methyl salicylate, a synthetic birch volatile (no attractant sources involved). A replicated dose-response study (3 doses, >600 trees) at a scale of 50m pine forest edge sections show a dose-dependent reduction of larval winter nests of pine processionary moth (*Thaumetopoea pityocampa*). Mate location was similarly affected, as measured by male catches in pheromone traps.

Conclusions: Our data support a reduction of efficiency in both host and mate location by NHV. This is evidence for the SDH at the habitat-level in forest insects. However, the identities of chemical cues used by the conifer bark beetles and the pine moth to avoid angiosperms seem to differ drastically.

Multi-scale effects of humans on forest insect-microbe symbioses

Diana Six[1], Bernard Slippers[2]

[1]University of Montana, Missoula, MT, United States, [2]Forestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, South Africa

Humans exert considerable influence on forest ecosystems, both directly and indirectly. Direct effects occur through use for habitation, wildlife and biodiversity preserves, recreation, spiritual connections, and to extract wood, herbs, medicines, and food. Many of earth's natural forests have been cleared for human settlement, livestock grazing, fuel wood, and cropland. In other cases, afforestation efforts have attempted to restore croplands back to native forest conditions or to initiate plantations of exotic trees on previously un-forested lands to provide critical sources of wood and pulp. Indirect effects are also diverse and come through such varied sources as adjacent land use types, pollution drift, and climate change. Both direct and indirect effects affect forests at multiple scales on a continuum from the individual tree to the globe. While anthropogenic effects are often the focus of research on impacts on individual species, especially threatened or endangered species, or on economically important pests, little focus has been directed on investigating effects on outcomes of interactions among organisms, and fewer still on effects on symbioses. Many insects, for example, are drivers of forest structure, composition and function. These same insects are mostly, if not all, involved in symbioses with microbes that facilitate their ability to use trees as a resource. The potential for anthropogenic activities to enhance, suppress, or entirely decouple such symbioses across multiple scales should be of considerable concern.

The activity and effects of Indoxacarb on subterranean termites

Michael Rust[1], Raj Saran[2]

[1]University of California Riverside, Riverside, CA, United States, [2]MGK Corporation, Minneapolis, MN, United States

The novel semicarbazone insecticide, indoxacarb, applied to soils is active against the western subterranean termite, *Reticulitermes hesperus* Banks. When applied topically to termites, it is extremely toxic to termites with an LD_{50} of 1.6 ng/termite. When termites are confined to treated soils, brief 1-hour exposures of 100- and 200-ppm indoxacarb killed 100% of the workers in 7 days. The indoxacarb causes a delayed toxicity. Soils treated at ≥ 25 ppm prevent tunneling and kill 100% of the workers within 5 days. Termites exposed to 10 ppm indoxacarb tunnel < 0.3 cm, but some termites survive at this low dose. When donor termites were exposed to 100 and 200 ppm indoxacarb, they were killed within 7 days. Unexposed recipient termites held with the donors were also killed with 7 days. Indoxacarb horizontally transferred from donors to recipients. The delayed toxicity of indoxacarb assists in this horizontal transfer.

The scarab digestive tract as a target for microbial pathogens

Drion Boucias, Regina Kleespie, Trevor Jackson

[1]University of Florida, Florida, United States, [2]AgResearch Limited, Lincoln, New Zealand

Introduction: Microscopic studies were conducted to examine the cytological features of the various tissue, cellular, and sub-cellular domains comprising the alimentary tract of the root-feeding scarab *Costelytra zealandica*.

Methods: Digestive tracts were dissected from third instar larvae, placed in fixative, dehydrated, and either embedded in paraffin, in plastic resin, or subjected to critical point drying (CPD). Stained paraffin and thick sections were examined with light microscopy, thin sections were examined with TEM, and coated CPD dissected tissue preparations examined with SEM. Digital images were prepared and processed using conventional morphometric imaging software.

Results: The various imaging technologies provided an overview of the topography the alimentary tract, and detailed the different cells and structures that comprised the foregut, midgut, and hindgut regions. The foregut was relatively short and possessed a bulb-like crop whereas the midgut tissue extended throughout the entire body length. This tissue, compartmentalized with clusters of secretory or assimilatory cell domains, contained a well-developed fishnet-type peritrophic membrane. The well-muscled pyloric sphincter was designed to pull the peritrophic membrane posteriorly moving the food bolus into the hindgut. The scarab hindgut contained a unique fermentation sac that provided harborage to a plethora of microbes. The rectum and associated cryptonephridial complex was connected to the malpighean tubules.

Conclusions: The digestive tract has multiple unique morphological adaptations designed for digestion of plant roots. The different tissues contained unique domains that play a key role in the susceptibility/resistance of this insect to soil-borne microbes.

The physiological integration of simultaneously selected life history traits

Goggy Davidowitz[1], Derek Roff[2], Frederik Nijhout[3]

[1]University of Arizona, Tucson, Arizona, United States, [2]UC Riverside, Riverside, California, United States, [3]Duke University, Durham, North Carolina, United States

Body size and development time are complex, whole-organism traits, that require integration at multiple levels. Integration at the level of the whole organism is mediated by the endocrine system. We present a physiological / endocrine mechanism that regulates over 95% of the variation in body size and development time in the tobacco hornworm: growth rate (GR), the critical weight (CW) that measures the timing of the onset of the cessation of juvenile hormone secretion (which initiates the processes leading to pupation), and the time interval between attainment of the critical weight and secretion of ecdysteroids (the interval to cessation of growth, ICG). Knowledge of the physiological mechanism allows us to make explicit predictions, based on physiological first principles, as to how these life history traits should respond to simultaneous selection. Initial results support 11 of our 12 *a priori* predictions. When the two life history traits are selected in the same direction (both upwards or both downwards), the response to selection is determined primarily by the timing of the two hormonal events (CW and ICG). When the two life history traits are selected in opposite directions (one up, the other down) the response to selection is determined largely by growth rate (GR). These results indicate that, under simultaneous selection, the integration of complex traits differs depending on the direction of selection.

The Southern African Butterfly Conservation Assessment (SABCA) takes flight

Silvia Mecenero

Animal Demography Unit, Dept. Zoology, University of Cape Town, Cape Town, South Africa

The Southern African Butterfly Conservation Assessment (SABCA) is a four year project aimed at increasing understanding of the distribution and diversity of butterflies in the atlas region (South Africa, Lesotho and Swaziland), thereby contributing towards effective conservation planning and management. SABCA is a three-way partnership between the South African National Biodiversity Institute, the Lepidopterists' Society of Africa (LepSoc) and the Animal Demography Unit (University of Cape Town).

The project comprises three main activities: creating a comprehensive database of existing records in museum and private collections, field surveys prioritised in areas identified by gap analysis, and an online virtual museum which accepts photographic specimens from the public.

Almost all data in South African institutions have been digitised (~ 120 000 records). The data is reformatted, vetted and geo-referenced before being uploaded into the SABCA database. About 250 000 records reside with LepSoc members. Field surveys have begun in most provinces, and progress in filling in gaps is being made. The virtual museum has attracted great public interest, about 200 photographic submissions are received every month. Both the field surveys and virtual museum have made important new observations on threatened species and range expansions.

Data collected from these three activities will be used to assess the conservation status of each butterfly species according to the IUCN criteria. An updated Red Data Book and atlas will be produced to inform conservation planning, decision making and policy development for butterflies. The resultant project outputs will ultimately contribute towards understanding ecosystem health and climate change.

Species File Software and the Orthoptera Species File

David Eades[1], Daniel Otte[2], Piotr Naskrecki[3]

[1]Illinois Natural History Survey, Champaign, Illinois, United States, [2]Academy of Natural Sciences, Philadelphia, Pennsylvania, United States, [3]Conservation International, Cambridge, Massachusetts, United States

Species File Software was first developed as the computer programming needed to manage the Orthoptera Species File Online. It is now a set of programs that manage databases and websites for all the orders of Polyneoptera and for a few groups outside of Polyneoptera. A database is edited over the Internet, which allows multiple authors to share in managing the data. In addition to the usual nomenclatural information, databases may contain specimen level data and keys (both dichotomous and matrix-based). Integration of these items in a single database facilitates keeping current with new research. The program screens data as it is entered and blocks many errors including changes that would violate the International Code of Zoological Nomenclature. Users may indicate which kinds of data are of interest, and pages will then display only the kinds of data selected. Data from species files is passed on to Species 2000 and other data aggregators. Work is in progress to exchange data with ZooBank. An endowment that supports eight persons assures continuing development in the future. The software is useful for any group subject to the Zoological Code and is available free.

Fly as cancer model? Genomic analysis of Drosophila's hypoxia tolerance

J.M. Gomez[1], T. Tomita[2], N.M. Romero[1], K. Clough-Gorr[3], M. Gassmann[4], H.F. Bunn[5], P. Wappner[1], T. Gorr[4]

[1]Instituto Leloir, Universidad de Buenos Aires, Buenos Aires, Argentina, [2]National Cancer Institute, National Institutes of Health, Bethesda, Maryland, United States, [3]University Hospital Bern and Spital Netz Bern Ziegler, University of Bern, Bern, Switzerland, [4]Institute of Veterinary Physiology, Vetsuisse Faculty and Zurich Center for Integrative Human Physiology, Zurich, Switzerland, [5]Department of Medicine/Hematology, Brigham and Women's Hospital, Harvard Medical School, Boston, United States

To understand, on a genomic level, the remarkable ability of Drosophila to survive severe and prolonged deprivations of oxygen, transcriptome profiles of S2 cells from late stage fly embryos were recorded through microarray and Northern blot surveys as a function of graded hypoxia. Both, fruitflies and S2 cells express with the hypoxia-inducible factor (HIF) the key regulator protein for survival and adaptation during oxygen deprivation. When flies are exposed to a severe O_2 shortage they will switch from tracheal defenses to a reduction of metabolic activities in order to acquire a new energy steady state (hypometabolism) and, as such, resemble the angiogenic-to-quiescence transition of many hypoxic tumors.

Increasing severity of the hypoxic stress was reflected in rising numbers and magnitudes of hypoxia-responsive gene regulations. Entrance of S2 cells into the ultimate hypometabolic defense mode saw marked transcriptional regulations of 'hypometabolic factor (HMF)' candidate genes, in correlation with a progressive reduction of ATP-costly biochemical functions such as protein or DNA synthesis and cell cycle progression. The biological role of several of these protein synthesis inhibiting and cell cycle arresting molecules is currently being studied by collaborative in vitro and transgenic approaches. To this end, we are focusing our investigations on the highly hypoxia inducible *Drosophila* gene Thor, a single-copy homolog of the mammalian 4E-binding protein (4E-Bp) family that all act as repressor of the rate limiting mRNA translation initiation factor 4E. Seemingly mimicked in malignancy, 4E-Bp1 genes/proteins were also found to be induced and/or activated by low oxygen in several human cancer cell lines. In support of a pro-survival role of inhibited protein synthesis and conserved ATP resources from "critters to cancer", Thor null fly mutants show limited adaptability and slowed recovery, while 4E-Bp1 knockdown cancer cells died off in much greater proportion, in response to severe hypoxia when compared with wildtype controls. We are currently analyzing the energetic consequences of 4E-Bp/Thor manipulations. We will further apply expression interference studies to other HMF factors in both fly and cancer systems. That way, we hope to raise the susceptibility of these cells towards hypoxic stress and conventional treatment modalities by virtue of blocking their hypometabolic defenses and to promote fly as a metabolic cancer model.

Bracovirus mediated evasion of the insect immune response

Michael Strand

University of Georgia, Athens, Georgia, United States

Insects rely upon a well-coordinated innate immune system for protection against invading pathogens and parasites. Larger, multicellular parasites are usually killed by encapsulation which involves attachment of multiple layers of hemocytes to the foreign target. Smaller pathogens, in contrast, are killed by a combination of hemocyte-mediated phagocytosis and humoral defenses. Despite the fundamental importance of these responses, our understanding of their regulation in relation to the counter strategies pathogens use to evade host defense responses is limited. Viruses in the family Polydnaviridae are symbiotically associated with parasitoid wasps and are among the most virulent immunosuppressive pathogens of insects. Polydnaviruses are divided into two genera, bracoviruses (BVs) and ichnoviruses (IVs), on the basis of their association with wasps in the families Braconidae and Ichneumonidae. Functional analysis of *Microplitis demolitor* bracovirus (MdBV) has also identified several key genes involved in immunosuppression of encapsulation, phagocytosis and the phenoloxidase cascade. Notably, most of these virulence factors target signaling pathways rather than effector molecules themselves. Overall, current results provide important insight on the evolution of polydnaviruses and identify key virulence determinants underlying immunosuppression.

The use of life-shortening *Wolbachia* strains to reduce dengue transmission by *Aedes aegypti*

Scott L. O'Neill

The University of Queensland, Brisbane, Queensland, Australia

Insect age is a critical factor influencing the dynamics of a range of insect transmitted diseases. Its importance is linked to the extrinsic incubation period (EIP) of a given pathogen within the vector. Since the EIP of many pathogens is quite long relative to the natural insect lifespan only old insects are of epidemiological importance. We have successfully transferred life-shortening *Wolbachia* symbionts into *Aedes aegypti*, the primary dengue vector that halve adult lifespan in the laboratory. These bacteria are maternally inherited at high frequency and induce complete cytoplasmic incompatibility which may facilitate their natural spread into field populations. Interestingly the infection appears to influence the ability of these mosquitoes to successfully utilize the blood of certain hosts for egg production. Laboratory data suggest that this approach may be able to significantly reduce dengue transmission potential of *Aedes* populations. This potential will soon be evaluated in a field cage setting in Nth Queensland.

Biosystematics and Evolution of true land bugs (Insecta: Heteroptera)

M. Javahery

McGill University, Ste.Anne de Bellevue, QC, Canada

A comparative study has been done of the morphology and taxonomy of male and female reproductive system, development, and characteristics of eggs in representatives of five families in infraorder of Cimicomorpha and 11 families in infraorder of Pentatomomorpha. A total of 48 genera and 77 species were studied. They included examples of Miridae, Nabidae, Phymatidae, Reduviidae, Tingidae (Cimicomorpha), and Acanthosomatidae, Alydidae, Aradidae, Coreidae, Cydnidae, Lygaeidae, Pentatomidae, Pyrhocoridae, Scutelleridae, and Thyreocoridae, (Pentatomomorpha). Embryonic development was monitored by dissection of eggs in isotonic NaCl solution. The reproductive systems of both sexes were taken from fresh material and observation made in 50% alcohol. Materials were collected from southeastern Canada, as well as Palearctic regions. The studies were based on characters of true phylogenetic value of eggs (shape, chorion sculpture, presence of a true operculum, the number and position as well as shape of the micropilar processes, and shape of egg-burster) and the mechanisms of egg eclosion, morphology of both males and females reproductive system. The phylogram and distribution in superfamily Pentatomoidea indicate that the genera *Elasmucha* and *Sehirus* are primitive and they are considered the probable outgroups. The data collected supports the suggestion that various shapes of eggs in the above families have evolved independently, and along different pathways from an ovoid ancestral egg.

Pathogenicity of *Thripinema fuscum* Tipping & Nguyen (Tylenchida: Allantonematidae) infecting *Frankliniella fusca* (Hinds) (Thysanoptera: Thripidae)

Kelly Dunford[1], James Becnel[2], Joseph Funderburk[3], Drion Boucias[1]

[1]University of Florida, Gainesville, Florida, United States, [2]USDA/ARS, Gainesville, Florida, United States, [3]University of Florida, Quincy, Florida, United States

The insect parasitic nematode *Thripinema fuscum* Tipping & Nguyen (Tylenchida: Allantonematidae) is a key regulator of *Frankliniella fusca* (Hinds) (Thysanoptera: Thripidae) in agricultural peanut across the southeastern United States. Parasitism by *T. fuscum* causes a significant reduction in both the feeding and fecundity rates of adult female thrips, and as a result, reduces the vector competence (acquisition and transmission) of *F. fusca* to spread Tomato spotted wilt virus (Bunyaviridae: Tospovirus). The potential of *T. fuscum* to act as a biological control agent of *F. fusca* has been recognized; however, very few studies have investigated the pathological changes induced by the entomogenous parasite. Future elucidation of the mechanisms responsible for shutting off egg production in parasitized thrips may provide novel avenues for regulating the intrinsic rate of increase of this pest insect. Understanding the mechanism(s) leading to reduced Tospovirus competency in parasitized thrips may also provide targets that suppress disease spread. To determine how the parasitic *T. fuscum* modulates the physiology of the thrips host and how such alterations influence vector competence, the impact of *T. fuscum* on host thrips was examined using a combination of light and electron microscopy. Changes to *F. fusca* tissues affected by Thripinema invasion and replication were recorded and a possible explanation of the cause (mechanical vs. chemical) given.

An EST database for the lepidopteran forest insect, *Choristoneura fumiferana*

Lan Li[1], Tim Ladd[1], Sichun Zheng[3], Peter Kell[2], Basil Arif[1], Arthur Retnakaran[1], Daniel Doucet[1], David Basham[1], Qili Feng[1]

[1]Great Lakes Forestry Centre, Sault Ste. Marie, Ontario,, Canada, [2]Department of Molecular and Cellular Biology, University of Guelph, Guelph, Ontario, Canada, [3]School of Life Sciences, South China Normal University, Guangzhou, Guangdong, China

The Lepidoptera *Choristoneura fumiferana* is one of the most widely distributed and destructive defoliators of forests in North America. An expressed sequence tag (EST) project has been initiated three years ago as the first step to understand the genomics and transcriptomics and to search for possible gene targets for biocontrol strategies. The EST database reported here is the first result from this EST project. The database contains 63,203 high quality ESTs generated from cDNA libraries of the epidermis, fat body and midguts of the larvae molting from the 5th to 6th instar stage. These ESTs were assembled into 15,239 putative transcripts. Annotation of these putative transcripts was conducted against NCBI databases and Swiss-Prot/TrEMBL protein database. Information of the annotated ESTs sequences, gene description and gene ontology in molecular function, biological process and cellular component is available to be retrieved by users using blast, keyword or clone ID search. The database, which is publicly available from URL: http://www.pestgenomics.org/database.htm, provides an informative platform for the scientific community to conduct gene cloning and identification of this forest insect and genomic comparison with other insects.

Implications of international sanitary and phytosanitary regulations for the southern African citrus industry

Vaughan Hattingh, Elma Carstens

Citrus Research International at Universtiy of Stellenbosch, Stellenbosch, South Africa

The southern African citrus industry is the second largest fresh citrus export industry in the world and depends on access to international markets. The industry is a major source of foreign earnings, provides employment for a large labour force and is socio-economically important to the southern African region. Agriculture's importance as an export industry extends to other fresh produce industries in southern Africa and further through Africa. Dismantling tariff and subsidy barriers to trade prospectively provides opportunity for Africa to strengthen its agriculture and its participation in international trade. However, recent intensification of restrictions on international fresh produce trade, in the form of sanitary and phytosanitary (SPS) regulations, restricts these opportunities. The International Plant Protection Convention stipulates that phytosanitary regulations require appropriate technical justification, to avoid unnecessary disruption of trade. This provides an advantage to nations with access to the scientific support and resources required to challenge or defend phytosanitary regulations, but Africa's access to such resources is limited. SPS obstacles to retention and expansion of the southern African citrus industry's global export status are addressed by an industry-funded research portfolio. The research includes projects on bio-security, control and eradication strategies, pest risk assessment and risk mitigation measures and focuses on fruit flies, certain lepidopteran pests, mealybugs and disease vectors. Closer collaboration between trading nations with the objective of facilitating trade, while managing the risk of new pest incursions, rather than maintaining protectionism, has the potential to alleviate many of the constraints imposed by the increased focus on SPS issues.

A new artificial diet for the sugarcane stalk borer *Eldana saccharina* Walker (Lepidoptera: Pyralidae) includes an endophytic fungus and excludes dicotyledonous plant material

Sharon McFarlane, Stuart Rutherford

South African Sugarcane Research Institute, Mount Edgecombe 4300, South Africa

In the early 1980's a chickpea based diet was developed to support the production of large numbers of *E. saccharina* eggs for sugarcane resistance screening, and enough larvae and pupae to support parasitoid rearing for field release. More recently research into the application of the sterile insect technique (SIT) to *E. saccharina* control depends on the production of good quality irradiated male insects that are released in large numbers into target wild populations. Larval diet can have a major impact on the development, survival, and reproductive success of these insects. For the purpose of SIT, the chickpea diet formulation produces too variable a product, with many larvae remaining at pupal harvest.

Recent West African evidence has shown that *Fusarium verticillioides,* when present epiphytically or endophytically in maize, can positively affect survival of larvae and their development. A survey of wild host plant species in KwaZulu-Natal for fungal endophytes has revealed that *Fusarium* is isolated more frequently from these plants than are other fungi. Bioassays were developed to screen isolates for potential mutualistic interaction with *E. saccharina*. Attenuated isolates were incorporated into test artificial diets and isolates were determined to be beneficial, antagonistic or neutral in terms of larval survival and development. The most beneficial, an isolate of *F. pseudonygamai*, greatly increased survival and growth when incorporated into diet as a three-week culture on rice. In the final new diet monocotyledonous plant material comprised of whole-wheat flour and dried sugarcane powder in addition to fermented rice. Chickpea, the main protein source in the old diet, was replaced by a combination of non-fat milk powder and spray dried whole egg powder. This was done in consideration of the "chemical legacy hypothesis" which suggests that the response of adult parasitoids to the frass of their host larvae depends partly on a learning process involving plant cues. In other words, if field released parasitoids are to have a greater probability of success, an artificial host diet should contain similar plant cues as would be found in the field. The development of the new diet was an iterative process during which alternative genetic modification strategies for the control of *E. saccharina* in sugarcane became apparent.

Is *Eldana saccharina* Walker (Lepidoptera: Pyralidae) infected by *Wolbachia*, anywhere in Africa?

Stuart Rutherford[1], Des Conlong[2], Deborah Sweby[1]

[1]South African Sugarcane Research Institute, PBag X02, Mount Edgecombe 4300, South Africa, [2]Department of Conservation Ecology and Entomology, Stellenbosch University, Private Bag X01, Matieland, 7602, South Africa

Bacteria belonging to the genus *Wolbachia* are found in the reproductive tissues of a wide range of arthropod species and are associated with a variety of reproductive anomalies. The importance of this phenomenon is as a potential component of population control since infection by *Wolbachia* usually results in either a disruption of the sex ratio of the insect population by male-killing, or cytoplasmic incompatibility between differently infected individuals. In the latter case it is thought that infection can contribute towards speciation or at least to the maintenance of reproductive barriers between diverged lineages.

According to a recent phylogenetic study, African *E. saccharina* separate into three distinct groups (West and Southern African and an Ethiopian group), which also appear to have different preferred host plants, different guilds of parasitoids and slightly different behaviours. These guilds of parasitoids and *E. saccharina* populations overlap in Uganda (East Africa).

At the outset of this study it was not known whether *Wolbachia* infects *E. saccharina* in wild-host plant populations anywhere in Africa. A sampling strategy was developed based on the hypothesis that specimens, from the southern most limit of *E. saccharina* distribution in KwaZulu-Natal South Africa, would be least likely to be infected. Conversely, specimens from Uganda, the apparent centre of diversity, would be more likely to be infected. Detection of *Wolbachia* infection has been routinely conducted by allele-specific polymerase chain reaction (PCR). In a preliminary study *Wolbachia* has been detected in East African specimens using *Wolbachia*-specific primers targeting four genes. Amplified PCR fragments are of expected sizes and sequencing confirms that *Wolbachia* is present. Here we report on the extent of *Wolbachia* infection in *E. saccharina* specimens from West Africa (Benin), East Africa (Uganda, Kenya and Ethiopia) and Southern Africa (Mozambique and South Africa).

Biological and habitat interventions for Integrated Pest Management systems

Des Conlong[2], Stuart Rutherford[1]

[1]South African Sugarcane Research Institute, Mount Edgecombe, KwaZulu-Natal, South Africa, [2]Departement of Conservation Ecology and Entomology, Stellenbosch University, Stellenbosch, South Africa

Conventional Integrated Pest Management (IPM) systems have concentrated on controlling pests through informed use of cultural and biological control and host plant resistance characteristics to minimise pesticide interventions. The basic foundation of successful IPM systems is a thorough knowledge of the target pest's life cycle, and its ecological and behavioural interactions with the environment and natural controlling factors in both its indigenous and crop habitats. Through this basic knowledge, a number of new interventions can be added to the IPM arsenal. These include management of the habitat to make the crop less suitable for colonisation by potential pests, and to increase natural enemy foraging and abundance in the crop habitat, Thus increasing the efficacy of conservation, inoculative and augmentative biological control. In addition, more is known about the impact of plant and insect pathogens and symbionts on target pest populations by making potential host plants more or less suitable for colonisation, thus adding a fourth trophic level to agro-ecosystem dynamics. Furthermore, the impact of these on fertility and offspring sex ratios (eg. *Wolbachia* isolates in pest and natural enemy populations) makes their exploitation, in combination with interventions such as Sterile Insect Technology (SIT), a real and practical possibility. Modern IPM is thus not only about insect/plant interactions, it is about holistic agro-ecosystem interactions, in which knowledge about plants, pathogens, endophytes, symbionts and insects are all combined to provide effective crop protection in an area-wide and environmentally friendly manner.

Changes to citrus IPM strategy in southern Africa

Tim Grout[1], Hendrik Hofmeyr[2], Sean Moore[3]

[1]Citrus Research International, Nelspruit, Mpumalanga, South Africa, [2]Citrus Research International, Citrusdal, Western Cape, South Africa, [3]Citrus Research International, Port Elizabeth, Eastern Cape, South Africa

Introduction: The climate in the citrus-production regions of southern Africa supports a wide variety of pests and their natural enemies. Until the mid-1990s, most exporting citrus growers practiced a form of IPM that relied on the conservation of wild natural enemies through the judicious use of pesticides. Depending on the amount of chemical intervention required for vectors and cosmetic pests, growers were variably successful in keeping key pests such as red scale (*Aonidiella aurantii*) and citrus mealybug (*Planococcus citril)* under biological control. False codling moth (FCM) (*Thaumatotibia leucotreta*) was largely controlled with the use of chitin synthesis inhibitors (CSIs) and a few insectaries provided natural enemies for augmentation purposes that were utilised by some growers.

Changes: Since 2000, increasing market competition has led to lower tolerances for phytosanitary pests that are below levels required to sustain biological control. Simultaneously, the number of pesticides available for use on export fruit has declined. These pressures, together with an increase in resistance to CSIs in FCM, have led to the commercial use of a granulovirus, the introduction of Sterile Insect Releases (SIR) and mating disruption, for the control of FCM. The availability of inexpensive generic imidacloprid formulations has increased the biorational use of this product as a soil drench for the control of red scale and suppression of mealybug. This treatment, or stem applications of acetamiprid or methamidophos, are used for the control of citrus psylla (*Trioza erytreae*). Buprofezin and/or parasitoid releases are being used for citrus mealybug control, while generic abamectin formulations provide for inexpensive control of *Scirtothrips aurantii* and several mites. Bait stations are increasingly being used for fruit fly control.

Conclusion: Biorational control strategies such as microbial control, SIR, mating disruption, attract-and-kill and soil- and stem-applied systemics now define citrus IPM in South Africa.

Regulation of humidity in honeybee hives

Michael B Ellis, Sue W Nicolson, Robin M Crewe, Vincent Dietemann

University of Pretoria, Pretoria, South Africa

Introduction: Many insects are able to modify adverse microclimatic conditions rather than attempting to evade or tolerate them. Honeybees (*Apis mellifera)* are able to regulate the temperature in their nest to optimise brood development. Survival of brood is also affected by humidity. However, it is not known whether honeybees regulate this parameter. We investigated how nest material and behaviour of the workers influence humidity.

Methods: We determined the water absorption capacity of comb containing the hygroscopic cocoons spun by larvae within their cells. We also monitored the behaviour of workers exposed to different humidities in a set of interconnected linearly arranged chambers.

Results: Comb containing cocoons absorbs a mean of 11.1% of its mass in water. Honeybee workers exhibit a mild hygropreference for approximately 75% RH in the absence of brood, and this preference is further weakened by the presence of brood. Fanning behaviour of workers is significantly increased by a rise in humidity.

Conclusions: Our results indicate that the buffering properties of cocoons could ensure a stable high humidity within the cell, thus favouring brood development. The mild hygropreference of workers can be explained if their dispersal throughout a humidity gradient enables them to actively counteract sub-optimal conditions where they occur. Indeed, through fanning behaviour, workers can expel humid air, thus decreasing humidity for effective nectar evaporation. We obtained evidence that humidity in honeybee hives is affected by both passive and active mechanisms allowing for the maintenance of distinct optima in various parts of the hive.

Extraocular photoreceptors and frontal grooves in Criocerinae (Coleoptera: Chrysomelidae)

Michael Schmitt, Uta Heidenreich

Zoologisches Forschungsmuseum Alexander Koenig, Bonn, Germany

Introduction: Extraocular photoreceptors are described for several holometabolous insects, including some Chrysomelidae. They are persisting larval stemmata and could play a part in triggering circadian rhythms. Presence of such “brain eyes” in leaf beetles other than *Leptinotarsa decemlineata* has not been shown before. Since in two chrysomelid subfamilies (Criocerinae and Sagrinae) conspicuous frontal grooves are characteristic, but no function is known to date, we examined if they work as gates for incoming light.

Methods: Isolated brains of 5 leaf beetle species and 4 hemimetabolous insects have been checked under a dissecting microscope. Ultrathin sections were made of brains of *Lilioceris merdigera* and investigated under TEM. Head capsules of 12 leaf beetle species have been dissected and photographed under transillumination.

Results: The frontal grooves were permeable for long-waved light in two criocerine species with black heads (*Lilioceris lilii* and *Crioceris asparagi*). In all species with lighter head capsules the sulci appeared darker than the rest of the head. Extraocular photoreceptors were found in all species of leaf beetles, but not so in all hemimetabolous insects. Under TEM, rhabdomeres and screening pigments could be shown.

Conclusion: All beetles studied have „brain eyes“, which are persisting larval stemmata. Their ultrastructure is exactly that of an ocular retinula. In species with black pigmented head capsules, the frontal grooves can act as light gates. However, since these grooves transmit less light than the remaining head in species with lighter head capsules, the evolutionarily primary role of these grooves cannot have been light transmission.

Managing termite pests in Australia: The art of combining environmental sensitivities and economic rationalities

Theodore Evans

Commonwealth Scientific and Industrial Research Organisation, Canberra, ACT, Australia

Australia has around 20 species of wood-eating termites of economic significance, which are found all over Australia; with higher risk of termite infestation in the 30% of the country located in the tropics. There has been an almost 100 year continuous history of research into termite control and management in Australia; these methods have changed considerably in this time. Currently, there are many pest control methods; Australia now has one of the most diversified termite pest control markets in the world. This diversity is due, in part, to the readiness of pest control operators (PCOs) to change suppliers and methods to achieve most rapid control. This diversity is also due to environmental and economic concerns; in particular the potential toxic side effects of insecticides, and the availability of cheaper, generic insecticides. Termite pest control methods can be classified as either preventative or remedial treatments; most attempt to do both. These methods can also be classified according to the method used: physical, chemical or biological. Some methods were developed in other countries, usually by multinational companies, and so will be known elsewhere, but have required modification to Australian conditions. Other methods were developed in Australia, often by builders or PCOs, and so are not widespread. At this point in time in Australia, there no method or product dominates the pest control market, for several reasons: (1) all methods and products are effective; (2) methods can vary in ease of use and efficiency according to local conditions; (3) customer preferences.

Possibilities for biological control of the invasive spider mite *Tetranychus evansi* in Africa

David Bugeme[1], Knapp Markus[1], Nguya Maniania[1], Vitalis Wekesa[2], Imeuda Furtado[2], Gilberto de Moraes[2]

[1]ICIPE-African Insect Science for Food and Health, Nairobi, Kenya, [2]Departamento de Entomologia, Fitopatologia e Zoologia Agricola, Esalq, Universidade de Sao Paulo, Sao Paulo, Brazil

Introduction: The spider mite *Tetranychus evansi* is an invasive pest of tomatoes in Africa. It is causing severe yield losses in small-holder production systems. No effective natural enemies are present in the field in Africa.

Methods: Surveys for natural enemies of *T. evansi* were conducted in South-America for introduction into Africa. Elsewhere, the entomopathogenic fungi *Beauveria bassiana* and *Metarhizium anisopliae* isolates were investigated for their potential in the control of *T. evansi* in the laboratory, greenhouse and in the field.

Results: The predatory mite *Phytoseiulus longipes* was the most promising candidate and was imported into Kenya after extensive laboratory and greenhouse testing. A pilot release experiment did not lead to establishment in Kenya.

On another hand, in the laboratory *B. bassiana* and *M. anisopliae* isolates infested *T. evansi*, with the most pathogenic isolate inducing a mortality of up to 95.5%. In the greenhouse, fungal isolates in both water and oil formulations significantly reduced the population density of mites on tomato leaves, but conidia formulated in oil outperformed the ones formulated in water. Similar results were observed in the field at 3 weeks post-spraying. However, at 5 weeks post-spraying there were no significant differences between the two fungal formulations and the synthetic acaricide.

Conclusions: Further releases and trials are required to make a judgement about the potential of *P. longipes* as a classical biological control agent for *T. evansi*. However, this study underlines the potential of the *M. anisopliae* isolate ICIPE78 as an alternative to acaricides for *T. evansi* management.

The role of GBIF's ECAT programme in access to taxon names

David Remsen[1], Christopher Lyal[2]

[1]Global Biodiversity Information Facility, Copenhagen, Denmark, [2]The Natural History Museum, London, United Kingdom

Attempts to mobilize and serve biodiversity data are significantly hampered by retrieval impediments due to the 'names problem' in biology. This results from taxonomic and nomenclatural changes impacting on the names of species, imperfect penetration of those changes to the non-taxonomist users of the names, multiple co-occurring taxonomic views, and difficulty in mapping concepts and names used in one source to those employed in another. All biodiversity data mobilization initiatives find themselves challenged to reconcile problems of synonymy, orthography, and homonymy as it relates to basic search and retrieval of species information. This is particularly so for those operating at large scales, such as GBIF and the Biodiversity Heritage Library, where records number in the tens of millions, comprise a vast array of sources, and span the full taxonomic and temporal range of post-Linnaean biology. The GBIF ECAT program seeks to collectively access taxonomic and nomenclatural authority files and redirect their content into an applied informatics tool to address these access impediments.

Completing the Catalogue of Life for insects

Christopher Lyal

The Natural History Museum, London, United Kingdom

Over the past few years there has been an explosion in the number of databases and lists of insect species names being created and made available on the web and otherwise. Some have been presented in such a way that they can be accessed simultaneously through web portals, allowing searching of multiple datasets. Such portals include the major initiatives Species 2000 and ITIS, working together as the 'Catalogue of Life' and providing a single authoritative taxonomic view of species content to the Global Biodiversity Information Facility, GBIF. Currently the Catalogue of Life contains over 1 million species, but is by no means complete. A grant application is being presented this year to facilitate that completion by providing a 'nomenclator layer' of names and references, and tools to start building full synonymic databases. However, its ultimate success, and our success in building a catalogue of all insect names, will depend on the involvement of taxonomists around the world, and enabling their database to be linked to a global system. Future workshops will refine the process and the participation, but the completion of the Catalogue of Life for insects starts now.

Area-wide integrated pest management for tsetse flies: The role of sterile insects

Marc Vreysen[1], Udo Feldmann[1], Andrew Parker[2], Jorge Hendrichs[1]

[1]Insect Pest Control Sub-Programme, Joint FAO/IAEA Programme of Nuclear Techniques in Food and Agriculture, Department of Nuclear Applications, International Atomic Energy Agen, Vienna, Austria, [2]Joint FAO/IAEA Programme of Nuclear Techniques in Food and Agriculture, FAO/IAEA Agriculture and Biotechnology Laboratory, Entomology Unit, Seibersdorf, Austria

The concept of area-wide integrated pest management (AW-IPM) against specific tsetse populations has gained in significance during the last ten years. The approach targets entire populations of tsetse within a delimited geographical area and integrates in a phased manner a combination of control tactics that are best suited for the specific characteristics of the target area. AW-IPM aims at combining control tactics which are effective at high tsetse population densities, such as the SAT (sequential aerosol technique) with those that are effective at low population densities such as the sterile insect technique (SIT). In addition, it takes into account different favourable climatic, agroc-ecological and seasonal trends. The creation of sustainable tsetse-free areas on Africa mainland is feasible, provided the operations are carried out on an area-wide basis. The elimination of *Glossina pallidipes* from 11 000 km² in Zululand, South Africa in the 1950s, using a combination of aerial spraying of insecticides, game/habitat destruction, and mass-trapping, is a case in point. The area is to date still free of *G. pallidipes*.

New tools such as tsetse population genetics and geographic information systems/remote sensing are providing more evidence that the tsetse belt is not continuous, but is, in many instances, fragmented. These population islands offer opportunities for the creation of sustainable tsetse-free areas using AW-IPM principles. The role of sterile insects in these AW-IPM programmes should be carefully assessed and they should only be used in those topographical and ecological situations where they offer a comparative advantage over other control tactics.

DNA-based approaches to the identification of forensically important Australian *Chrysomya* (Diptera: Calliphoridae)

Leigh A. Nelson[1], James F. Wallman[2], Mark Dowton[1]

[1]*Centre for Medical Bioscience, School of Biological Sciences, University of Wollongong, NSW 2522, Australia,* [2]*Institute for Conservation Biology, School of Biological Sciences, University of Wollongong, NSW 2522, Australia*

Introduction: A DNA-based approach shows potential for the identification of taxa for which the use of morphology, or the association of different life stages, is problematic. The identification of several forensically important Australian *Chrysomya* species is hampered by their similar morphologies, even as adults.

Methods: Four DNA regions were tested for the identification of members of this genus, collected from the east coast of Australia: 1) the ribosomal 28S, 2) the second ribosomal internal transcribed spacer (ITS2), 3) the mitochondrial control region and 4) the 'barcode' region of the first subunit of the mitochondrial cytochrome oxidase I (COI).

Results and Conclusions: With the exception of the COI 'barcode', difficulties were experienced with amplification and sequencing, attributable to high intra-individual sequence variation (heteroplasmy) in those regions. The 658 bp fragment of the COI gene was sequenced from 56 specimens, representing all nine Australian *Chrysomya* and three calliphorid outgroups. The COI sequence divergences were calculated using the Kimura-two-parameter distance model, and a bootstrap neighbour-joining (NJ) tree was generated to provide a graphic display of the patterns of divergence among the species. The COI barcode successfully identified the Australian *Chrysomya,* with all species resolved as reciprocally monophyletic groups on the NJ tree, with strong bootstrap support. Intraspecific sequence divergences averaged 0.097% (range = 0-0.612%), while interspecific divergences averaged 6.499% (range = 0.458-9.254%). The overlapping sequence divergences for the *Chrysomya* is attributable to the low sequence divergence (mean = 0.484%) between the sister species *Chrysomya megacephala* and *Chrysomya saffranea.*

Spatial analysis of earthworm predation by generalist carabid predators using molecular analysis of gut contents

Andrew King[1], James Bell[2], David Bohan[2], William Symondson[1]

[1]Cardiff University, Cardiff, United Kingdom, [2]Rothamsted Research, Hertfordshire, United Kingdom

Earthworms have a key role in many soil processes, including soil turnover, aeration, drainage and the breakdown and incorporation of organic matter. As earthworms are a major component of the invertebrate biomass in European soils, they are a significant source of prey for many mammals, birds and invertebrate predators.

Carabid beetles, such as *Pterostichus melanarius* and *P. madidus*, are recognised predators of crop pests such as slugs and/or aphids, capable of affecting their temporal and spatial population dynamics.

Molecular approaches can be used to identify trophic links in agricultural food webs, to measure the responses of generalist predators to changes in prey diversity and density, and to assess the role of alternative prey, such as earthworms, in sustaining predators at times of low target prey abundance. Both monoclonal antibodies and general earthworm PCR primers have revealed significant proportions of *P. melanarius* populations testing positive for earthworm.

We have now developed species-specific, and in some cases lineage-specific, PCR primers for all the earthworm species at our field site. Extreme genetic divergence amongst two species, *Allolobophora chlorotica* and *Apporrectodea rosea*, necessitated the development of different primers for each lineage. The primers for all species and lineages were combined within a multiplex PCR to simultaneously screen for the presence all species of earthworm in the guts of each predator.

The application of this approach to the analysis of spatial and temporal interactions between carabids and multiple earthworm species in the field will be presented.

Vibratory signals in stingless bee recruitment: Investigations of transmission pathways allow the identification of potential receivers

Michael Hrncir

University of São Paulo, Ribeirão Preto, Brazil

When returning from profitable food sources, stingless bee foragers generate thoracic vibrations inside their nest, predominantly during trophallactic food transfers. Since it proves difficult to pinpoint the receivers of these putative signals (due to sometimes very subtle behavioral changes), the true meaning of these vibrations for recruitment processes is not entirely unscrambled. Yet, detailed analyses of the potential pathways, through which the thoracic vibrations are transmitted from the foragers to the hivebees, allow at least defining and confining the crowd of potential receivers. Assuming similar physiological properties of the mechanosensory organs in honeybees and stingless bees, (1) a "long-range", (2) a "medium-range", and (3) a "short-range" transmission pathway can be postulated. (1) *Substrate vibrations*. Thoracic vibrations are strongly attenuated on all natural substrates found within meliponine nests. Nevertheless, hivebees should be able to detect the substrate vibrations at distances of up to 3-5 cm from the vibrating forager (on entrance structure and involucrum). Consequently, substrate vibrations could be used by both food receivers and potential recruits to detect and approach a forager. (2) *Airborne sounds*. Most hivebees attending trophallaxes stay within 5 mm from the vibrating forager and (almost) touch her body with their antennae. Within this range, the forager-generated particle velocity is strong enough to be perceived by the hivebees. (3) The most efficient transmission is through *direct physical contact* during trophallaxis. Here, food-receivers are directly vibrated by the forager, and the frequency content and temporal pattern are directly passed on to the receiver bees. [FAPESP 06/50809-7 and 06/53839-4]

Phytosanitary constraints: South africa's export regulatory system

Isabella Bezuidenhout

Directorate Plant Health, Department of Agriculture, Pretoria, Gauteng, South Africa

As a result of agreements negotiated at the World Trade Organisation (WTO), traditional trade protection measures such as tariffs and quotas are falling away. But to some extent they are being replaced by domestic technical regulations that permit countries to bar products from entering their markets if the products do not meet certain standards. Arbitrary and restrictive sanitary and phytosanitary measures continue to represent a major obstacle to international trade of agricultural products. South Africa's entry into the international arena has been an area of tremendous change. In line with domestic liberalisation policies and export promotion strategies, South Africa has become an active member in international trade and a member of various international organisations. The new global environment for international trade places a huge responsibility on the National Plant Protection Organization of South Africa (NPPO) to facilitate safe agricultural trade with its international trading partners. Effective national export control systems are critical to enable a country to enhance its competitiveness and international market access of plants, plant products and other regulated articles. In South Africa an effective and efficient export regulatory system is undermined by the existence of inadequate and/or obsolete standards and standard operating procedures, absence or inadequate information on pests, insufficient human resources, inadequate pest surveillance, inspection and certification, pest free areas and areas of low pest prevalence not yet identified, smuggling through porous borders, and inadequate information sharing on pests.

The origin of the South African weed population of *Pereskia aculeata* (Cactaceae) and new potential biological control agents

Iain Paterson[1], Doug Downie[1], Stefan Neser[2], Martin Hill[1]

[1]Rhodes University, Grahamstown, South Africa, [2]ARC-Plant Protection Research Institute, Pretoria, South Africa

New biological control agents are required to control the invasive weed *Pereskia aculeata* Miller (Cactaceae) in South Africa. Identifying the regions of origin of weed biotypes has been important in a number of biological control programmes and is likely to affect the control of *P. aculeata* because of the plant's vast and distjunct native distribution. DNA sequencing of the TrnL-F intergenic spacer, the nuclear gene Phytochrome C and Inter-Simple Sequence Repeats using 14 primers indicate that the weed population originates from the southern part of the plant's native range in Misones Province, Argentina. South African plants are placed in a distinct clade which indicated either single or multiple introductions from this region. Surveys of the phytophagous insects associated with *P. aculeata* have been conducted in Misones Province and 4 other regions within the plant's native range. Misones Province had the largest diversity of phytophagous insects associated with *P. aculeata* followed by 3 regions in Brazil. It has been suggested that the Caribbean is the region of origin of the species but this region supported a depauperate insect fauna. As the origin of the South African weed population and the region with the most diverse insect fauna associated with *P. aculeata* Misones Province is the most appropriate region to survey for biological control agents. Of the 23 phytophagous insects associated with *P. aculeata* in this region 5 have potential and should be considered for host specificity testing based on their distributions and modes of damage.

Analysis of a market-focussed biorational product business

Sean Moore

Citrus Research International, Port Elizabeth, South Africa

Introduction: In 2003 the Citrus Growers Association formed a company – River Bioscience – to commercialise research innovations from its subsidiary, Citrus Research International.

The products: The first product commercialised by River Bioscience was the *Cryptophlebia leucotreta* granulovirus (CrleGV). Recently, River Bioscience acquired three other products. These are another baculovirus, the *Helicoverpa armigera* nucleopolyhedrovirus (HearNPV), a fruit fly bait station and a fruit fly monitoring system. The success of Cryptogran (the CrleGV product) can be attributed to: the dearth of other products in the market place at the time of launching; the high priority requirement to control the target pest; and the product's efficacy, which is comparable to that of existing chemical options. Helicovir (the HearNPV product) is fully developed but is awaiting registration. It is envisaged that acquiring market share with this product will be a lot more difficult than was the case with Cryptogran. This is due to the slow speed of kill of the product and the availability of chemical alternatives. Grower education will therefore be of paramount importance in obtaining acceptance of Helicovir.

The company: The success of the company can be attributed to: the market-focus rather than product-focus of the company; the relationship and credibility which the company has with its market; and the expertise of the company's distribution network. If River Bioscience had not acquired other products, in addition to Cryptogran, within three years from start up, the company would have been exposed to great risk.

Conclusions: The most influential factor in the success of the company and its products is the market focus of the company.

Polyandry or polygyny in the social Hymenoptera: two routes to genetic diversity

William Hughes[1], Francis Ratnieks[2], Madeleine Beekman[3], Ben Oldroyd[3]

[1]University of Leeds, Leeds, United Kingdom, [2]University of Sussex, Brighton, United Kingdom, [3]University of Sydney, Sydney, Australia

Understanding the evolution of multiple mating by females (polyandry) is an important question in behavioural ecology. A series of fitness benefits of polyandry for social insect queens have been suggested and significant progress has been made in providing experimental evidence for particular hypotheses in particular taxa. Here I will adopt for the social Hymenoptera, the potential powerful approach of a comparative analysis to examine the support it provides for the various hypothesised costs and benefits of polyandry. Many of the postulated fitness benefits of polyandry are based upon an increase in intracolonial genetic diversity, which also results from colonies having multiple queens (polygyny). I will therefore also examine the comparative relationship between polyandry and polygyny to see if it provides any support for the evolution of one or both traits having been driven by a benefit from intracolonial genetic diversity.

A case study of an invasive species: Why outbreak and why decline?

Zhen Zhang, Hongbin Wang, Xiangbo Kong, Pei-yi Zhang, Jun Liu

Research Institute of Forest Ecology, Environment and Protection, Chinese Academy of Forestry, The key Laboratory of Forest, Beijing, China

Abstract: The red turpentine beetle (RTB), *Dendroctonus valens* LeConte native in North and Central America, was introduced into China in early 1980's, and since 1998 it had caused severe damage to *Pinus tabulaeformis* in China, especially in an outbreak period from 1998 to 2002. The analyses indicated there were a few main factors which influenced the successful establishment of this species in China. (1) when RTB first attacked the pine there were no competitors, other borers infested the pine only after the tree became weak or dying by RTB; (2) RTB had high adaptation ability to the environment because of the wide distribution range, large host range and big body size; (3) the main host species, *Pinus tabulaeformis*, was attractive to the beetle; (4) RTB had a characteristics of low special aggregation;(5) there existed of huge pure pine stands or the mixed stands had limited resistance to infestation of RTB. The environmental or management factors caused the population outbreaks included drought in the spring, illegal cutting, heavy tapping and unsuitable management. The RTB population declined in recent years because there were more rainfall, the host attractiveness decreased, the local natural enemies were established, and various management measures were implemented, such as mass trapping using semio-chemicals, introduction of natural enemies, prohibition of illegal cutting, and also the treatment of stumps after cutting.

Forest inventory data: A basis for conservation of ground dwelling beetles in managed landscapes

Colin Bergeron[1], John Spence[1], Jan Volney[2]

[1]University of Alberta, Edmonton, Alberta, Canada, [2]Northern Forestry Centre, Edmonton, Alberta, Canada

Introduction: Ground dwelling beetles (Coleoptera: Carabidae) can teach us much about biodiversity conversation in managed landscapes. This study aims to quantify how ground beetles interact with different forest habitat components. It further seeks to determine if operational maps derived from air photo interpretation (1:20 000) adequately reflects these interactions in ways that allow the design of conservation strategies in managed landscapes.

Methods: A systematic grid of 200 sites was established on 84 km^2 of Boreal Mixedwood forest in Western Canada at the Ecosystem Management Emulating Natural Disturbance research site. Disturbance history, forest structure and composition, and ground dwelling beetles were sampled in every sites.

Results: Occurrence of most common ground beetle species was explained by the distribution of the most common tree species as is well reflected in forest inventory data (FID). Uncommon carabid species were associated with tree species uncommon on this landscape and these associations were not well reflected in the FID. The uncommon tree and beetle species occurred in places where the disturbance regime differs from the rest of the landscape.

Conclusions: FID predicted the occurrence of most common beetle species. They can therefore be used for conservation-oriented management planning. However, the occurrence of uncommon species in areas with long fire return intervals or frequent flooding is not well predicted by forest inventory data. Hence, other surrogates need to be investigated for use in conservation of the uncommon, and likely more vulnerable, species in managed landscapes.

Realities and prospects for microbial control of citrus pests in South Africa

Sean Moore[1], Antoinette Malan[2], Wayne Kirkman[1], Tim Grout[3], Tarryn Goble[4]

[1]Citrus Research International, Port Elizabeth, South Africa, [2]University of Stellenbosch, Stellenbosch, South Africa, [3]Citrus Research International, Nelspruit, South Africa, [4]Rhodes University, Grahamstown, South Africa

Introduction: Several pathogens have been recorded from citrus pests in South Africa. However, the exploitation of these pathogens on a commercial level is a relatively new practice in the southern African citrus industry.

Realities: Currently only *Bacillus thuringiensis kurstaki* (Bt) and the *Cryptophlebia leucotreta* granulovirus (CrleGV) are registered for use on citrus. Bt is used for controlling bollworm, *Helicoverpa armigera*, apple leafroller, *Tortrix capensana* and citrus butterflies, *Papilio* spp. CrleGV has been used commercially for control of the false codling moth, *Thaumatotibia leucotreta*, for four years now. An application for the registration of the *Helicoverpa armigera* nucleopolyhedrovirus (HearNPV) has also been submitted after several years of successful trials against *H. armigera*.

Prospects: In addition, several other projects to investigate and develop entomopathogens for control of citrus pests are underway. Entomopathogenic nematodes (EPNs) have shown great promise in laboratory biossasys for control of *T. leucotreta*. The integration of EPNs and CrleGV into a phenologically discerning programme for season-long control of *T. leucotreta* is discussed. EPNs could also be used for control of other pests which have a soil-borne stage in their life-cycle, such as fruit fly, *Ceratitis capitata* and *H. armigera*. Research projects are currently underway to investigate the use of hyphomycete fungi for control of final instar larvae and pupae of pests which occur in the soil. These include the pupae of *T. leucotreta*, *C. capitata* and the citrus thrips, *Scirtothrips aurantii*.

Conclusion: Much potential exists for further exploitation of entomopathogens for control of various pests on citrus. Microbial control options can form an integral part of a greater IPM strategy.

Composition and phenology of insect pests of *Capsicum baccatum* (Solanaceae) cultivated in the Makana District, Eastern Cape Province, South Africa

Colleen Hepburn, Sarah Radloff, Martin Villet, Martin Hill

Rhodes University, Grahamstown, South Africa

The composition and phenology of insects occurring on Cherry Peppers, *Capsicum baccatum*, grown in the Makana District was quantified during the study period, November 2005 to November 2006. Data from a pilot sampling trial were analyzed to establish the number of plants to be scouted per site and the most effective scouting techniques to use. Five different types of monitoring traps were placed in each of the eight study sites. Collection of trap catches and scouting of fifteen individual plants per site was undertaken on a weekly basis over the 52-week study period. The most commonly trapped potential insect pests were African Bollworm *Helicoverpa armigera* (Hübner), False Codling Moth *Thaumatotibia leucotreta* (Meyrick), Mediterranean Fruit Fly *Ceratitis capitata* (Wiedemann) and several species of thrips. The majority of damage caused to the *Capsicum baccatum* crop was due to *Ceratitis capitata* populations. Although *Helicoverpa armigera* and *Thaumatotibia leucotreta* adults were present in the monitoring trap catches, the scouting data showed larval counts of both species were nominal. Using the scouting data gathered and the mean number of pods per plant, a measure of plant damage was estimated. Statistical analyses established the efficacy of the monitoring traps for each pest and tested for differences among and between study sites. Surveillance programmes, Integrated Pest Management and intervention strategies are considered for application in *Capsicum baccatum* cropping systems.

Advances in the study of scent trails in stingless bees (Apidae: Meliponini)

Dirk Louis P. Schorkopf

University of Vienna, Vienna, Austria

Introduction: Meliponine bees are uniquely among flying insects for their scent trail laying behaviour: Bees of the worker caste of several species signalize food sources by scent marking them, therefore informing nest mates of its existence and position. Many interpretations and hypothesis concerning scent trail laying in meliponines are now in doubt and somewhat controversial when inspecting them in greater detail.

Methods: I first reviewed the advances of scent trail laying research in meliponines. I then compared the research methods and interpretations of the past on scent trail laying with the more recent outcomes and own observations. The following questions where treated in more detail: 1) which methods were used to challenge a particular question in respective studies 2) in which way did the methods of the past and recent studies differ 3) is it possible to explain some controversial hypothesis and interpretations between the studies merely by the use of different methods 4) where some methods particularly useful to answer a particular question regarding scent trail laying in meliponines?

Results: Since the discovery of scent trail laying in Meliponini several (however, less than 30) relevant studies have been published. Interestingly researchers in general preferred to use a new method or to change important aspects of already published methods when trying to answer the same questions which make a comparison difficult or in some cases even impossible. Some difference in methodology, however, was due to the use of sophisticated instruments rarely available in the past. Some controversial interpretations between the studies can possibly be explained by the use of different methods and the use of different species. Although some methods seem to be more efficient in answering a particular question on meliponine scent trail functionality, still much too few studies are available to draw secure conclusions.

Conclusions: Although some valuable insights on scent trail laying in meliponines are already available the study of scent trails in Meliponini has just begun. A more careful evaluation of the methodology, also as to their comparability to past studies will be very helpful to answer the many questions still remaining.

Insect rearing for commercial virus production

Sean Moore[1], Wayne Kirkman[2], Craig Chambers[1]

[1]Citrus Research International, Port Elizabeth, South Africa, [2]River Bioscience, Port Elizabeth, South Africa

Introduction: Since 2004 the *Cryptophlebia leucotreta* granulovirus (CrleGV) has been commercially produced in South Africa for use against the false codling moth, *Thaumatotibia leucotreta*, on various agricultural crops. This is the first baculovirus to be commercially produced in South Africa.

Host: The first requirement for successful production of the virus is an effective and efficient mass rearing process for the host, as virus production is *in vivo*. In order to achieve this, effective means for the following had to be established: surface sterilisation of eggs; production of a suitable artificial diet for larvae; and moth eclosion and oviposition systems. Quality control is of paramount importance. This entails regular recording of the host biology, cleanliness and environmental parameters. This enables rapid attendance to any unacceptable deviations.

Pathogen: Virus production must be spatially separated from host production, with no flow from the former to the latter. For virus production, the most suitable larval life-stage is inoculated with an LC_{90} concentration of virus and incubated for the optimal time period until harvesting. Great care must be taken to minimise contamination of larvae with bacterial and fungal pathogens. Quality control entails quantification of all important biological and environmental factors. Deviation from set standards may result in disqualification of virus from being formulated and bottled.

Conclusions: The most important factors in the successful production of a baculovirus in order to meet the demands of a commercial market are: documented protocols, well-trained staff and dedication to quality control.

Does *Xylaria* play a specific role in the fungus-growing termite mutualism?

Anna A. Visser[1], Vera D. Ros[1], Eline Hartog[1], Z. Wilhelm De Beer[2], Bernard Slippers[2], Michael Wingfield[2], Janette Mitchell[3], Thomas Lœssøe[4], Alfons J.M. Debets[1], Thomas W. Kuyper[5], Rolf F. Hoekstra[1], Duur K. Aanen[1]

[1]Laboratory of Genetics, Wageningen UR, Wageningen, Netherlands, [2]Forestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, South Africa, [3]Agricultural Research Council, Plant Protection Research Institute, Pretoria, South Africa, [4]Department of Biology, University of Copenhagen, Copenhagen, Denmark, [5]Department of Soil Quality, Wageningen UR, Wageningen, Netherlands

Introduction: Fungus-growing termites live in obligate mutualistic symbiosis with species of the basidiomycete genus *Termitomyces*, which is grown in monoculture on a substrate of dead plant material. When the termite colony dies, or when nest material is incubated without termites in the lab, often species of the ascomycete genus *Xylaria* appear and rapidly cover the fungus garden. Considering its high prevalence, is *Xylaria* specialized in occupying termite nests or is it just an opportunistic visitor? As a first attempt to answer this question, we tested specificity of *Xylaria* for fungus-growing termites at the termite genus, species, or single colony level.

Methods and Results: In South Africa, 120 nests of eight termite species from three termite genera were sampled for *Xylaria*. *Xylaria* appeared on 70% of the incubated combs. Using ITS and 28S sequences, and including non-termite associated *Xylaria* GENbank sequences, we show that one clade comprising 63% of all isolates is specific for fungus-growing termites. The remaining 37% strains possibly represent endophytes. The termite-specific *Xylaria* clade does not show strong specificity at subsequent lower taxonomic levels, viz. at the termite genus, species, or colony level.

Conclusions and Discussion: Our results suggest that *Xylaria* does not play a very specific role in the fungus-growing termite mutualism. We are currently testing if *Xylaria* is more specialized on the substrate of the fungus garden. This would explain why *Xylaria* is so prevalent in termite nests and does show specificity for fungus-growing termites in general, while lacking specificity for groups within fungus-growing termites.

Successful invasion of red turpentine beetle *Dendroctonus valens* LeConte (Coleoptera: Scolytidae): Evidence of the empty niche hypothesis

Zhen Zhang, Pei-yi Zhang, Jun Liu, Hong-bin Wang, Xiang-bo Kong

Research Institute of Forest Ecology, Environment and Protection, Chinese Academy of Forestry The key Laboratory of Forest, Beijing, China

Abstract: The red turpentine beetle (RTB), *Dendroctonus valens* LeConte, originally distributed in North and Central America, was introduced into China in early 1980's and since 1998 it has caused great damage to Chinese pines, *Pinus tabulaeformis* Carr. The pine wood boring insect community structures in invaded area were studied to explore the reason of the successful invasion of the RTB. The results indicated that when RTB first attacked the pines there were no competitors, other borers came only after the pines became weak or dying by RTB. At later stages of attack RTB mostly coexisted and competed with *Melanophila farmanekin* and *Asemum amurense*. An important local natural enemy, *Temnochila sp*. was found which prefers RTB to other wood borers. There are also records of other local natural enemies which can prey or parasite on RTB. Thus, its successful invasion can not be explained by the lack of natural enemies while the empty niche hypothesis may provide a more likely explanation.

Effects of host and non-host volatiles on the behavior of red turpentine beetle *Dendroctonus valens* LeConte (Coleoptera: Scolytidae) and its natural enemies

Zhen Zhang[1], Hong-bin Wang[1], Li-xian Cui[2], Da-zhuang Huang[2], Xiang-bo Kong[1], Yong-jie Zhang[3], You-ju Jin[3]

[1]Research Institute of Forest Ecology, Environment and Protection, Chinese Academy of Forestry The key Laboratory of Forest, Beijing, China, [2]Agricultural University of Hebei, Baoding/Hebei, China, [3]College of Biological Sciences and Biotechnology, Beijing Forestry University, Beijing, China

Red turpentine beetle (RTB), *Dendroctonus valens* LeConte (Coleoptera: Scolytidae), is an invasive species in China which originally distributed in North and Central America. Since 1998 it has caused grave damage to Chinese pines, *Pinus tabulaeformis* Carr in China. In door and field testing proved that (*S*)-(+)-3-carene was the most attractive host monoterpene to the Chinese population of RTB and its natural enemy, *Prostomis* sp. though other monoterpenes such as α-pinene, and β-pinene had also more or less their attractive effects. To the contrast, myrcene and (+)-limonene were repellents to RTB. Eight compounds (cis-3-hexen-1-o, trans-2-hexen-1-ol, nohyl aldehyde, 1-octen-3-ol, ethanol, 1-hexen-3-ol, benzaldehyde and salicylaldehyde) had significantly repellent effects on RTB, however, three other compounds(3-octanol, cis-2-hexen-1-ol, trans-2-hexenal) had been determined to have no significant repellent effects on RTB by the y-tube test. However, some of them were effective at lower concentration (1/1000), while others were more effective at higher concentration of 1/100. All the tested volatiles, except ethanol, were demonstrated to be effective repellents to RTB with rotor trap tests in the field.

Post-release evaluation of the seed feeding bruchid beetle *Sulcobruchus subsuturalis* in the biological control of *Caesalpinia decapetala* an invasive weed in South Africa

Faith Kalibbala, Edward Witkowski, Marcus Byrne

University of the Witwatersrand, Johannesburg, South Africa

Introduction: The release of the seed beetle *Sulcobruchus subsuturalis* for biological control of *Caesalpinia decapetala* in South Africa has been ongoing since 2000. This is the first post release evaluation of the efficacy of the agent against the weed.

Method: We assessed the phenology of *C. decapetala* and *S. subsuturalis* at two sites and the establishment of the beetle on the weed at 25 sites. In addition, the effects of *S. subsuturalis* on seed densities, seed germination and seedling recruitment were measured. Predation by native ants and attacks by native parasitoids were also examined at two release sites.

Results: Mature pods were available on the tree from spring to summer when the beetle is expected to be reproductively active. The proportion of beetle infested seeds collected from study sites was low (0 to 15.5%). Consequently high seed densities and seedling recruitment were observed in the field. In the laboratory, seed infestation levels were high and germination was less than 10% and seedling emergence as low as 2.1%. Predation by native ants (*Crematogaster* species, *Pheidole megacephala*, *Messor natalensis* and *Tetramorium avium*) reached 100% within 10 days. Egg parasitism ranged between 80 and 93.1%. The parasitic wasp *Dinarmus altifrons* was recovered developing inside a *C. decapetala* seed infested with *S. subsuturalis*.

Conclusion: Releases of *S. subsuturalis* against *C. decapetala* should continue, but improved by inundative rather than inoculative releases; every year between September and March (summer); and involve land owners, farmers and nature reserve authorities in release activities.

Molecular evolution and functional significance of *Drosophila* neuropeptide copies

Christian Wegener, Anton Gorbashov

Emmy Noether Neuropeptide group, Animal Physiology, Philipps-University, Marburg, Germany

Arthropod neuropeptides often occur in multiple sequence-related copies within a single prepropeptide. For example: the prepropeptide encoded by the *fmrf* gene contains 24 different FMRFa-like peptides in the cockroach *Periplaneta americana* [1], and 13 FMRFa-like peptides in *Drosophila melanogaster* [2].

A long-standing and unanswered question addresses the functional significance of these multiple sequence-similar copies. We choose a comparative genomic approach to this question and analyzed the amino acid sequence variability of neuropeptides in the 12 *Drosophila* species with fully sequenced genomes. To support the actual expression of predicted neuropeptides, we directly profiled major neuropeptide release sites of four species belonging to the main *Drosophila* subtaxa by MALDI-TOF mass spectrometry. This profiling provides the first biochemical identification of neuropeptides in *D. virilis, D. mojavensis, D. pseudoobscura*, and *D. sechellia*.

Our results show that the peptide hormone complement has been stable throughout the 60 million years of diversification within the genus *Drosophila*. They further suggest that all peptide copies are -to varying degrees- subjected to evolutionary constraints and do not neutrally mutate. Moreover, the degree of peptide sequence conservation correlates well with literature data on the pharmacological efficacy of individual peptide copies.

Taken together, our results suggest that multiple peptide copies are not mutually redundant, but have either specific functions or are important in line with the "more-of-the-same" concept.

Application of classification tree methods to the study of insect population dynamics

Chris J K MacQuarrie, D. Langor, John Spence

[1]University of Alberta, Edmonton, Alberta, Canada, [2]Canadian Forest Service, Northern Forestry Centre, Edmonton, Alberta, Canada

Introduction: One of the primary goals of insect population dynamics is to identify causes of mortality and quantify their relative impact. However, this task can be difficult if there are multiple potential causes for each insect death or specific causes cannot be identified. Often these problems can be resolved by rearing and rigorous experimentation. However, for many species, particularly aliens or invasives, this may be impractical or impossible. I show that via the application of classification trees to insect mortality data it is possible to perform detailed investigations of potential causes of insect mortality in a field setting.

Methods: I sampled larval populations during an outbreak of alien *Profenusa thomsoni* Konow in an urban birch (*Betula* L.) forest in Anchorage, Alaska, USA. The health (alive or dead) of each larvae was recorded as was the size of its host leaf; the amount of defoliation; the number of conspecifics; the crown position the larvae was collected from; and the time of sampling. I then used classification tree analysis to split the data into homogenous groups of live and dead larvae based on the values of the other variables as a way to associate biological processes with mortality. This procedure was repeated for each of *P. thomsoni*'s five larval instars that complete their development in the host leaf.

Results: Larval mortality of *P. thomsoni* was best explained by a combination of competition and resource exhaustion. However, the specific variables selected, and their magnitude differed among instars. Interestingly, the relationship between leaf area and survivorship observed in the classification trees suggested a novel hypothesis to explain overutilization of host leaf resources by leafminer females. These results suggest females may deposit too many offspring in host leaves as a way of minimizing the effect of plant defences. In addition, mortality was also associated with smaller leaves, a pattern than may reflect increased competition for limited resources, but also suggests that smaller-leaved birch varieties may be less susceptible to *P. thomsoni* damage.

Conclusions:. It is difficult to quantify the population dynamics of species like *P. thomsoni* that are not easy to rear or sample. Classification trees can be used to identify biologically important variables for poorly understood species and as way to generate hypotheses consistent with the data that should be given high priority for future experimentation.

The effect of predator and alternative prey density on cutworm survival, activity, and growth

Steven Frank[1], Paula Shrewsbury[2], Ellery Vodraska[2]

[1]Texas A&M University, College Station, Texas, United States, [2]University of Maryland, College Park, Maryland, United States

Introduction: Conservation biological control seeks to increase predator abundance to impose predation pressure on herbivores and prevent plant damage. However, many conservation biological control practices increase alternative food in addition to predator abundance. Moreover, research has demonstrated that predator activity or presence in a habitat can have negative indirect effects on herbivores by altering their behaviour and feeding efficiency. The objectives of the study were to 1) determine the effect of alternative food density on predation of cutworms by *H. pensylvanicus*; 2) determine the effect of predator density on predation of cutworms; 3) examine daily activity patterns of predators and cutworms; and 4) determine whether cutworm activity and growth is affected by predator density.

Methods: Experiments were conducted in PVC tubes on bluegrass turf maintained as a golf course fairway. Predator and cutworm activity was monitored every two hours on two nights of the experiment. After six days surviving cutworms were counted and weighed.

Results: Increasing alternative prey density reduced predation of cutworms. Predation was greatest at high predator density with no alternative food. However, cutworms were less active as predator density increased. In addition, when predator density was low cutworms were more active and grew faster than when predator density was high.

Conclusion: This research demonstrates that alternative food reduces the impact of predators on pest survival. However, high predator density is still detrimental to pest growth. Thus, indirect effects of predators on pest fitness deserve greater attention in pest management.

Cry2Ab resistance in *Helicoverpa armigera* and factors influencing the evolution of resistance to transgenic cotton in Australia

Rod Mahon, Karen Olsen, Sharon Downes

CSIRO, Canberra ACT, Australia

The transgenic cotton Bollgard II expresses the *Bacillus thuringiensis* toxins Cry1Ac and Cry2Ab. Bt-cotton is effective against many Lepidoptera including *Helicoverpa armigera* and *H. punctigera*. *H. armigera* has been able to evolve resistance to conventional insecticides and therefore threatens the long-term usefulness of Bt-cotton wherever this species is found. We have examined the frequency of alleles that confer resistance to Bt toxins in Australian populations of *H. armigera*. While Cry1Ac resistance has not been found, Cry2Ab resistance alleles occur at a frequency of 0.003. Resistance is the result of mutation(s) at a single autosomal locus and is recessive and is not cross-resistant to Cry1Ac. This is fortunate, as Bollgard II is grown extensively in Australia (>80% of all cotton). If both toxins are expressed at optimal levels, this variety should remain efficacious against Cry2Ab-resistant insects. However there is evidence that the titre of toxins vary throughout the growing season providing opportunities that favour rare homozygous Cry2Ab resistant insects. Nevertheless, we have no evidence that the frequency of resistance is increasing. We examined the hypothesis that Cry2Ab resistant insects suffer fitness costs that counters positive selection. We compared Cry2Ab resistant to near-isogenic susceptible insects under a variety of conditions. No fitness costs were found. Our present understanding of Cry2Ab resistance in *H. armigera* suggests that, because resistance is recessive, an increase in frequency of the resistance allele will be slow, but such an increase is inevitable.

Resource flow and digestion in the imported fire ant

Bradleigh Vinson, Asha Rao, Freder Medina, Karen Snowden

Texas A&M University, College Station, United States

Workers gather resources from the environment as well as cycle resources within the colony. But where these resources go depends on the type of resource (protein, lipid or carbohydrate), the nature of the resource (solid or liquid), and the source of the resource (directly from the environment or processed by worker or processed by larvae). For example, workers collect a variety of resources with the carbohydrates primarily going to and needed by workers. On the other hand, when they collect lipids or proteins, the liquids are fed mainly to the queens, alates and larvae. Particulates in the above resources are separated from liquids by workers and fed to larvae along with any collected solid resources. The larva processes these resources, but there are bacteria associated with the larvae that also appear to play an important role in processing these resources. In the larvae, some of these resources are extra–orally digested, others are regurgitated and yet others are passed as meconium prior to pupation. Some of these reprocessed resources are then redistributed to the colony. Here, we examined these various routes of resource flow and the manipulation involved along with the role of bacteria in fire ant resource utilization.

Termites as ecosystem engineers: increasing ecohydrological function and soil health in the savanna grazing lands of tropical northern Australia.

Tracy Dawes-Gromadzki, Adam Liedloff, Austin Brandis

CSIRO, NT, Australia

Healthy soils underpin healthy landscapes, through their effective capture, retention and recycling of water and nutrients. Declining soil health has become a critical issue within the Great Barrier Reef Lagoon catchments along north-east Queensland that primarily support cattle grazing. Symptoms include increased soil compaction, reduced water infiltration and increased sediment, nutrient and water run-off. Improving soil hydrological function is critical to reducing such effects. Termites are key drivers of this process through the creation and maintenance of macropores, which facilitate the capture and infiltration of rainfall. However, the activity and diversity of termites and other soil macroinvertebrates varies greatly across these landscapes in association with patchiness in perennial vegetation. Cattle grazing can also have marked effects on vegetation patch structure and dynamics and consequently on the structure of soil macroinvertebrate assemblages. Understanding these functional relationships and the consequences for soil health is critical to sustainable pasture and livestock production and the quality of water in run-off entering the Great Barrier Reef Lagoon. We are investigating the functional role of invertebrates in soil eco-hydrological processes and how this varies with vegetation patchiness and grazing management near Charters Towers, north Queensland. The results are also being used to feed into the Savanna.au computer simulation model to predict how changes in soil health affect soil water infiltration and runoff. We present an overview of results that suggest heavy grazing intensity leads to a decline in soil health through a reduction in macroinvertebrate activity, macropore density and the ability of these landscapes to capture rainfall.

Integration of neuropeptidergic signaling and stress behaviors via the AMP-activated kinase in *Drosophila*

Erik Johnson[1], Colin Bretz[1], Lindsay Williamson[1], Nevzat Kazgan[2], Jay Brenman[2]

[1]Wake Forest University, Winston-Salem NC, United States, [2]University of North Carolina, Chapel Hill, NC, United States

Introduction: Stress, defined as a challenge to homeostasis, can culminate in stereotypical behavioural and physiological changes. These alterations to behavioural and physiological programs are coordinated by a variety of neuropeptide and hormone transmitters. However, the mechanisms underlying stress perception and subsequent hormonal release are unclear. We have investigated the actions of the AMP-activated kinase (AMPK) in *Drosophila*, in pursuit of a better understanding of these mechanisms. AMPK signalling is thought to serve as an intracellular sensor of energetic status as it is activated by AMP and is allosterically inhibited by ATP.

Methods: The functional AMPK is a heterotrimer consisting of a catalytic alpha and regulatory beta and gamma subunits. By virtue of this assembly, we have generated specific mutations in the alpha subunit and displays dominant negative activity. We have employed the yeast binary system to manipulate AMPK signalling in a variety of different cellular and peripheral cellular populations.

Results: Ubiquitous expression of this dominant negative construct causes a dramatic hypersensitivity to starvation stress, as evaluated by lifespan. Furthermore, starvation conditions which generate hyperactivity in normal flies, leads to enhanced hyperactivity in this altered genetic background. However, expression of the dominant negative in neuroendocrine cells that express the Adipokinetic Hormone (AKH) leads to increased longevity and a reduction of starvation-induced hyperactivity, which is a similar phenotype as those reported for AKH cell ablation.

Conclusions: AMPK function is dependent upon cellular context and regulates starvation-induced behavioural and physiological changes. AMPK not only serves a role as an energy sensor, but also as a crucial link between stress hormone signalling and alterations in cellular and organismal physiologies under stress.

Community responses to multiple global change drivers

Jason Tylianakis

University of Canterbury, Christchurch, New Zealand

Introduction: All organisms are embedded in complex networks of feeding interactions with other species (food webs), and the structure of these networks may be critically linked to their stability and function. Empirical food webs necessarily require the pooling of interactions sampled over a given period and/or region, and thus provide a static representation of a dynamic community. The effects of global changes on this structure, and the extent to which pooled networks represent the structure of networks at smaller spatiotemporal scales are unclear.

Methods: Communities of cavity-nesting bees, wasps and their parasitoids were sampled over 17 months in 48 sites of five land use types in coastal Ecuador. Frequencies of parasitoid-host interactions were used to construct quantitative food webs, which were compared across habitats.

Results: Habitat modification significantly altered the structure of food webs, with webs in modified habitats having a more uneven structure. Modified webs also had reduced interaction turnover, and a greater proportion of potential interactions were actually realised.

Conclusions: Global change may have significant effects on food web structure and spatiotemporal variability in this structure. Such complex effects of individual global change drivers on network structure and interaction turnover become compounded when multiple interacting drivers operate simultaneously.

Cladistic analysis of assassin bugs (Heteroptera: Reduviidae): Morphological and molecular data

Christiane Weirauch, James Munro

Department of Entomology, University of California, Riverside, California, United States

Introduction: With more than 6600 species worldwide Reduviidae or assassin bugs are the second largest and one of the most diverse groups of True Bugs. Assassin bugs show remarkable morphological and biological diversity and an exceptional range of adaptations to prey capture. Despite these features, systematic studies on Reduviidae have been neglected over the past decades. Apart from the need for descriptive and revisionary work, the higher-level classification of Reduviidae is in poor condition. This is reflected in the fact that, depending on author, 21 to 32 subfamily-level names are recognized. Several subfamily-level taxa are poorly defined and their relationships are obscure.

Methods: A cladistic analysis of higher-level taxa of Reduviidae based on 162 morphological characters and 75 ingroup and outgroup species is presented. We are currently testing this hypothesis with a matching molecular data set for ~ 90 ingroup taxa, comprising 18 subfamilies and 28 tribes. The dataset comprises ~3000 base pairs of ribosomal mitochondrial and nuclear gene regions that are aligned using secondary structure models. The data are analyzed using parsimony, maximum likelihood and Bayesian methods.

Results;. The morphology-based hypothesis on higher-level groups of Reduviidae shows – to name only a few groups – the Phymatine Complex to be basal within Reduviidae, Triatominae as monophyletic and closely related to part of the Reduviinae and to Stenopodainae, Harpactorinae as monophyletic, and Reduviinae as polyphyletic. The analysis of molecular data corroborates most of these results, including a closer relationship of blood-feeding Triatominae with Stenopodainae and part of the Reduviinae.

Entomopathogenic fungi vs semiochemicals: Mutualistic affair against pests

Nguya Maniania[1], Felix Nchu[1], Susan Dimbi[2], Sunday Ekesi[1]

[1]International Centre of Insect Physiology and Ecology (icipe), Nairobi, Kenya, [2]Crop Protection Division, Tobacco Research Board, Harare, Zimbabwe

Introduction: Inundative and augmentative are the main methods employed for introduction of entomopathogenic fungi (EPF) into the ecosystem. However, a new strategy is currently being considered, whereby insect pathogens are disseminated (autodissemination) among target pest populations by using devices that attract insect pests into a focus of the pathogen. Contamination devices (Cd) have been developed for the introduction of EPF against a number of insects and the strategy relies largely on insect's semiochemicals.

Materials and Methods: Different Cds were tested for suppression of tsetse, fruit flies and ticks in the field. Cd was mounted on tsetse trap and flies that are attracted are forced to go through the Cd where they are contaminated with conidia before they exit. In the case of fruit flies, the Cd was baited with protein bait. In the case of ticks, an attraction-aggregation-attachment-pheromone trap was developed to infect tick attracted to the trap with different fungal formulations.

Results: Conidia applied in Cds significantly reduced tsetse and fruit fly populations in the field. A high level of mycosis was observed among tsetse and fruit fly samples brought to the laboratory. A reduction of ticks was also observed with the different fungal formulations tested. However, emulsifiable formulation was the best.

Conclusions: Semiochemicals and EPF have a mutual relationship that will go a long way. The availability of pheromones and other lures for the most important pests makes autodissemination technique an alternative that is less costly and effective than conventional method of application and deserves further studies.

The pest status of diamondback moth (Lepidoptera: Plutellidae) in South Africa: the role of parasitoids in suppressing the pest populations

Robert S. Nofemela, Morake S. Mosiane, Rami Kfir

ARC - Plant Protection Research Institute, Private Bag X134,, Pretoria 0001, South Africa

Introduction: Diamondback moth, *Plutella xylostella* (Lepidoptera: Plutellidae), is major pest of *Brassica* crops in South Africa. Investigations were carried out on the role of parasitoids in suppressing the pest populations.

Methods: Cabbage, *Brassica oleracea* var. *capitata* L. (Brassicaceae), seedlings were transplanted three consecutive times every year for five years (2003-2007) in a field in the North West Province of South Africa. At weekly intervals, 30 plants selected randomly were inspected and the numbers of *P. xylostella* larvae, pupae and parasitoid cocoons found in each plant were recorded. Three sex pheromone traps, placed around each field, were also monitored every week for the flight activity of male moths.

Results: Trap catches corresponded with infestations on the crop. Infestations were low during late spring to autumn (November - May) often fluctuating between zero and two larvae per plant. The only period that infestations were high was during late winter and spring (August - October). A negative correlation between infestations and parasitism levels was observed. Parasitism of *P. xylostella* larvae was high reaching 100% on several occasions during November – May each year, but lower (<50%) in winter and early spring. Eight indigenous parasitic Hymenoptera were reared from *P. xylostella* larvae, of which *Cotesia plutellae* (Braconidae) and *Oomyzus sokolowskii* (Eulophidae) were the most abundant.

Conclusion: Parasitoids suppressed *P. xylostella* populations during November – May, and in general the pest populations declined during the study period. However, additional control measures may be required during June – October to supplement low parasitism levels.

Bee perception of warmth as a floral reward

Adrian Dyer[1], Heather Whitney[2], Sarah Arnold[3], Beverley Glover[2], Lars Chittka[3]

[1]Monash University, Clayton, Vic., Australia, [2]University of Cambridge, Cambridge, United Kingdom, [3]Queen Mary University of London, London, United Kingdom

Introduction: Insects preferentially visit warmer flowers. Bumblebees (*Bombus terrestris*) do this even in the context of all flowers presenting equivalent nutritional rewards, potentially providing an evolutionary advantage for plants that present warmer flowers. Understanding why bees exhibit this behaviour requires separating factors including perceived flower warmth and sucrose concentration.

Methods: Exp 1: Bee visits to model flowers were tested in lab conditions considering temperature as a cue to make decisions to collect sucrose (20°C flowers) or avoid quinine (28°C flowers). Exp 2: Bee visits to feeders that varied in temperature (20°C or 28°C) or sucrose concentration (21.5%, 23%, 25% or 30%) were evaluated using a three way ANOVA.

Results: Exp 1: Bees had to land on flowers to perceive a temperature differences in stimuli. Once landed, bees rapidly learnt to use temperature as a cue to make correct decisions using either their antennae or tarsal receptors. Exp 2: With increasing sucrose concentration (at identical temperature) bees preferentially visit a sweeter feeder ($p=0.002$); and if a less sweet feeder is at a higher temperature this does not affect bee preferences for visiting a sweeter feeder ($p=0.672$).

Conclusions: Bees process the parameters of temperature and sucrose concentration separately. These cues are processed hierarchically by bees with sucrose concentration being the more important factor influencing choices. However, at an equal sucrose concentration bee preference for warmer flowers provides an effective way for plants, which can effectively modulate flower temperature, to maintain pollinators.

Evolution of odour coding in moths

Sonja Bisch-Knaden, Marco Schubert, Celine Heinl, Silke Sachse, Bill S. Hansson

Max-Planck Institute for Chemical Ecology, Department of Evolutionary Neuroethology, Jena, Germany

Introduction: Odour information is coded as an olfactory map in the antennal lobe glomeruli. Among different moth species there are similar numbers of glomeruli and thus probably similar numbers of receptor types. This concordance might have created also similar coding patterns in the antennal lobe.

Methods: By using calcium imaging to measure the representation of a diagnostic set of odours (aromatics, terpenes, alcohols, aldehydes, ketones) in different moth species we tested this hypothesis. We used low odour concentrations (0.5 µg to 5 µg) to determine the position of the most sensitive glomerulus for each odour. To compare the localization of this glomerulus within and between species, the size and orientation of the antennal lobes were normalized.

Results: We measured odour-evoked calcium responses in the antennal lobes of *Manduca sexta* (n=13, Sphingidae) and *Spodoptera littoralis* (n=9, Noctuidae) and found several similarities: e.g. within each species the response sites for the terpenes geraniol and linalool were indistinguishable ($p>0.9$) but both odours activated glomeruli at a different location than the aromatic phenyl acetaldehyde ($p<0.01$, repeated measures ANOVA plus Tukey-Kramer test). Furthermore, the between species comparison showed that these odours activated corresponding sites in the antennal lobe ($p>0.8$), as did the other seven odorants tested with the exception of octanol ($p<0.05$) and octanal ($p<0.001$). We are in the process of analyzing two more sphingid and noctuid moths respectively.

Conclusions: The spatial pattern of olfactory coding seems to be widely conserved between the two moth species investigated of the families Sphingidae and Noctuidae, separated by approximately 60 million years in evolutionary time.

The prohormone convertase AMONTILLADO represents a key enzyme in the production of bioactive peptide hormones

Christian Wegener[1], Cordelia Imig[1], Matthias Vömel[1], Jörg Kahnt[2], Jeanne Rhea[3], Michael Bender[3], R. Elwyn Isaac[4]

[1]Emmy Noether Neuropeptide group, Animal Physiology, Philipps-University, Marburg, Germany, [2]Max-Planck Institute of Terrestrial Microbiology, Marburg, Germany, [3]Department of Genetics, University of Georgia, Athens/Georgia, United States, [4]Institute of Integrative and Comparative Biology, University of Leeds, Leeds, United Kingdom

Subtilisin-like prohormone convertases (PCs) are major enzymes involved in the processing of bioactive peptides from larger precursor molecules. *amontillado* (*amon*) codes for *Drosophila* PC2 and is expressed in endocrine and nervous tissue. Flies deficient in *amon* show defects in growth, carbohydrate metabolism and ecdysis. This suggests that a deficiency in *amon* disrupts peptidergic endocrine pathways. It is, however, unknown if and which peptide hormones are affected.

We used direct MALDI-TOF mass spectrometric (MS) profiling. This technique allows to detect the whole peptide hormone complement up to 2.5 kDa in individual neurohemal organs of *Drosophila*. MS profiles of the ring gland from wildtype and heat-shock rescued *amon*-deficient larvae did not show significant differences. In *amon*-deficient larvae, peptide hormones were mostly undetectable. A deficiency in *amon* thus seems to impair the production of all peptide hormones in the detected mass range. In the adult brain, neuropeptides where also detectable in *amon*-deficient flies, but apparently at lower concentrations. We are currently conducting a more detailed analysis by quantifying peptide concentrations.

Our results so far suggest that *amon* is a key enzyme in the production of *Drosophila* neuropeptides. The general importance of this peptidase for peptide processing is being investigated by ectopic expression of neuropeptides using specific and pan-neuronal GAL4-drivers, and then by characterising their cellular distribution. The observed distribution is then correlated with that of *amon* and peptidergic neurons. In combination with MS, this will allow an assessment of whether *amon* is the only PC involved in neuropeptide processing, or whether other neuronal PCs may also have a role.

Female Sex Pheromone of Simao Pine Caterpillar Moth, *Dendrolimus kikuchii*: SPME Collection, Electrophysiological Analysis, and Field Evaluation

Xiang bo kong[1], Xiao ling Sun[2], Zhen Zhang[1], Hong bin Wang[1], Cheng hua Zhao[3]

[1]Research Institute of Forest Ecology, Environment and Protection, Chinese Academy of Forestry; The Key Laboratory of Forest Ecology and Environment, State Forestry Administration, Beijing, China, [2]Tea research institute, Chinese Academy of Agricultural Sciences, Hangzhou,Zhejiang Province, China, [3]Institute of Zoology, Chinese Academy of Sciences, Beijing, China

Abstract - Sex pheromone components of *Dendrolimus kikuchii* Matsumura (Lepidoptera: Lasiocampidae) were demonstrated as (*Z,E*)-5,7-dodecadien-1-yl acetate (*Z*5,*E*7-12:OAc) and (*Z,E*)-5,7-dodecadien-1-ol (*Z*5,*E*7-12:OH) by means of solid phase microextraction (SPME) collection, electrophysiological tests, Coupled gas chromatography (GC)-mass spectrometry (MS) analyses, microchemical analyses, and field evaluations. GC and GC-MS analyses of solvent extracts determined that the average amount of *Z*5,*E*7-12:OAc and its corresponding alcohol per calling female gland extract was 1.2 ± 0.9 ng (± SD) and 0.2 ± 0.1 ng (± SD) (*N* = 30). In contrast, in solid phase microextraction (SPME) collection from calling females, *Z*5,*E*7-12:OAc (KIs: DB-WAX, 2,051; DB-5, 1,636) appeared as the single dominant peak, comprising13.5-33.4% (*N* = 3) of the sampled volatile. Whereas, *Z*5,*E*7-12:OH (KIs: DB-WAX, 2,147; DB-5, 1,511) comprises only1.3-2.3% of that (*N* = 3). Biological activities of pheromone candidates were assessed in GC-EAG and field bioassays. Males antennae were responsive strongly to *Z*5,*E*7-12:OAc, and weakly to *Z*5,*E*7-12:OH with synthetic compounds, and the same phenomena were observed from the solvent extracts of the pheromone glands. Further field trials determined that the complete fight behaviours were elicited by *Z*5,*E*7-12:OAc and *Z*5,*E*7-12:OH in a 5:1 ratio, and (*Z,E*)-5,7-Dodecadien-1-yl propionate and/or (*Z*)-5-dodecenyl acetate had a synergistic effect on male attraction to the acetate/alcohol pheromone blend.

Spatial distribution and movement of lesser grain borer, *Rhyzopertha dominica* F.

Godfrey Ching'oma, James Campbell, Sonny Ramaswamy

Kansas State University, Manhattan, United States Minor Outlying Islands

Information on spatial and temporal dynamics of the lesser grain borer, *Rhyzopertha dominica* (F.), in agricultural landscapes is not adequate. This research was undertaken with the objective of determining the flight capacity, seasonal patterns and spatial distribution. A mark-release-recapture study was undertaken on the Konza Prairie Biological Research Station, Kansas State University, Manhattan, Kansas during 2003 and 2004 to assess potential dispersal capacity of this species. The beetles were reared in the laboratory and one- to two-week-old unsexed beetles were released in the center of a grid of 46 Lindgren funnel traps placed in concentric circles at 50, 100, 200, 400, 600, 800, and 1,000 m from the center towards north, north-east, east, south-east, south, south-west, west, and northwest directions away from the release point. Of a total of 62,400 beetles released over multiple dates, 872 (1.4%) were recaptured. Beetles dispersed a mean (±SEM) distance of 380.4 ±10.5 m, with a range of 50 and 1,000 m (maximum distance in grid). However, Delta sticky traps placed as far away as 3.6 km from the release center recaptured a few (n=3) marked beetles suggesting that *R. dominica* is capable to fly significantly longer distances than our recapture grid. Beetles were also trapped at two- to three-week-intervals in an agricultural landscape in Dickinson Co., Kansas, using a grid of 203 aggregation pheromone baited sticky traps from May to November 2003 and April to November 2004, to assess the spatial-temporal distribution of beetles in relation to farm bins and other geographic features. During spring of both years, beetles were captured near wooded areas, whereas during summer beetles were trapped in both wooded areas and near farm grain storage locations and during fall were trapped predominantly in wooded areas.

Wasp-bracovirus associations: the grail quest for the ancestor virus

Annie Bézier[1], Marc Annaheim[2], Juline Herbinière[1], Christoph Wetterwald[3], Gabor Gyapay[4], Sylvie Bernard-Samain[4], Patrick Wincker[4], Isabel Roditi[2], Manfred Heller[2], Maya Belghazi[5], Jérôme Lesobre[1], Rita Pfister-Wilhem[2], Georges Periquet[1], Catherine Dupuy[1], Elisabeth Huguet[1], Nathalie Volkoff[6], Beatrice Lanzrein[2], Jean-Michel Drezen[1]

[1]IRBI CNRS, University of Tours, Tours, France, [2]Institute of Cell Biology, University of Bern, Bern, Switzerland, [3]Department of Clinical Research, University of Bern, Bern, Switzerland, [4]CEA/Genoscope, Evry, France, [5]Proteomic analysis center, Marseille, France, [6]BIVI INRA, University of Montpellier, Montpellier, France

Introduction: Comparative genomic studies have highlighted the role of symbiotic associations in biological evolution. However very few of these relationships involve viruses, except the remarkable associations of polydnaviruses (PDVs) with tens of thousand species of parasitic wasps that develop within the body of lepidopteran larvae. PDV particles, injected along with parasite eggs into the host body, act by manipulating host immune defences, development and physiology thereby enabling wasp larvae to survive in a potentially harmful environment. The virus is completely dependent on the wasp for particles production that occurs exclusively in specialized cells of the ovaries. Surprisingly, the genome enclosed in the particles encodes almost no viral structural protein but mostly factors used to manipulate the parasitized host. It was thus questioned whether PDVs were true viruses or a genetic secretion somehow created by the wasp.

Methods: Combined genomic and proteomic analyses were used to identify viral components of polydnaviruses in the braconid species *Chelonus inanitus* and *Cotesia congregata* which belong to the most distantly related subfamilies of bracovirus-associated wasps.

Results: We characterized a large set of virus genes encoding structural components of PDV particles in both species.

Conclusions: We demonstrated the viral nature of PDVs associated with braconid wasps

Deadly dosages: Tree killing as a life history in insect-fungal symbioses

Paal Krokene

Norwegian Forest and Landscape Institute, Ås, Norway

Combined bark beetle-fungus attacks are a key factor in conifer ecosystems in the Northern Hemisphere, where they regularly cause massive tree mortality. Central to the success of the bark beetle-fungus complex is the fact that bark beetles are among the few insects that are capable of breaching the potent anatomical and chemical defenses of healthy tree stems. These defenses include constitutive or preformed mechanical and chemical defenses, such as mechanically though sclerenchyma cells, cells specialized for synthesis and storage of phenolic compounds, and resin producing structures. Overlaid with these constitutive defenses is a capacity to up-regulate additional, inducible defenses in response to an attack, such as cell wall lignification and formation of traumatic resin ducts and wound periderms. In addition, acquired or systemic resistance, which may be considered a long-term consequence of induced defenses, may prime the tree for dealing more effectively with future attacks. The single most important characteristic of tree killing bark beetles is probably their ability to engage in pheromone-coordinated mass attacks that exhaust host resistance. However, since aggregation pheromones also occur in many bark beetles that do not kill trees pheromones can only be considered as a preadaptation for the evolution of tree killing. Other such necessary but insufficient conditions for tree killing is some degree of tolerance to host defenses, large contiguous forests with low host species diversity, and association with fungi that increase the virulence of each attack and help exhaust tree defenses.

Allatostatin A, a candidate peptide in olfaction driven behavior

Sabine Kreissl, Christine Strasser, Giovanni Galizia

University of Konstanz, Konstanz, Germany

Introduction: The growing number of known endogenous neuropeptides in insects adds to the complement of neuroactive substances contributing to network activities within central nervous systems. To study the role of neuropetides in coding of olfactory stimuli and in olfaction related behavior, we are mapping the peptide complement within the olfactory system of the honeybee *Apis mellifera.* Of several candidate peptides, we have here chosen Allatostatin A as one of the most prominent in olfactory neuropiles of the honeybee.

Methods: Brains were immunostained for Allatostatin A (AST), a family of neuropeptides sharing the c-terminal sequence YXFGLamide. Double labeling of GABA and Allatostatin and simultaneous staining of Allatostatin and antennal sensory neurons provided details on colocalisation and spatial arrangement. The wholemounts were scanned by confocal microscopy.

Results: The antennal lobes housed 20 somata of local AST neurons, all coexpressing GABA. Their neurites invaded the core regions of glomeruli T1-T3, and the entire glomeruli in T4. There was sparse overlap between AST neurites and receptor axons. In the mushroom bodies, which are multimodal second order neuropiles, we found AST stained neurites that likely originate from the A3 cluster of mushroom body extrinsic neurons.

AST was also present in the central body, optic lobes, tritocerebrum and subesophageal ganglion.

Conclusions: In all arthropods studied so far, AST exerted an inhibitory function. The distribution of AST neurites in bees suggests a role in shaping olfactory responses, maybe adding functional diversity to the network of inhibitory neurons within the olfactory system.

Predator trophic composition influences the relationship between predator diversity and herbivore suppression

Deborah Finke[1], Robert Denno[2]

[1]University of Missouri, Columbia, Missouri, United States, [2]University of Maryland, College Park, Maryland, United States

Introduction: Natural pest suppression is a valuable ecosystem service provided by insect natural enemies which may be threatened by declining biodiversity. However, the impact of the loss of predator diversity on pest populations may ultimately depend on the trophic relationships among enemies in the assemblage, specifically the occurrence of intraguild predation. In the absence of intraguild predation, declining predator diversity may, in fact, negatively impact herbivore suppression. However, if intraguild predators are present, predator diversity may relax the impact of predation on herbivores and dampen positive effects of predators on basal resources. Alternatively, habitat complexity, by providing a refuge from intraguild predation, might enhance the collective ability of predators to limit herbivore populations and thus indirectly benefit plant biomass.

Methods: Using a salt-marsh food web, we investigated the interactive effects of predator species richness (1-3 species) and trophic composition (strict predators, intraguild predators, or a mixture of the two) on prey suppression and primary production. We also assessed the effects of habitat vegetational complexity on the occurrence of intraguild predation and the ability of a diverse predator assemblage to control herbivore populations.

Results: We found that the trophic composition of the predator assemblage determined the impact of increasing predator species richness on natural pest suppression. Increasing the diversity of strict predator species additively enhanced herbivore suppression. Whereas, increasing intraguild predator species richness diminished herbivore control. However, complex-structured habitats enhanced prey suppression by the predator assemblage including intraguild predators by providing a refuge for predators.

Conclusions: The trophic composition of a predator assemblage may interact with habitat complexity to determine the impact of altered predator diversity on valuable ecosystem services such as natural pest suppression.

Analysis of the parameters improving oviposition of *Musca domestica* (Diptera: Muscidae) in a pig manure degrading pilot plant

Berta Pastor[1], Ana Isabel Martínez-Sánchez[1], Santos Rojo[1], Peter Takac[2], Milan Kozanek[2]

[1]Instituto Universitario CIBIO. Universidad de Alicante, Alicante, Spain, [2]Institute of Zoology. Slovak Academy of Sciences, Bratislava, Slovakia

Introduction: The intensive model of pig production in most Europe produces a huge volume of manure in very concrete areas, which makes the treatment of this waste very complicated. Inside this context appears ECODIPTERA (LIFE-environment UE project), which will try to prove that using larvae of dipterans to degrade pig manure is a reliable strategy. One of the main aspects of this technology is the volume of eggs required for the process. In order to obtain an optimal biodegradation it is required a continuous egg production, which can decompose big quantities of pig manure.

Methods: Two factors influencing the ovipositional behaviour were studied: a) maturation of adults with different diets (sugar, dried milk and yeast) and b) presentation of ovipositional substrate by the design of appropriate structures. For this purpose, four different treatments were compared: control (1), cross of paper placed on substrate (2), paper cover protecting the substrate (3) and a combination of the last two treatments (4).

Results & Conclusions: The diet that provided the highest volume of eggs was the mixture of sugar, dried milk and yeast one. Egg hatchability varied depending on the diet; after ten days hatchability decreased in sugar diet but was constant in the rest of diets. Substrate presentation affected the volume of eggs collected in each treatment: egg layings were bigger in treatment 4 (cross and cover), followed by treatment 3. The lowest quantities of eggs were recorded in uncovered treatments, 1 and 2.

Routes and modalities of invasion of *Harmonia axyridis*: a microsatellite-based population genetics survey

Eric Lombaert[1], Thibaut Malausa[1], Anne Loiseau[2], Benoit Facon[2], Thomas Guillemaud[2], Arnaud Estoup[2]

[1]INRA, Sophia Antipolis, France, [2]INRA, Montferrier sur Lez, France

Using standard population genetics inferential methods as well as more sophisticated ones (i.e. Approximate Bayesian Computation), we aim to retrace the routes of invasion of the Asian ladybird *H. axyridis* (*H.a*) in North and South America, South Africa and in northern Europe. This work is based on the analysis of the genetic variation of *H.a.* populations measured at microsatellite loci that have been recently optimized in the species. It should, amongst other things, allows understanding if the invasion is due to a single introduction of a particular commercialized strain or natural population of *H.a*., or if it is the consequence of many introductions with potential hybridization/introgression events between genetically differentiated strains/populations. This INRA research program benefits from a large sampling network based on national and international cooperation. We present here some unpublished results on *H.a* genetic variation based on a preliminary dataset including genotypes obtained at eighteen microsatellite markers.

Repellency, toxicity and tunneling activity of *Coptotermes heimi* (Wasmann) (Isoptera: Rhinotermitidae) in response to Biflex, Termidor and Tenekil

Farkhanda Manzoor, Nadeem Sheikh, Syed Nasir

1Department of Zoology, Lahore College for Women University, Lahore, Pakistan. Lahore, Punjab, Pakistan

In laboratory tests, repellency, toxicity and tunneling ability of field collected termite, *Coptotermes heimi* (Wasmann) was evaluated against three insecticides biflex (Bifenthrin), termidor (Fipronil) (Pyrazole) and tenekil (Polychlorinated petroleum hydrocarbon). For toxicity, different concentrations 0.78125, 1.5625, 3.125, 6.25, 12.5, 25, 50 ppm of biflex, termidor and tenekil were used to observe F-1 (0.97) mortality of termites. Biflex and termidor proved to be more toxic at 50 ppm in comparison with tenekil (after 8h exposure). LC_{50} values of biflex, termidor and tenekil against *Coptotermes heimi* were 1.78, 2.00 and 9.99 ppm respectively for 8h treatment. Similarly, LC_{50} values of biflex, termidor and tenekil against *Coptotermes heimi* were 14.6, 14.6 and 37.5ppm respectively for one month old treated soil. For repellency test, only biflex was repellent at 50 ppm in freshly treated and one month old treated soil. Termidor and tenekil did not prove its repellency at any concentration. These insecticides also affected survival and reduced the tunneling ability of termite workers in the treated soil. Results of the tunneling assay revealed that all termiticides (at every concentration) were able to stop termite penetration to the treated soil, either by killing or repelling them. Termite workers tunneled deeply in the lower concentrations (0.78125ppm) of these insecticides in comparison to the strong doses (50ppm). This study provided us some valuable information regarding their efficacy in the lab which could provide useful information for its field applications.

The *Tribolium* genome project: annotation and functional analysis of the first beetle genome

Marcé Lorenzen[1], Susan Brown[2], Yoonseong Park[3], Stephen Richards[4], Richard Beeman[1]

[1]USDA-ARS-GMPRC, Manhattan, KS, United States, [2]Division of Biology, Kansas State University, Manhattan, KS, United States, [3]Dept of Entomology, Kansas State University, Manhattan, KS, United States, [4]Human Genome Sequencing Center, Baylor College of Medicine, Houston, TX, United States

The genome of the red flour beetle, *Tribolium castaneum*, has been sequenced, and a working assembly (Tcas_3.0) will soon be released (www.hgsc.bcm.tmc.edu/projects/tribolium) and is being updated at NCBI. The addition of this insect to the genome club is of particular interest because *Tribolium* is both the first coleopteran and first pest insect to have its genome sequenced. The coverage is estimated to be ~96% of euchromatin, and 92% of the assembled genome (140/152 Mb) has been anchored to linkage groups via high-resolution recombinational mapping. GLEAN and NCBI RefSeq sets serve as the official gene predictions. The genome sequence and associated annotation tracks can be viewed in the Genboree genome browser (www.genboree.org); at NCBI; and in GBrowse at BeetleBase (www.bioinformatics.ksu.edu/BeetleBase), which will be the permanent curation/viewing site. Since *Tribolium* is an agricultural pest, we and our collaborators are interested in the identification of potential biopesticide targets. Specifically, we are employing transposon-based mutagenesis, RNA interference (RNAi) and microarray analysis to evaluate genes involved in chitin/cuticle metabolism, osmoregulation, neurotransmission, immunity, digestion and hybrid incompatibility. The status of the *Tribolium* genome project will be discussed and an overview of the available information, tools and resources will be presented.

Insect resistance management strategy for PTM-resistant 'Spunta' potatoes.

Walter Pett[1], David Douches[1], Diedrich Visser[2], Hector Quemada[1], Johan Brink[1], Kelly Zarka[1], Karim Maridia[1], Francisco Santos[1], Kobie de Ronde[2]

[1]Michigan State University, East Lansing, Michigan, United States, [2]ARC-Vegetable and Ornamental Plant Institute, Pretoria, South Africa

Introduction: We have developed a genetically modified 'Spunta' potato (Spunta G2) containing the *Bacillus thuringiensis* (Cry1Ia1) gene for the control of the potato tuber moth, *Phthorimaea operculella*, (PTM) in South Africa. To comply with South Africa's Genetically Modified Organisms (GMO) Act, 1997 (Act no. 15 of 1997) one of the components of a regulatory dossier should address insect resistance management.

Methods: Laboratory leaf bioassays studies evaluating PTM development and survival were conducted using solanaceous plants found in South Africa. The plants tested included; S*olanum melongena L.*, *Solanum elaeagnifolium Cav., Solanum incanum L., Solanum mauritianum Scop., Solanum. nigrum L.*, *Solanum sp., Datura ferox L., Physalis peruviana* L.*, Lycopersicum esculentum* Mill. PTM-resistant 'Spunta', non-transformed 'Spunta', and 'BP1' were also tested. Field trials were conducted to record the number of PTM damaged plants, mines, and larvae per plant on PTM-resistant 'Spunta', non-transformed 'Spunta', 'BP1', eggplant, and tomato.

Results: Greater than 60% PTM survival was observed on eight of the solanaceous plants tested in our laboratory feeding studies. PTM damage, mines, and larvae were detected on non-transformed 'Spunta', 'BP1', eggplant, and tomato in our field trial. No damage was detected on the PTM-resistant 'Spunta" plants.

Conclusions: Our results indicate that there are numerous solanaceous plant species that will serve as alternate hosts for PTM. Therefore, we propose a non-structured refuge as a strategy for managing the evolution of resistance in Spunta G2, relying on alternate hosts as well as non-transformed potatoes.

Insect resistance management strategy for PTM-resistant 'Spunta' potatoes.

Walter Pett[1], David Douches[1], Diedrich Visser[2], Hector Quemada[1], Johan Brink[1], Kelly Zarka[1], Karim Maridia[1], Francisco Santos[1], Kobie de Ronde[2]

[1]Michigan State University, East Lansing, Michigan, United States, [2]ARC-Vegetable and Ornamental Plant Institute, Pretoria, South Africa

Introduction: We have developed a genetically modified 'Spunta' potato (Spunta G2) containing the *Bacillus thuringiensis* (Cry1Ia1) gene for the control of the potato tuber moth, *Phthorimaea operculella*, (PTM) in South Africa. To comply with South Africa's Genetically Modified Organisms (GMO) Act, 1997 (Act no. 15 of 1997) one of the components of a regulatory dossier should address insect resistance management.

Methods: Laboratory leaf bioassays studies evaluating PTM development and survival were conducted using solanaceous plants found in South Africa. The plants tested included; S*olanum melongena L.*, *Solanum elaeagnifolium Cav., Solanum incanum L., Solanum mauritianum Scop., Solanum. nigrum L.*, *Solanum sp., Datura ferox L., Physalis peruviana* L.*, Lycopersicum esculentum* Mill. PTM-resistant 'Spunta', non-transformed 'Spunta', and 'BP1' were also tested. Field trials were conducted to record the number of PTM damaged plants, mines, and larvae per plant on PTM-resistant 'Spunta', non-transformed 'Spunta', 'BP1', eggplant, and tomato.

Results: Greater than 60% PTM survival was observed on eight of the solanaceous plants tested in our laboratory feeding studies. PTM damage, mines, and larvae were detected on non-transformed 'Spunta', 'BP1', eggplant, and tomato in our field trial. No damage was detected on the PTM-resistant 'Spunta" plants.

Conclusions: Our results indicate that there are numerous solanaceous plant species that will serve as alternate hosts for PTM. Therefore, we propose a non-structured refuge as a strategy for managing the evolution of resistance in Spunta G2, relying on alternate hosts as well as non-transformed potatoes.

G protein-coupled receptors from tick (*Rhipicephalus microplus*) and mosquito (*Aedes aegypti*): biological significance and peptidomimetic design for target validation

Patricia Pietrantonio[1], Ronald Nachman[2], Suparna Taneja-Bageshwar[1], Christopher Jagge[1]

[1]*Department of Entomology, Texas A&M University, College Station, TX, United States,* [2]*Southern Plains Agricultural Research Center, USDA, College Station, TX, United States*

Introduction: The female of the mosquito *Aedes aegypti* (Diptera: Culicidae) is a vector of arboviruses causing yellow fever and dengue fever. The tick *Rhipicephalus* (*Boophilus*) *microplus* (Acari: Ixodidae) is the principal tick vector in cattle worldwide. In both, transmission of disease agents is directly linked to the female's obligatory haematophagia for reproductive success. There is no vaccine for dengue, nor a recombinant vaccine against the *Babesia sp.* pathogen causative of bovine babesiosis. The G protein-coupled receptors putatively involved in water balance in these two arthropods are being characterized as potential targets for novel pesticide development.

Methods: Functional studies *in vitro* and *in vivo* are designed to elucidate receptor function and biological significance. RNAi of these receptors was attempted with variable results. The rational design of peptidomimetics based on the insect kinin analog FFSWGa is conducted for receptor target validation. Peptidomimetic design is improved through iterative calcium bioluminescence assays using tick and mosquito kinin receptors expressed in mammalian cells.

Results: We cloned the dih1 (DH_{44}) receptor (GPRdih1) from mosquito renal tubules and report evidence of temporal variation of the GPRdih1 transcript, suggesting that receptor biology (transcriptional expression) in the Malpighian tubule may be linked to hormone release during peaks of diuresis. Six insect kinin analogs were synthesized in which Ser, the primary peptidase hydrolysis site, was replaced with the bulky alpha-amino isobutyric acid (Aib) molecule, and in which the secondary peptidase hydrolysis site was also blocked for biostability. These mimetics were active on tick and mosquito kinin receptors.

Strategies for Insect Resistance Management (IRM) for Bt crops in Brazil and Argentina

Samuel Martinelli[1], Fabiano Ferreira[1], Odnei Fernandes[1], Graham Head[2], Gillermo Videla[3]

[1]Monsanto do Brasil Ltda., São Paulo, São Paulo, Brazil, [2]Monsanto Co., Saint Louis, Missouri, United States, [3]Monsanto LAS, Buenos Aires, Argentina

Genetically modified crops expressing *Bacillus thuringiensis* proteins (Bt crops) have been used for controlling certain lepidopteran and coleopteran pests in various countries. Bt crops provide benefits to farmers and the environment by reducing dependency on conventional chemical pesticides. Nevertheless, due to the continuous expression of these proteins, the evolution of resistance might occur and put at risk the use of this technology. Therefore, to prevent or delay the emergence of insect resistance to Bt crops, the biotechnology industry and farmers have been working together to develop insect resistance management (IRM) programs. Brazil and Argentina have been cropping Bt cotton, and Argentina also has a history of cultivating Bt maize. The plans currently in place in Brazil and Argentina are scientifically rigorous yet practical attempts to significantly delay the evolution of Bt resistance. The details of implementation, and resistance and compliance monitoring, will be covered in this presentation.

Training for biocontrol and sterile insect technique under the same roof: benefits of maintaining the two activities within the same industrial entity

Shimon Steinberg

Bio-Bee Sde Eliyahu Ltd., Bet Shean Valley, Israel

Bio-Bee has been mass producing and releasing natural enemies for biological control of pests since 1983. In 2004, Bio-Bee established a daughter company, Bio-Fly, to rear the Mediterranean fruit fly and supply sterile males for its control through Sterile Insect Technique (SIT). Examples are presented that demonstrate the added value of training for both biocontrol and SIT within the same industrial entity: (i) Pupal products are available for both biological control agents and the medfly. Therefore, quality assessment parameters, such as percent emergence and flight ability, can be determined for the aphid parasitoid, *Aphidius colemani*, and the medfly by using similar methods. These determinations enable adjustments to be made from the number of pupae produced to the number of functional adults released in the field, (ii) For pirate bugs and predatory mites, as well as the medfly, rates of emergence and mortality do not always correlate with adult fitness. This may be due to the same causes both in biocontrol and SIT, (iii) Possibly, the relationship between product control parameters and field performance of the end product can be predicted in both biocontrol and SIT, and (iv) The novel application of SIT to control leafminer flies, *Liriomyza* spp., synergizes with biocontrol of the pest. Bio-Fly produces and sterilizes males and females of the leafminer, *L. bryoniae*, and mass produces its parasitoid, *Diglyphus isaea*. Bio-Bee is a pioneering effort in mutual "fertilization" in education and training for biocontrol and SIT, emphasizing methods for mass production and quality assurance.

Critical oxygen responses in *Drosophila melanogaster* reared in hypoxia or hyperoxia

C Jaco Klok, Jon F Harrison

Arizona State University, Tempe, AZ, United States

Introduction: Atmospheric oxygen availability has long been hypothesized as having important historical effects on insect body size. In *Drosophila melanogaster* adult body size relates positively with rearing oxygen over multiple generations. By contrast leg tracheal dimensions relate, independent of size, negatively with oxygen. How do size and tracheal changes affect the matching of oxygen delivery capacity to oxygen needs? One prediction is that hypoxia reared flies would have lower critical PO_2 values ($CritPO_2$), due to reduced sizes and larger tracheal diameters.

Methods: Metabolic rates (MR) were recorded from adults and larvae reared for 9-11 generations in 10, 21 and 40% O_2. During respirometry % O_2 was steadily decreased, inducing activity (agitation) and an eventual drop in MR. We evaluated MR-$CritPO_2$ as % O_2 where MR drops, and activity-$CritPO_2$ as % O_2 inducing a sharp activity increase.

Results: All adults maintained steady MRs down to ≈2% O_2, before MRs dropped precipitously, independent of rearing O_2. The 40% O_2 reared adults' activity-$CritPO_2$ was 8% O_2 vs 6 to 5% for 21 and 10% O_2 reared adults. MR-$CritPO_2$ for 40% O_2 reared larvae was 8% and 4% for 21 and 10% O_2 reared larvae. Activity-$CritPO_2$ was ≈8% in 40% O_2 reared larvae while 10 and 21% reared larvae had no discernable activity increase. Amazingly, all larvae were able to continue activity even in 20 minutes of anoxia.

Conclusions: The adults' lower MR-$CritPO_2$'s and lack of rearing O_2 effects are consistent with adults having more extensive oxygen delivery capacities for flight. By contrast, the higher larval MR-$CritPO_2$'s and rearing O_2 effects are consistent with the oxygen induced diameter changes of their major longitudinal tracheae. Similarly, rearing oxygen had a narrow effect on adult activity-$CritPO_2$, while only the hyperoxic-reared larvae were noticeably more agitated by decreasing O_2. Continued larval activity despite 20 min of functional anoxia, suggests they have considerable capacity for anaerobic ATP generation.

Establishing the noxious/beneficial status of the zoophytophagous mullein bug, *Campylomma verbasci*

Olivier Aubry[1], Daniel Cormier[2], Gérald Chouinard[2], Timothy Work[1], Éric Lucas[1]

[1]Département des Sciences Biologiques, Université du Québec à Montréal, Montréal, Québec, Canada, [2]Institut de recherche et de développement en agroenvironnement, St-Hyacinthe, Québec, Canada

The mullein bug, *Campylomma verbasci* Meyer (Heteroptera : Miridae) can be an important pest in north American apple orchards. Initially, this zoophytophagous insect can be deleterious during the first larval instars since and can damage apple fruits. After that, it becomes beneficial by preying on mites (mainly *Panonychus ulmi* (Koch) (Acarina: Tetranychidae)). Here we 1) study *in situ* the link between mullein bug and red mite populations and 2) evaluate damage production of apple fruits according to fruits' diameter and cultivar. Densities of the bug in apple orchards were not correlated with densities of red spider mites. The number of feeding punctures did not differ between small (10-13mm) or large (14-17mm) fruits, however, the *Red Delicious* cultivar experienced more attacks than either *Ginger Gold* or *Honey Crisp* cultivars. The behaviour of this insect is discussed with regard to size and cultivar of apple fruits tested. Finally, we propose a new tool for establishing the noxious/beneficial status of the bug directly in orchards.

Anti-plasmodial, anti-trypanosomal and anti-parastic natural products of some selected Kenyan medicinal plants

Joseph Keriko[1], Elizabeth Kigondu[3], Mercy Githua[1], Mary Ndungu[1], Geoffrey Rukunga[3], Gathu Nyaga[1], Ahmed Hassanali[2], Isaiah Ndiege[4], Grace Murilla[5]

[1]Jomo Kenyatta University of Agriculture and Technology (JKUAT), [2]International Centre of Insect Physiology and Ecology (ICIPE), [3]Kenya Medical Research Institute (KEMRI), [4]Kenyatta University (KU), [5]Trypanosomiasis Research Centre (TRC), Nairobi, Kenya

Introduction: Protozoa disease including malaria,and leisimaniasis are a major threat to world health and are becoming more prevalent in developed World due to suppression of the immune system. Hazards associated with the continued use of conventional synthetic insecticides have also greatly hampered the control of protozoal diseases. Data shows that plants extracts have been used both in traditional medicine and in pest management practices for centuries with great success. Thus, extraction, separation and purification of the active principles from plants could produce template compounds for such control.

Methods: Plants parts such as the leaves, stems and root backs of some selected Meliaceae family of plants including some selected species of plants namely; *Suregada zanzibariensis*, *Albizia coriaria Aloe nyeriensis* were solvent extracted, fractionated, separated, purified and the isolated compounds structurally elucidated. Bioassay tests were carried out on both the fractions and pure compounds using various bioassay standard methods.

Results: Eighteen extracts from seven Meliaceae family of plants were tested in vitro against two strains of *Plasmodion falciparum*. Nine extracts were found to be active. Mathanol total extracts of the leaves of *S. Zanzibariensis* showed the highest anti-plasmodial activity. The same extract including the stem bark *of A. Coriaria* and *A. nyeriensis* exhibited good anti-leishmanial activity. Some active compounds were isolated.

Conclusion: In general Meliacese plants and related species of plants shows some potential as sources of anti-protozoal dungs. More *in vivo* activities tests are in progress in order to try to develop potential anti-plasmodial and anti-leishmanial dugs.

Genome-wide insertional mutagenesis in the red flour beetle, *Tribolium castaneum*

Marcé Lorenzen[1], Jochen Trauner[2], Teresa Shippy[3], Gregor Bucher[4], Ernst Wimmer[4], Richard Beeman[1], Martin Klingler[2], Susan Brown[3]

[1]USDA-ARS-GMPRC, Manhattan, KS, United States, [2]Department of Developmental Biology, University of Erlangen, Erlangen, Germany, [3]Division of Biology, Kansas State University, Manhattan, KS, United States, [4]Blumenbach Institute of Zoology and Anthropology, Dpt. of Dev. Biol., Georg-August-University, Göttingen, Germany

Introduction: Despite the fact that beetles are the most species-diverse eukaryotic order, the red flour beetle (*Tribolium castaneum*) genome is the first and so far only sequenced coleopteran genome (www.hgsc.bcm.tmc.edu/projects/tribolium/). Further progress in identifying and understanding the functions of the estimated 16,000 genes will require sophisticated methods of molecular dissection.

Methods: An *in vivo* system for generating new transposon insertions was used. This system utilizes transgenic strains generated using two different transposons (*piggyBac* and *Minos*). The *piggyBac*-based donor lines possess insertion-site-dependent reporter phenotypes dependent on enhancers flanking the insertion sites, as well as an insertion-site-independent reporter phenotype (eye-specific EGFP expression). Donor elements were remobilized via hybridization with *Minos*-based helper lines that supply a source of *piggyBac* transposase. Hybrid progeny (individuals carrying both elements in the same genome) were outcrossed and offspring carrying new insertions selected, as evidenced by loss of insertion-site-specific enhancer phenotype with retention of eye-specific EGFP expression. Insertion-site junctions were cloned, sequenced and their genomic locations determined.

Results: Depending on the donor/helper combination used, 75–100% of single-pair hybrid crosses produced new insertions. We have analyzed over 11,000 new transformants, of which at least 320 are recessive lethal, 24 recessive sterile, and over 200 possess new enhancer-trap phenotypes. Insertion junctions have been determined for many of these and often appear to be located within transcription units.

Conclusions: This highly efficient approach (synthetic hybrid dysgenesis) demonstrates that genome-wide, saturation mutagenesis is feasible in *Tribolium*, and perhaps in other economically important insects.

The *Tribolium* genome project and its potential impact on pest management

Marcé Lorenzen, Brenda Oppert, Richard Beeman

USDA-ARS-GMPRC, Manhattan, KS, United States

The genome sequence of the red flour beetle, *Tribolium castaneum*, a worldwide pest of stored products, has recently been determined (www.hgsc.bcm.tmc.edu/projects/tribolium/). *Tribolium* is the first agricultural pest insect and the first beetle for which the complete genome sequence has been described. *Tribolium* has become a powerful model for molecular genetic and functional genetic studies of pest biology and evolutionary/developmental biology. The *Tribolium* genome offers a rich source of potential targets for novel biopesticides. We have been mining the genomic data for candidate genes, as well as utilizing functional genomics (transgenics and RNA interference) to identify, characterize, and exploit physiological targets for pest control. Among the genes being considered as potential targets are those involved in chitin/cuticle metabolism, osmoregulation, neurotransmission, digestion and immunity. In *Tribolium*, RNA interference (RNAi) can be used to specifically inactivate any gene in all tissues after single injections of the appropriate double-stranded RNAs. The successful deployment of RNAi for pest control will depend on oral delivery of dsRNA produced in transgenic crops. Orally administered dsRNA has been shown to trigger gene silencing in several arthropods; *Ixodes scapularis* (tick), *Epiphyas postvittana* (moth), *Diabrotica virgifera virgifera* (beetle) and *Leptinotarsa decemlineata* (beetle). Continued work on this problem will lead to the identification of biopesticide target genes particularly amenable to oral RNAi-mediated knockout. Some examples of the results from our gene mining efforts will be presented along with an update on our progress towards functional analysis.

Lifting the historical impediment: BUGZonline, an electronic portal to the bibliography of New Zealand terrestrial invertebrates 1775-1993.

Stephen Pawson, Raphael Didham

[1]Scion, Christchurch, New Zealand, [2]University of Canterbury, Christchurch, New Zealand

The 'historical impediment' describes an inability to source early literature to assist in current research. This manifests as a lack of adequate indexing, or the lack of access to printed copies of publications. New Zealand is fortunate in that it has an almost complete bibliography of terrestrial invertebrate literature compiled over three decades. The BUGZ project began with the aim of lifting the historical impediment by utilising new OCR and database technology to provide free, full text, fully indexed access to the 16,043 references listed in the bibliography.

The resource now provides access to over 200,000 pages of invertebrate literature, including journal articles, books, monographs, theses, reports and popular literature. Content can be searched either by title, author, year, full-text or taxon, and articles can be browsed by title or author. Once found pages can be viewed individually as images or downloaded as a complete .pdf document (page range .pdf's are also available). A powerful feature of BUGZonline is the inclusion of UbiO's FindIT and LinkIT technologies; this allows users to select known taxonomic names associated with viewed pages and subsequently link them to external content from other providers such as Genbank and GBIF.

The BUGZ electronic portal is free to all users thanks to New Zealand's Terrestrial and Freshwater Biodiversity Information System who funded the project. Access to the portal is via www.bugz.org.nz – check it out today.

Effects of *Orius laevigatus* (Fieber) on the population dynamics of *Amblyseius swirskii* (Athias-Henriot) and *Bemisia tabaci* (Gennadius) in sweet pepper greenhouses

Hwang-Yong Kim, Jeong-Hwan Kim, Yong-Heon Kim, Yong-Hwi Lee

National Institute of Agricultural Science and Technology, Suwon, Kyung-gi, Republic of Korea

Introduction: In recent, *Bemisia tabaci* causes serious damage on sweet pepper in Korea. So the famers often release *Amblyseius swirskii* to control the whitefly. However, the predatory mite is also a prey to the other kind of predatory bug *Orius laevigatus* which is usually released to control thrips in sweet pepper greenhouse.

Methods: Filed experiment has been performed as follows. *A. swirskii* was released in sweet pepper greenhouse (10,000m^2), before the detection of *B. tabaci*. Every week, we have observed changes in population density of *A. swirskii* and *B. tabaci*. Later, to control the thrips on flowers, *O. laevigatus* was also released. And then the density of *O. laevigatus* has been monitored, too.

Results: Just one application of *A. swirskii* was effective to control *B. tabaci*. The predatory mite was settled down successfully on flowers and leaves. Just one application of *O. laevigatus* was also effective to control thrips. Although most of all *A. swirskii* has disappeared from the flowers after the application of *O. laevigatus*, the predatory bug has no significant influence over *A. swirskii* in the leaves. And consequently, *B. tabaci* has been continuously controlled in low density.

Conclusions: In the case of Korean sweet pepper greenhouse, combined application of *A. swirskii* and *O. laevigatus* was effective to control *Bemisia tabaci* and *Frankliniella occidentalis*.

Beyond barcoding: Genomic approaches to molecular systematics and diagnostics

Stephen Cameron

CSIRO Entomology, Canberra, ACT, Australia

DNA Barcoding has reinvigorated interest in molecular diagnostics however, despite the arguments of its proponents, barcoding does not provide solutions in all instances or for all groups. In instances where barcoding fails, genomic data is a rich source for alternative markers with higher accuracy or resolving power than the blind use of barcodes. Three approaches will be discussed:

1. mt genome mining to determine which genes have the optimal rates of variability;
2. functional barcoding by identifying gene variants responsible for resistance, virulence etc;
3. ecogenomics approaches to blind biodiversity assessments and comparisons between environments.

Collectively these approaches provide more experimentally verifiable approaches to three of the main goals of DNA barcoding – species level systematics, molecular diagnostics and biodiversity monitoring.

Respiration under high metabolic load in *Rhodnius*

Timothy Bradley

University of California, Irvine, California, United States

Three respiratory patterns have been described in insects: Discontinuous, Cyclic and Continuous. The Discontinuous Gas Exchange Cycle (DGC) can be distinguished by the presence of an open phase in which the spiracular valves are fully open, and a closed phase during which oxygen uptake into, and carbon dioxide release from, the insects are essentially precluded. The Cyclic pattern is characterized by cyclic carbon dioxide release with no evidence of a closed phase. The Continuous pattern shows no obvious cyclic pattern. I will discuss the effects of changing metabolic demand on the respiratory patterns of insects. In particular, one can differentiate the separate influence of oxygen demand and carbon dioxide accumulation on different portions of the respiratory control process. Examples from my own research will emphasize studies with the insect *Rhodnius prolixus*, but examples from other species will be discussed as well. The critical parameters influencing respiratory pattern are the size and design of the tracheal system and the rate of oxygen use (aerobic metabolic rate). The minute to minute balance between these two variables, one delivering oxygen, the other removing it, determines the pattern of respiration exhibited by the insect at any given time.

Genetic structure, origins, and evolution of biotypes in the *Bemisia tabaci* species complex

Margarita Hadjistylli[1], Judith Brown[2], George Roderick[1]

[1]University of California, Berkeley, Berkeley, California, United States, [2]University of Arizona, Tucson, Arizona, United States

Introduction: The sweetpotato whitefly, *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae), is a cryptic species complex with its members (biotypes/haplotypes) exhibiting high genetic differentiation but no morphological variation. In this study, we examined genetic structure of worldwide populations and tested for evidence of allopatric diversification.

Methods: We genotyped individuals from 25 worldwide populations representing major biotypes/haplotypes at 15 microsatellite loci. We calculated pairwise genetic differentiation (F_{ST}) using the software Arlequin and assessed gene flow and genetic structure between populations using maximum likelihood and Bayesian inference approaches in the programs Migrate and Structure.

Results: Our analyses show significant genetic differentiation among most populations, especially between distinct geographic locations, suggesting allopatric divergence. High differentiation was detected even between biotypes overlapping in range, such as B and Q in the Mediterranean, suggesting strong reproductive isolation. Yet, biotypes B and Q seem to have diverged more recently than others, pointing to a common diversification center in the Mediterranean/North Africa/Middle East region that could explain the evolution of similar high pest attributes because of the long history of agriculture in the area. Our results are supported by the mitochondrial C01 gene phylogeny obtained for the same samples in a parallel study. Genetic data from biotypes B and Q are now used to understand how historical demography may have contributed to their diversification and worldwide expansion.

Conclusion: High genetic structure in the *B. tabaci* complex suggests that biotypes constitute genetic entities that are in the process of divergence into distinct species, especially when isolated by large geographic distances.

Odor representation in *Drosophila* local neurons

C Giovanni Galizia, Ana F Silbering

Universität Konstanz, Konstanz, Germany

Introduction: Olfactory coding is intrinsically combinatorial, involving the activity of several populations of neurons simultaneously. Furthermore, olfactory coding is hierarchical, with several processing steps leading from receptor neurons to central brain areas. We investigate odor representations both vertically and horizontally along these lines exploiting physiological and genetic tools in *Drosophila melanogaster*.

Methods: We recorded odor evoked responses in the antennal lobes of fruit flies, and characterized complete concentration-response curves. Using specific promotors, we expressed the calcium sensitive reporter GCaMP in olfactory sensory neurons, in three populations of local neurons, and in projection neurons. Data were recorded with a cooled 12-bit CCD camera, and further processed using IDL and R. Signals were evaluated in identified glomeruli across animals.

Results and Conclusions: The results indicate that the neural network within the antennal lobe is actively involved in shaping odor responses. In particular, both spatial and temporal aspects of odor-response profiles differed for the three populations of local neurons. Furthermore, responses in projection neurons could not be predicted by responses in sensory neurons alone. Also when all local neuron activity in that glomerulus was taken into account, no reliable prediction was possible. These results indicate that the responses in a glomerulus, at the level of projection neurons, is modulated both by single-glomerulus input and by network activity across glomeruli.

Eldana saccharina Walker (Lepidoptera: Pyralidae) assessment in the ZSAES sugarcane varieties' breeding and selection program: the road to ZN10 limited release in the Zimbabwe Sugar Industry

Audrey R.S Mutambara-Mabveni, Marvellous Zhou

[1]*ZSAES, Chiredzi, Zimbabwe,* [2]*ZSAES, Chiredzi, Zimbabwe*

Introduction: The sugarcane variety selection program in Zimbabwe was initiated in 1976 with the stated objective of increasing cane yield, quality and pest and disease resistance. About 100 crosses are made annually, under contract, by the South African Sugarcane Research Institute and the selections done in the southeast lowveld of Zimbabwe. The crosses series started in 1993 resulted in the limited release of cross 93-2317 (variety ZN10) in the Zimbabwe Sugar Industry in 2007. For this series, *Eldana saccharina* damage assessments were started in year 8 (pre-release variety trials stage) of the 13-year process.

Methods: Standard *E. saccharina* assessments were carried out in all pre-release variety trials with the 17 crosses/selections that reached year 8 of the 1993 series. Randomly selected sugarcane stalks were visually inspected for borer entry and exit holes, to determine the number of cane stalks bored. The stalks were then split longitudinally to determine the proportion of internodes bored per stalk. Larvae were collected and identified and damage ascribed to *E. saccharina* or any other borer. Data were analysed with SAS statistical software (SAS Institute Inc., 1999-2001).

Results: Statistical analysis indicated that there were significant differences ($p<0.001$) among the 17 crosses, in response to natural infestations by *E. saccharina.* Cross 93-2317 was among the least damaged crosses. The first ratoon crop was the most damaged, while crops harvested in the mid-season (June, July, August) were the least damaged. There were significant differences ($p<0.001$) in the performance of the crosses when grown in different localities. Cane older that 11.5 months had higher infestation levels compared to younger cane.

Conclusion: Cross 93-2317 has tolerance/resistance to *E. saccharina* damage among other desired attributes, such as high cane yield, high sucrose and tolerance to smut. Cross 93-2317 was recommended for limited release in the Zimbabwe Sugar Industry as variety ZN10. *E. saccharina* poses a threat to the growing of ZN10 in the Zimbabwe Sugarcane Industry, and infestation levels increase as the cane matures.

Peptidergic and monoaminergic mechanisms regulating circadian rhythms in insects

Makio Takeda, Susumu Hiragaki, Le Thi Duie Trang

Kobe University, Kobe, Hyogo, Japan

Recently, the molecular mechanism underlying circadian rhythm has been investigated in some model insects such as *Drosophila melanogaster,* cockroaches, and silkmoths. About a dozen of genes have been found in *D. melanogaster* .They form interlocked negative feedback loops. Homologous genes have been found in other insects but with some unique features to each species. The output pathways to regulate peripheral rhythms seem to vary. Unlike central cog mechanisms, the output pathway has not been worked out even in *D. melanogaster.* A convincing factor regulating this pathway is PDF, pigment dispersing factor in *D. melanogaster.* Since PDF-ir resides in the putative circadian pacemaker cells that express most of the clock gene products and that using mutants causing different degrees of optic lobe deformation, the number of PDF-expressing neurons and the strength of rhythmicity have a strong correlation. Also, a *pdf* mutant lost the rhythmicity. However, it is not likely that all output pathways are PDF-regulated, since *lark* mutant produces abnormal eclosion rhytms but locomotor activity rhythm is intact and pdf receptor is not expressed in neurosecretory cells.

Although surgical operations point to the accessory medulla region of the cockroach as the most critical locus to keep normal circadian rhythms, the IHCinvestigations have demonstrated that clock proteins-like antigens are not restricted to a particular part of the brain. We will show data indicating not only PDF but other factors are involved in circadian regulation. The classical scheme that the circadian pacemaker of the orthopteroid insects is located at the accessory medulla using PDF as an output messenger will be reappraised by focussing other factors, since this site expresses several other peptide-like immunochemical reactivities, such as BPP/NPF, glicentin, PHI, gastrin/CCK in *P. americana*, while some peptides like ATH, ASH and GABA caused phase shifts in *Leucopheae*. Melatonin and 5HT also are important in regulating circadian system in cockroaches and moths. There are several NAT genes but some have E-box in the regulatory region, and this is the access point of clock core mechanism to output pathway. I will show the neuroanatomical structure of peptides and indolamine mechanisms regulating circadian system and give its functional implications.

Dynamic of differentiation and hybridization in *Carabus solieri* : a comparison of morphological, genetic and colour variation throught a zone of genetic exchanges

Paul Alibert[1], Sabrina Gaba[2], Stéphane Garnier[1]

[1]CNRS-Université de Bourgogne UMR 5561 Biogéosciences, Dijon, France, [2]Unité de recherche Biologie et Gestion des Adventices-INRA Dijon, Dijon, France

Zones of genetic exchanges between differentiated entities provide valuable informations on the patterns of species distribution and the dynamic of divergence and speciation in time and space. Despite a rather restricted range (southern and Ligurian Alps in Europe) the ground beetle *Carabus solieri* exhibit significant morphological, genetic, and colour variations fitting with a clear geographical structuration. The present work focuses on a transition zone between two subspecies of *C. solieri* differing for all three features and examines their patterns of transition along a transect across the range of the subpecies and the zone of genetic exchanges. Morphological variation was assessed using outline analyses (Dual Axis Fourier Shape Analysis) of two external and genital characters: pronotum and aedeagus shapes, respectively. Genetic variation was appraised using 10 microsatellites loci and colour was captured, separately for the pronotum and the elytra, with a video camera and quantified using the position of the specimens in the RGB and HLS spaces. Variation along the transect of the morphological, genetical and colour caracters are fittet to maximum likelihood clines. Cline widths and position of cline centers are then estimated and compared between the different markers. A strong concordance and coincidence among clines is expected to reveal a selection acting on the whole genome whereas differences in cline positions and widths can suggest that selection operates differentially on the different characters (including between external and genital traits). Dynamic of introgression and selection of the putative hybrid zone are discussed in the light of these results.

Termites may be a friend to farmers: Ecosystem services in wheat paddocks in Australia

Theodore Evans[1], Tracy Dawes-Gromadzki[2]

[1]*Commonwealth Scientific and Industrial Research Organisation, Canberra, ACT, Australia,*
[2]*Commonwealth Scientific and Industrial Research Organisation, Darwin, NT, Australia*

Termites, along with ants and earthworms, the 'soil macrofauna', are known as ecosystem engineers' because of their ability to move soil and so affect mixing of soil layers by re-distributing soil types, aeration and water movement. These processes are known to be beneficial to other, smaller organisms and to plants in natural landscapes, which suggests that they may be desirable to have in production landscapes. However, soil macrofauna are vanishingly rare in Australian agricultural landscapes used for cropping, especially the very large areas used for wheat, barley, oats and canola, due to the regular disturbance to the soil from ploughing and other tillage – even some forms of seeding. Conservation tillage practices combined with stubble retention, originally implemented to minimize erosion of topsoil, have enabled the return of some termite species (and other soil organisms) to re-establish in these landscapes. The termite species are all grass harvesters belonging to *Amitermes*, *Drepanotermes*, *Nasutitermes* or *Tumilitermes*, which consume the stubble, dead leaves and roots of the crop plants. The effect of the soil macrofauna on the soil and productivity in wheat crop lands was examined in a two factor experiment, with insect exclusion (using a synthetic pyrethroid insecticide) and tillage as the factors. Soil macronutrients, water content and infiltration, and crop production are measured annually. The results to date for this preliminary experiment will be presented.

RNAi mediated silencing of essential multigenes of baculovirus induces higher level of resistance in transgenic silkworm, *Bombyx mori*

Subbiah Edupalli[1], Sriramana Kanginakudru[1], Corrine Royer[2], Vankadara Sivaprasad[3], - Chandrashekaraiah[3], Bernard Mauschamp[2], Gerard Chavancy[2], Pierre Couble[4], Javaregowda Nagaraju[1]

[1]Centre of Excellence for Genetics and Genomics of Silkmoths, Laboratory of Molecular Genetics, Centre for DNA Fingerprinting and Diagnostics,, Hyderabad 500 076, India, [2]Unité Nationale Séricicole,, 25 Quai, JJ Rousseau 69340, La Mulatière, France, [3]Andhra Pradesh State Sericulture Research and Development Institute,, Kirikera, Hindupur, Andhra Pradesh, India, [4]Centre de Genetique Moleculaire et Cellulaire, Universite Claude Bernard, 69622 Villeurbanne Cedex, France

Introduction: RNA interference (RNAi) approach has been used for anti-viral therapy with varied degree of success in different eukaryotic systems. In the study reported here we speculated that by simultaneously abrogating several essential genes of invading Bombyx mori Nuclear Polyhedrosis Virus (*Bm*NPV) it is possible to mount higher level of protective effect against viral infection in silkworm.

Methods: Towards achieving this goal, we constructed *piggybac* transposon-mediated transgenic silkworm strains that expressed double-stranded RNA (dsRNA) specific to four essential viral genes placed in tandem in flip-flop (MFF) orientation. We also obtained transgenic silkworms that expressed only *sense* (S) or *antisense* (AS) forms of these baculoviral genes.

Results: Our results show significant inhibition of baculovirus proliferation in MFF transgenic lines as compared to, *sense* , *antisense*, and their hybrids. The MFF harbouring transgenic lines registered significantly higher level of resistance to baculovirus infection as compared to the silkworm lines carrying single essential bauloviral target gene as reported in our earlier study (Kanginakudru et al. 2007 Insect Molecular Biology **16,** 635–644).

Conclusion: These results suggest that the RNAi pathway can be successfully exploited in developing baculovrus resistant silkworm strains which could find commercial applications in sericulture.

Study on the potential of native fungal isolates and *Metrahizium anisopliae* var. *acridum* for greater wax moth, *Galleria mellonella* (L) in Ethiopia.

Hellen Namusana, Emiru Seyoum, Bekele Jembere

Addis Ababa University, Addis Ababa, Ethiopia

Introduction: The greater wax moth is widely distributed in Ethiopia and various control measures had been used against the greater wax moth but use of pathogens in general and fungi in particular. It has been well documented that the entomopathogenic fungi, *Metarhizium* and *Beauveria* have proved to be potential candidates for many insect pests. Thus, this study investigated the potential of *Metarhizium anisopliae* var. *acridium* (IMI330189) and *Beauveria* (IITA 18) in comparison with two local isolates were compared against, adult wax moths. The possible effect of the fungal isolates on the honeybee colonies was also investigated.

Materials and methods: The effects of six fungal isolates including, DLCO-AA5, DLCO-AA14, DLCO-AA83, DLCO-AA 109, IITA 18 and IMI 330189 were evaluated in the laboratory for their pathogenicity to adult greater wax moths. Spore dilutions were prepared in 0.5% Tween 80. Adults were treated by spraying 2 ml of conidial suspensions ranging from $4x10^4$ to$4x10^7$ conidia /ml.

Results: Adult GWM were found to be susceptible to all isolates and concentrations used. Comparison of post treatment mortality of adult, greater wax moth (GWM) at the lowest concentration ($4x10^4$ conidia/ml) revealed that infection of $\geq$ 90% could be achieved by day 13 post inoculation. Investigations into effects of mycosis on percentage emergence of adults fungal from fungal treated pupae of the GWM showed no significant difference ($P>0.05$) between the different fungal isolates and controls. With all fungal concentrations (($4x10^4$ to $4x10^7$ conidia/ml) used, percentage emergence of over 86.1% was observed in adult GWM.

Implications of global environmental change for above- and belowground insect-insect and insect-plant interactions

Greg Masters[1], Felix Wackers[2], Alan Gange[3], Joanne Staley[4]

[1]CABI-LEC Alliance, Lancaster, United Kingdom, [2]Lancaster University, Lancaster, United Kingdom, [3]Royal Holloway, Egham, United Kingdom, [4]Imperial, Ascot, United Kingdom

Interactions between species are a central tenet of entomology and ecology, but it is only relatively recently that we have started to understand the importance of the belowground system in such multitrophic communities. Recent advances have led to a greater understanding of the important role that insect-insect and insect-plant interactions have in driving the complex interplay between above- and belowground systems. The mechanisms and processes of such interactions potentially are numerous and can include changes in host-plants, in terms of overall level and allocation of water content, C, N and secondary metabolites, as well as altered plant phenology, stature, morphology and community structure. However, it is these same mechanisms and processes within communities and plants that will be affected by Global Environmental Change (GEC). We consider GEC to be primarily climate change but also to include pollution and changes in land-use. All of these environmental drivers, but particularly climate change, can affect physiological, autecological and population/community mechanisms underlying multitrophic interactions.

Although the implications of GEC for ecosystems, communities, populations and individual insect and plant species are increasingly understood, we know little about how such changes will affect multitrophic interactions, particularly between above and belowground systems.

Here, we examine the potential consequences of GEC for above- and belowground interactions by using conceptual and model laboratory and field above- and belowground insect herbivore systems, which manipulate temperature and water relations in line with climate change predictions. From this evidence, existing models of above-belowground interactions will be examined when subject to a climate manipulations. Although species may respond idiosyncratically, our aim is to seek general response patterns., limited evidence available.

Interactive auditory communication in mosquitoes

Ben Warren[2], Robbie Girling[1], Gabriella Gibson[1], Ian Russell[2]

[1]National Resources Institute, Chatham, United Kingdom, [2]University of Sussex, Brighton, United Kingdom

Introduction: It has been well documented that mosquitoes detect near field sounds (<10 cm away) using their Johnston's organ, an auditory structure located at the base of their antennae. Furthermore, male mosquitoes are known to be attracted by sound, within a frequency range similar to that of the females' flight tones, but nothing is known of female responses to sound. We investigated how males and females respond to one another's flight tones in species where male and female flight tones are similar (*Toxorhynchites brevipalpis*) and where they vary greatly (*Culex* spp.).

Methods: The sounds produced by tethered flying male and female mosquitoes were recorded using a particle velocity microphone (Knowles NR-3158) and analysed using Spectrogram 12 (Visualization Software, LLC) software. Flight tones were recorded from individuals of each sex, same-sex pairs and opposite-sex pairs.

Results: Individuals of *Tx brevipalpis* flown together in male-female pairs initially flew at their own endogenous wing beat frequencies, but in response to the other's flight tones they gradually converged on a common fundamental wing-beat frequency. In contrast, male-female pairs of *Culex* spp. converged not at their fundamental wing-beat frequencies but at higher harmonics, which are at frequencies outside their auditory range. Same-sex pairs of all the species tested did not converge either at a common fundamental or harmonic frequency.

Conclusions: We have discovered a form of auditory communication between male and female mosquitoes, which may be involved in mate recognition.

Botanical pesticides for stored grain protection: from the laboratory to the farm

Brighton Mvumi[1], Alex Chigoverah[1], Kenias Nyevedzanai[1], Phosiso Sola[2], Phillip Stevenson[4], Gudeta Sileshi[5], Steven Belmain[3], David Hall[3], Stephen Nyirenda[6], John Kamanula[7]

[1]University of Zimbabwe, Harare, Zimbabwe, [2]Southern Alliance for Indigenous Resources, Harare, Zimbabwe, [3]Natural Resources Institute, University of Greenwich, Chatham Maritime, Kent, United Kingdom, [4]Royal Botanic Gardens, Richmond, Surrey, United Kingdom, [5]World Agroforestry Centre (ICRAF), Lilongwe, Malawi, [6]Department of Agricultural Research Services, Mzuzu, Malawi, [7]Mzuzu University, Mzuzu, Malawi

Introduction: Storage insect pests remain one of the biggest threats to food security in sub-Saharan Africa where grain is usually stored for at least 6 months. Normally, farmers would use synthetic chemical pesticides but they are facing challenges in using these pesticides including unavailability, resistance development, high cost and adulteration. Therefore, farmers resort to using pesticidal plants which they have tried and tested over many years. Although much laboratory work has been conducted by many researchers, the results have been of limited use in the field.

Methods: Field trials were set-up in Zimbabwe using *Bobgunnia (Schwarztia) madagascarensis*, *Dichrostachys cinerea, Bauhunia thoningii, Lippia javanica* and *Aloe* spp. previously identified by the farming community. The plant materials were applied at 2% w/w on threshed maize and beans or cowpeas as fruit or leaf powder, except for *Aloe* spp. which was used as an ash. Actellic Super dust (at label rate) and neem, *Azadirachta indica* (at 2%w/w) were used as positive controls while untreated grain served as negative control. Grain was sampled from each treatment at the beginning of the experiment and at 8-week intervals subsequently, and analysed in the laboratory for insect numbers and species, and grain damage.

Results: Preliminary results indicate that the plant materials did have some effect but not sufficient to suppress grain damage and insect multiplication as much as Actellic Super dust or neem. Among the plants tested, *B. madagascarensis* showed the greatest pesticidal potential.

Conclusions: Considerable grain protection was achieved with *B. madagascarensis* applied at the rate of 2% w/w. Further studies are required to explore dose-response modelling and to identify the active ingredients so as to optimise the use of pesticidal plants.

Plant volatile and pheromone baited traps for the strawberry blossom weevil

Atle Wibe[1], Helena Bichão[2], Anna-Karin Borg-Karlsson[3]

[1]Bioforsk - Norwegian Institute for Agricultural and Environmental Research, Tingvoll, Norway, [2]NTNU - Norwegian University of Science and Technology, Trondheim, Norway, [3]KTH - The Royal Institute of Technology, Stockholm, Sweden

Introduction: The strawberry blossom weevil, *Anthonomus rubi*, is a major pest insect of cultivated strawberry in northern part of Europe. The weevils deposit eggs in the flower buds before it sever the buds from their stalks, leading to a direct loss of crop. The aim of this project is to develop an effective plant protection method without eradicants, to be used in both conventional and organic agriculture.

Methods: Volatiles emitted by the strawberry plants were collected using SPME and identified by GC/MS. To identify important volatiles for host location some compounds were tested as stimuli in electrophysiological studies of the insect antenna. In a field study using funnel traps two potential plant volatiles PV1 and PV2 and the pheromone blend Grandlure (Ph) were tested. The volatiles were tested separately and in mixtures.

Results: The chemical analysis of the host volatiles identified several compounds present in different quantities. Some of these compounds elicited electrophysiological responses in the insect antennae. In the field study traps baited with Ph caught more weevils than the traps baited with PV1 or PV2. Traps baited with PV1+PV2 or PV1+Ph caught about the same as traps baited with Ph. When the traps were baited with PV2+Ph or PV1+PV2+Ph a significant increase of caught weevils were recorded.

Conclusions: The results have shown that there may be a synergistic effect between PV2 and Ph when used as bait for trapping strawberry blossom weevils. This can be important knowledge for developing a new plant protection method for strawberry.

An integrated molecular and histological study on the impact of sublethal effects of Fenoxycarb on the European honeybee, *Apis mellifera*

Kevin Heylen[1], Johan Billen[1], Roger Huybrechts[1], Lutgarde Arckens[1], Bruno Gobin[2]

[1]Katholieke Universiteit Leuven, Leuven B-3000, Belgium, [2]Zoology Department, Sint-Truiden B-3800, Belgium

The aim of our research was to investigate if a synthetic Juvenile hormone (JH)-analog (the insecticide Fenoxycarb) potentially affects physiological processes in the honeybee. We evaluated effects on both the molecular level (gene and protein expression in the brain) and the organ level (hypopharyngeal gland development). Both mRNA and protein expression profiles were analysed in age-matched treated and control bees to identify relevant components using microarray and 2D-DIGE (2-dimensional fluorescence difference gel electrophoresis). Analysis of brains resulted in a list of 21 genes that were consistently differentially expressed in microarray experiments for 2 different colonies, while 7 differential protein spots were shared in 2D-DIGE experiments on 3 different colonies. So far, four protein spots were successfully identified using MS, of which two also appeared in the microarray list. When we focused on a specific gene involved in the transition from nurse to forager, bees treated with the JH-analog showed different expression to control bees. Moreover, histological studies on the important and JH-sensitive hypopharyngeal glands were also performed to look for morphological differences between treated and control bees. Age related degeneration of the hypopharyngeal gland progressed faster in bees, treated with Fenoxycarb, in comparison to control bees. Our data show that effects of JH-analogs on bees can be detected at the molecular and developmental level which provides a potential tool for side-effect evaluation.

Effects of potato viral infections in the biology and preference of aphid vectors and their epidemiological implications

Juan M. Alvarez, RajagopalBabu Srinivasan

University of Idaho, Aberdeen, Idaho, United States

Introduction: Virus infections influence the quality of plants directly affecting the performance of aphids feeding on these plants. PVY and PLRV are the two most economically important viruses in the potato crop in Idaho, the number one potato producing state in the United States. The two viruses can frequently be found on the same plant. The objective of this study was to determine the consequences of single and mixed infections on the insect vectors and how these infections in turn affect the vector dynamics and disease epidemiology.

Methods: Tissue culture plantlets were single and mix infected with PVY (including necrotic strains) and PLRV and the life histories (nymphal period, adult longevity, daily fecundity and intrinsic rate of increase) of the two most important aphid vector species were studied on these plants using leaf cages. Settling bioassays with alatae and apterae aphids were conducted on single and mixed infected plants.

Results: Aphid fecundity was significantly higher on mixed-infected plants than on singly-infected plants or non-infected plants. Both winged and wingless aphids preferentially settled on PVY-PLRV infected plants than on singly-infected plants or non-infected plants. Mixed-viral infected plants with these two heterologous viruses exhibited more severe symptoms than singly-infected plants.

Conclusions: Mixed infections have resulted in synergistic interactions, drastically altering plant viral-susceptibility and physiological status, which severely altered host plant symptom expression patterns as well as vector-preference behavior. Some of these interactions may provide an explanation for the recent spike in incidence of PVY necrotic variants in Idaho and some other regions.

Effects of potato viral infections in the biology and preference of aphid vectors and their epidemiological implications

Juan M. Alvarez, RajagopalBabu Srinivasan

University of Idaho, Aberdeen, Idaho, United States

Introduction: Virus infections influence the quality of plants directly affecting the performance of aphids feeding on these plants. PVY and PLRV are the two most economically important viruses in the potato crop in Idaho, the number one potato producing state in the United States. The two viruses can frequently be found on the same plant. The objective of this study was to determine the consequences of single and mixed infections on the insect vectors and how these infections in turn affect the vector dynamics and disease epidemiology.

Methods: Tissue culture plantlets were single and mix infected with PVY (including necrotic strains) and PLRV and the life histories (nymphal period, adult longevity, daily fecundity and intrinsic rate of increase) of the two most important aphid vector species were studied on these plants using leaf cages. Settling bioassays with alatae and apterae aphids were conducted on single and mixed infected plants.

Results: Aphid fecundity was significantly higher on mixed-infected plants than on singly-infected plants or non-infected plants. Both winged and wingless aphids preferentially settled on PVY-PLRV infected plants than on singly-infected plants or non-infected plants. Mixed-viral infected plants with these two heterologous viruses exhibited more severe symptoms than singly-infected plants.

Conclusions: Mixed infections have resulted in synergistic interactions, drastically altering plant viral-susceptibility and physiological status, which severely altered host plant symptom expression patterns as well as vector-preference behavior. Some of these interactions may provide an explanation for the recent spike in incidence of PVY necrotic variants in Idaho and some other regions.

Evolution of segmentation mechanisms in insects, as revealed by a study on the cricket *Gryllus bimaculatus*

Taro Mito, Taro Nakamura, Tetsuya Bando, Hideyo Ohuchi, Sumihare Noji

The University of Tokushima, Tokushima, Japan

The mode of segmentation in short and intermediate germ insects differs from that in *Drosophila*, a long germ insect. In order to elucidate segmentation mechanisms of short/intermediate germ insects, we have investigated functions of orthologues of the *Drosophila* segmentation genes as well as regulatory interactions among those genes, with a phylogenetically basal, intermediate germ insect, *Gryllus bimaculatus*. With RNAi-based analyses of gene functions in *Gryllus* embryogenesis, we previously demonstrated the divergent aspects of the segmentation mechanism in *Gryllus*, which are following: (1) Caudal (Cad) probably acts as a crucial morphogen with a posterior-to-anterior gradient, regulating the gap genes *hunchback* (*hb*) and *Kruppel* (*Kr*). (2) *even-skipped* regulates *hb* and *Kr* expression in a gap pattern. (3) *extradenticle* regulates *hb* and *eve* expression in the gnathal region, fulfilling a gap-like function. (4) Wingless/Armadillo signaling is involved in posterior elongation/segmentation, activating *cad* expression. Recently, we found that *Gryllus* has two *orthodenticle* (*otd*)-related genes, *Gb'otd1* and *Gb'otd2*, probably orthologous to *otd1* and *otd2* in other insects, respectively. *Gb'otd1* is expressed during blastoderm stage, whereas *Gb'otd2* expression starts later in a germband stage. An RNAi analysis revealed that *Gb'otd1* is required for patterning of the head and thorax, a larger domain than that regulated by *Drosophila otd,* through regulation of gap genes. Our findings indicate that the regulatory networks of segmentation genes and network components differ between *Gryllus* and *Drosophila*. This implies that molecular mechanisms of segmentation changed dynamically during insect evolution, whereas the segmented body plan itself remained substantially unchanged.

Activity of the homing endonuclease gene I-*Ppo*I in the germline of transgenic *Anopheles gambiae* mosquitoes

Nikolai Windbichler, Philippos Aris Papathanos, Andrea Crisanti

Imperial College, London, United Kingdom

Homing endonuclease genes are rare cutting DNA endonucleases that combine the capability to selectively disrupt specific gene sequences with the ability to spread from a few individuals to an entire population through homologous recombination repair events. Because of these properties HEGs are regarded as promising candidates to transfer genetic modifications from engineered laboratory mosquitoes to wild type populations including *Anopheles gambiae* the vector of human malaria. We have shown that the I-*Ppo*I homing endonuclease recognises and cleaves its highly conserved recognition site, located within the 28S rRNA genes on the X chromosome of *A. gambiae*, with high efficiency in cell lines, embryos and transgenic mosquitoes. We have proposed a gene drive system for mosquitoes that is based on this finding and aims to selectively incapacitate X-carrying spermatozoa. Such a system could be used to control the size of field populations by imposing severe sex biases or to drive transgenes through a population. We have generated a number of transgenic *A. gambiae* mosquito strains that express a fusion protein of the I-*Ppo*I homing endonuclease and the eGFP fluorescent marker under the control of the male germline specific beta2 tubulin promoter. We are measuring the effect on sex ratios and fecundity in male and female crosses of these transgenic lines to assess the potential of this system for mosquito vector control approaches.

Biology and larval feeding rate of *Scaeva albomaculata* (Diptera: Syrphidae) on *Macrosiphum rosae* (Linnaeus) (Homoptera: Aphididae) in laboratory conditions

Farzad Jalilian[1], Naser Moeeny Naghadeh[2], Seyed Mahdi Mahjoob[1], Mohammad Taghi Tohidi[1]

[1]Razi University, Kermanshah, Iran, [2]Agricultural research Center, Kermanshah, Iran

Introduction: Biological characteristics and larval feeding rate of hoverfly, *Scaeva albomaculata* (Macqaurt) were investigated on *Macrosiphum rosae* (L.) at laboratory conditions.

Material and Methods: The experiments were carried out in growth chamber at 27±2ºC, RH 60±5% and a photoperiod of 16:8 (L : D).

Results: The egg, 1st, 2nd, 3rd larval instars, prepupa and pupal developmental times were determined as 4.50 ± 0.42, 2.5 ± 0.22, 3.83 ± 0.37, 1.16 ± 0.16, 5.50 ± 0.71, 5.50 ± 0.71 days, respectively. Adult longevity was considerably increased (32.75 ± 2.78 days) when they fed with honey solution, while in food free conditions, they were alive only 4.33 ± 0.88 days. The results indicated that each female produce 110.5 ± 10.74, eggs during oviposition period, 88.50% of these eggs hatched to first instar larvae. There were significant differences ($P<0.01$) between daily feeding rate of the first, second and third instar larvae. Each larva fed 511.37 aphids during larval period and revealed a high potential of feeding on *M. rosae*. The third instar larvae had an important role in feeding rate of larval period and 78.32% of total larval feeding was due to this instar. Per capita daily feeding rate of the first, second and third instar larvae were 7.94, 33.06 and 104.48 , respectively.

Conclusions: Because of high feeding rate, the hoverfly, *S. albomaculata* can be used in biological control and integrated management programs of *M.rosae*.

Integration of growth and positional information by *Dachsous-Fat* signaling in leg regeneration of the two-spotted cricket *Gryllus bimaculatus*

Tetsuya Bando, Yuko Maeda, Fumiaki Ito, Taro Nakamura, Taro Mito, Hideyo Ohuchi, Sumihare Noji

University of Tokushima, Tokushima, Japan

Tissue regeneration, which is a mechanism recovering a lost part of tissue, is well known phenomenon in several animals and is classically categorized into two modes; morphallaxis and epimorphosis. Two-spotted cricket *Gryllus bimaculatus* recovers distal missing part in epimorphic manner. However, we do not know how regenerating cells know their positional information and how the regenerating cells know how many times they should divide to restore the lost part. Here we show that Fat signaling that widely regulate proximodistal patterning, planer cell polarity and cell proliferation in *Drosophila* is also involved in cell proliferation and positional information of leg regeneration in the cricket. Nymphal RNAi for *Gryllus* homologues of *fat*, *dachsous*, *expanded*, *merlin* and *warts* caused enlargement at blastemata of regenerating legs by over cell proliferation, while nymphal RNAi for *Gryllus* homologues of *fat*, *dachsous* and *dachs* recovered the lost part, but the lengths of regenerating legs were shortened depending on the amputated positions. These nymphs also showed defects in normal and reversed intercalary regeneration, showing loss of positional information in the balstemata. We found that in regenerated legs exhibiting nymphal RNAi for *fat*, *dachsous* and *dachs*, lost parts were recovered in a morphallactic manner. Our results suggested that different signaling cascades leading to cell growth and positional information are integrated by the Dachsous-Fat signaling during leg regeneration.

Effect of ionizing (gamma) and non-ionizing radiation (UV) on the development of *Trichogramma turkestanica*

Aydin S. Tuncbilek[1], Fahriye Sumer[2], Ulku Canpolat[3]

[1]Erciyes University, Seyrani Faculty of Agriculture, Department of Plant Protection,, Kayseri, Turkey, [2]Erciyes University, Faculty of Sciences and Literature, Department of Biology, Kayseri, Turkey, [3]Erciyes University, Faculty of Sciences and Literature, Department of Biology, Kayseri, Turkey

Introduction: Ionizing (gamma) and non-ionizing radiation (UV) were used to determine possible effectiveness on the development of *Trichogramma turkestanica*

Methods: Various instars of *Trichogramma turkestanica* (Hymenoptera: Trichogrammatidae) were exposed to gamma radiation for different doses (0-25 Gy) and ultraviolet (UV) radiation with 254nm wavelength (UV-C) for different durations (0-10 min) to assess their effect on each instars and their potential in breaking the developmental cycle of the egg parasitoid.

Results: The egg of *T. turkestanica* was more sensitive to gamma radiation and there was no adult emergence at the dose of 25 Gy. Pupal stage was more resistant to gamma radiation and adult emergence was not stopped within the investigated doses. The prepupa of *T. turkestanica* was more sensitive to UV radiation and there was no adult emergence at the duration of 4 minutes and above. Egg stage was more resistant to UV radiation and adult emergence was not stopped within the investigated doses. Longevity of irradiated adult was gradually decreased with increasing doses when compared with untreated control. Influence of irradiated host eggs on *T. turkestanica* will be discussed.

Conclusions: Biological effect of gamma radiation on *T. turkestanica* was different from UV radiation.

Invasion of Europe by the western corn rootworm, *Diabrotica virgifera virgifera*: multiple transatlantic introductions with various reductions of genetic diversity

Marc Ciosi[1], Nicholas J Miller[2], Kyung Seok Kim[2], Rosanna Giordano[3], Arnaud Estoup[4], Thomas Guillemaud[1]

[1]Equipe; Biologie des Populations en Interaction, UMR 1301 IBSV INRA-UNSA-CNRS, Sophia Antipolis, France, [2]USDA-ARS, CICGRU, Genetics Laboratory, Iowa State University, Ames, IA, United States, [3]Illinois Natural History Survey, Division of Biodiversity and Ecological Entomology, Champaign, IL, United States, [4]INRA, UMR CBGP (INRA / IRD / Cirad / Montpellier SupAgro), Montferrier-sur-Lez, France

The early stages of invasion involve demographic bottlenecks that may result in lower genetic variation in introduced populations than in the source populations. Previous population genetic studies of invasive species have reported very different levels of losses of genetic variability in comparisons of source and invasive populations. Descriptions of invasive species for which multiple introductions from a single source population have been demonstrated may be a particularly informative subject of study. The western corn rootworm (WCR), *Diabrotica virgifera virgifera*, native to Central America, is such a species as it has been shown to have been repeatedly introduced in Europe from North America. Using several genetic markers, we investigated within- and between-population variation, in WCR from North America and Europe, to investigate the possible routes by which the WCR was introduced into Europe and to assess the effect of introduction events on genetic variation. From 1992 to 2007, we detected five independent introductions from the northern US to Europe and four intra-European founder events. The loss of genetic diversity following these introductions differed considerably between events, suggesting substantial differences in the initial variation of colonizing individuals as well as foundation and/or establishment conditions. We also showed that as a result of multiple introductions, the nuclear genetic variability present in the US source population has been largely redistributed among the various introduction foci in Europe.

Differential gene expression patterns correlate with caste fate in the honey bee, *Apis mellifera*

Zilá Simões

FFCLRP of University of São Paulo, Ribeirão Preto, Brazil

Differential gene expression splits definitively the fate of the two female *Apis mellifera* morphs during specific moments of postembryonic development in a process denominated caste determination. The morphological, behavioral and physiological characters specific to each caste are outcomes of this process that initiates with the differential feeding of queen and worker larvae. Some traits are fixed for the rest of the life for these two morphs, however some characters still retain important traces of plasticity, at least in workers. One of the immutable traits established during metamorphosis is the differentiation of the corbicula, a pollen basket surrounded by strong bristles on the metathoracic leg of workers. We investigate how the development of this worker caste-specific structure relates to the expression of patterning genes, such as *Ubx* and *abd-A,* during specific moments of caste differentiation. More flexible life history traits relate to reproduction and division of labor. For example, the functionally sterile workers still retain the possibility to activate their ovaries and lay eggs, especially under queenless conditions, and this depends on the expression of specific genes. Important candidate genes for the regulation of fertility are *vitellogenin (vg)*, *lipophorin (lp*) and genes encoding their specific receptors. Analyzing the expression of these genes in honey bee queens and workers we observed a clear, albeit inverse relation to oogenesis.

Financial support: FAPESP (05/03926-5)

Ancient agriculture in ants: exploring the complexity of social insect-microbe associations

Cameron Currie

University of Wisconsin, Madison, WI, United States

The formation of beneficial host-microbe symbioses have driven most major evolutionary transitions towards increased biological complexity, and the pervasiveness of these associations and their ecological dominance in virtually every ecosystem illustrates the importance of symbiosis as a form of evolutionary innovation. One textbook example is the fungus-growing ant-microbe symbiosis. This symbiosis includes the conspicuous leaf-cutters, and involves the obligate cultivation of fungus for food by ants. Over the last decade it has become clear that the ant-fungus mutualism includes two additional integral symbionts: i) specialized parasitic fungi in the genus *Escovopsis,* which exploit the ants' fungus garden and ii) mutualistic filamentous bacteria that produce antibiotics that inhibit the garden parasite. In this talk, I will present evidence for the presence of two more lineages of microbial symbionts associated with fungus-growing ants: i) black yeast that exploit the ant-bacteria mutualism, and ii) nitrogen-fixing bacteria that appear to fertilize the ants' fungus garden. The fungus-growing ant-microbe symbiosis illustrates the potential importance of microbes in shaping the biology of social insects.

Bacteria mediate insect-plant-fungal associations in leaf-cutting ants

Cameron Currie

University of Wisconsin, Madison, WI, United States

Since the origin of life on Earth ~4.6 billion years ago, microscopic organisms have shaped all levels of biological organization and have evolved into the most abundant and diverse life forms on the planet. However, the importance of microbes is perhaps best exemplified by their crucial role as symbionts with plants and animals, including mediating virtually every plant-insect association on the planet. For example, herbivorous insects depend on microbes to aid in the digestion of plant material, while fungal and/or bacterial symbionts can help plants defend themselves from herbivorous insects. Leaf-cutter ants in the tribe Attini represent a well-known example of microbes mediating insect-plant associations. The ants forage on fresh leaf material, which they use to manure their fungal garden. Leaf-cutting ant represents one of the most dominant herbivores in the Neotropics, illustrating the success of this obligate and ancient ant-fungus mutualism. Recent work has revealed that this association is composed of a complexity community of microbes, which includes microfungal pathogens that exploit the ants' fungal gardens. To help protect the health of the fungus garden the ants engage in a third mutualism with antibiotic-producing bacteria. Here I explore the role of additional microbial symbionts in altering tri-trophic insect-plant-microbe associations.

Medium range olfactory responses of the malaria vector, *Anopheles gambiae* to synthetic odour blends

Fredros Okumu, Sarah Moore

Durham University, Durham, United Kingdom

Background: The interaction between the malaria vector, *Anopheles gambiae* and its human hosts is mediated mainly by olfactory cues emanated from the host. Several compounds from whole body odour, sweat and breath are proven mosquito kairomones.

Methods: We evaluated medium range attractiveness of selected carboxylic acids to *An. gambiae s.s* in a semi field screen house system. The optimal concentrations at which these compounds are attractive to the vector were determined by a series of binary assays in competition with a standardized control blend.

Results: The behaviourally active odour compounds evaluated included l-Lactic acid, Propionic acid (C3), Octanoic acid (C8), Isopentanoic acid (3mC4), Pentanoic acid (C5), Butyric acid (C4), Heptanoic acid (C7) and Tetradecanoic acid (C14). Data was analysed by binary logistic regression to estimate the attractiveness of the test blends relative to the control blend. We determined that C3, C4, C5 and 3mC4, are attractive at low concentrations but repellent at higher concentrations. C7, C8 and C14 however remained attractive at high concentrations. The most attractive blend formulated from the test compounds was only of limited attractiveness compared to human foot odours trapped in worn socks.

Conclusion: Our results provide additional proof that apart from the carboxylic acids, there are other compounds essential for the mediation of *Anopheles* olfactory responses to humans. However, our system was evidently advantageous for rapid through assessment and optimization of behaviourally active compounds. Further discussion on the behavioural assay strategies and future work including recombination with insect repellents within a push-pull framework is discussed.

Two species of backswimmers (Notonectidae) and one species of water boatmen (Corixidae) as basibionts of some protozoan ciliates

Ricardo Mariño-Pérez, Rosaura Mayén-Estrada

Laboratorio de Protozoología, Departamento de Biología Comparada, Facultad de Ciencias, Universidad Nacional Autónoma de México, C.P. 04510, Ciudad Universitaria, México, D.F., Mexico

Introduction: Epibiosis is an association between an epibiont (organisms growing attached to a living surface) and a basibiont (substrate organism, which is the epibiont's host), this is a common interaction between aquatic animals and protozoans, nevertheless in arthropods has been reported mainly for crustaceans. The aim of this work is to present data concerning to the epibiosis between three species of water true bugs and ciliates, from central Mexico.

Methods: The aquatic bugs were collected in a freshwater pond in Hidalgo state, Mexico. Six samples were taken between February and August 2005. In order to examine and observe the ciliates, each basibiont was dissected, including the pairs of legs.

Results: Two species of backswimmers were found, *Notonecta unifasciata* and *Buenoa pallens,* and one species of water boatmen, *Corisella edulis*. All the three species presented epibionts. The peritrich *Orbopercularia* sp. and two species of suctorians (*Discophrya elongata* and *Acineta tuberosa*) were found attached to *Corisella edulis. Discophrya elongata* was found mainly in the middle legs, *Orbopercularia* sp. was observed mainly in legs, head and dorsal abdomen. For *A. tuberosa* data were not conclusive. On *Notonecta unifasciata* we observed *D. elongata* attached to legs. A third species of suctorian (*Periacineta notonectae*) was found only attached to *Buenoa pallens*, mainly in the anterior legs.

Conclusions: The epibionts were attached to certain exoskeleton areas, for which we conclude that the ciliates distribution is related to the appendage's architecture (very modified in Nepomorpha), and also to the hydrodynamic advantages implied in the nourishment activities.

Pseudopeptide and nonpeptide mimetic agonists and antagonists of diuretic insect kinin and diapause hormone neuropeptide classes

Ronald Nachman[1], Qirui Zhang[2], Suparna Taneja-Bageshwar[3], Pawel Zubrzak[1], Geoffrey Coast[4], Patricia Pietrantonio[3], David Denlinger[2]

[1]US Department of Agriculture, College Station, TX, United States, [2]Ohio State University, Columbus, OH, United States, [3]Texas A&M University, College Station, TX, United States, [4]University of London, London, United Kingdom

Insect neuropeptides regulate critical processes and behaviors in insects, though they are unsuitable as tools to arthropod endocrinologists and/or as pest management agents due to unsuitable biostability and/or bioavailability characteristics. Peptidomimetic analogs can overcome these limitations and either over-activate or block critical neuropeptide-regulated functions. The stereochemical and conformational aspects critical for the successful interaction of two broad classes of arthropod neuropeptides with their respective receptors is discussed, and exploited to design/discover mimetic analogs with enhanced biostability, bioavailability, and selectivity.

The diuretic insect kinin (IK) class of neuropeptides share the evolutionarily conserved C-terminal pentapeptide motif Phe-X^1-X^2-Trp-Gly-NH_2, where X^1 = His, Asn, Ser, or Tyr and X^2 = can be Ala but is generally Ser or Pro. Evaluation of restricted-conformation IK analogs incorporating such moieties as tetrazole and amino-pyroglutamate (APy), mimics of the *cis*Pro, type VI beta turn, indicate that this is the conformation adopted at the receptor site. A discussion follows on the design of non-peptide mimetic agonist/antagonist analogs with enhanced biostability in expressed tick and mosquito IK receptors.

The diapause hormone (DH) neuropeptide group shares the conserved C-terminal motif Trp-Phe-Gly-Pro-Arg-Leu-NH_2. The DH's induce embryonic diapause in *Bombyx mori*, and adult diapuse-break in Heliothines. Evaluation of DH analogs incorporating a *trans*Pro mimetic component in the diapause-break bioassay indicates that this configuration is associated with an agonist response. A discussion follows on the design of pseudopeptide mimetic DH agonists and antagonists with enhanced potency, biostability, and bioavailability that may prove of future utility for disruption of this important behavior in pest insects.

Resistance to human pathogens through the manipulation of mosquito immune pathways

Lindsey Garver, Jose Ramirez, Yuemei Dong, Zhiyong Xi, George Dimopoulos

Johns Hopkins School of Public Health, Baltimore, Maryland, United States

Introduction: Immune responses mounted by pathogen transmitting mosquitoes are largely regulated by the Toll and Imd pathways, which control the nuclear translocation of two NF-kappaB-like transcription factors, Rel1 and Rel2, respectively. Activation of Rel1 and Rel2 by these pathways is controlled by the negative regulators Cactus and Caspar.

Methods: We have used RNA interference to assays the effect of Toll and Imd pathway activation on pathogen infection and the regulation of the mosquito transcriptome.

Results: We found that Rel2 activation resulting from AgCaspar depletion rendered Anopheles gambiae mosquitoes resistant to the human malaria parasite *Plasmodium falciparum* at the pre-mature oocyst stage. In a similar analysis we found that Rel1 activation resulting from AeCactus depletion rendered *Aedes aegypti* mosquitoes less susceptible to the dengue virus. High-density microarray-based, genome-wide expression analyses in both mosquito species identified a plethora of genes that were regulated by the activation of the two Rel factors via Cactus and Caspar depletion. The Toll pathway displayed in general a significantly more diverse role in mosquito biology than did the Imd pathway, which was more immunity-specific. The Toll and Imd pathways are also implicated in anti-microbial defenses and we show that the mosquito's endogenous microbial flora play a role in limiting pathogen infection, possibly through a basal level immune gene stimulation.

A novel experimental hut assay to test spatial repellency

Sarah Moore[1], Nicodem Govella[1], Benjamin Fuhrer[1], John Grieco[3], Tanya Russell[1], Gerry Killeen[1], Nicole Achee[3]

[1]IHRDC, Ifakara, Tanzania, United Republic of, [2]Durham University, Durham, United Kingdom, [3]United States Uniformed Health Services, Bathesda, United States

The debate over the mode of action of excitorepellent insecticides still continues. Is toxicity or spatial repellency the reason that they are so effective in reducing vector-borne disease? Can a spatial repellent with limited toxicity ever be useful in large-scale vector control programmes? Only with the use of standard reproducible assays, similar to those WHO protocols employed to measure the lethal dose of residual insecticides can this question be answered.

In order to address this issue a standard experimental hut assay was devised. This assay uses a readily transportable kit form experimental hut with standardised interception traps specifically designed to capture Afrotropical malaria vectors entering and exiting the huts. The hut assay uses a novel design that brings together aspects of traditional experimental hut assays, and new innovations. Using standardised protocols the assays measure: reductions in proportions of mosquitoes entering treated versus control huts – spatial repellence; time spent in huts by mosquitoes that enter – contact irritancy; mortality of those mosquitoes that enter huts.

Baseline experiments to explore natural mosquito entry and exit behaviour were conducted. These were followed by assays using low-toxicity botanical spatial repellents *Nepata cataria* and para-menthane 3,8, diol to measure the differences in entering and exiting behaviour, and the results are discussed in relation. The kit-form huts are currently in use in four East African field sites, and will allow direct comparison of mosquito bionomics, the mode of action of residual insecticides, and the efficacy of malaria-control tools such as LLIN between those sites.

Dynamics of an eruptive herbivore in a novel habitat: consequences of climate-induced range expansion by the mountain pine beetle

Allan Carroll, Katherine Bleiker, Gregory Smith

Natural Resources Canada, Canadian Forest Service, Victoria, BC, Canada

For insect herbivores, the most commonly predicted/measured response to a warming environment is a latitudinal and elevational shift in their geographic range. However, due to their relatively high mobility, the rate of change in the distribution of herbivorous insects is expected to exceed that of virtually all other organisms in their original habitat . Thus, in many cases the short-term response to climate change by herbivorous insects will comprise habitat invasion. As a result of novel trophic interactions in new habitats the dynamics of an insect herbivore will likely differ from that associated with the originating habitat. Therefore, reliable predictions of the potential impacts of climate-induced range shifts by herbivorous insects are precluded. Using the recent expansion of the mountain pine beetle (*Dendroctonus ponderosae* Hopkins) across the northern Rocky Mountains in North America as a case study, this paper will examine the dynamics of an eruptive forest herbivore in novel habitats and assess the potential for continued range expansion.

Winners and losers in a transformed landscape: butterfly diversity in remnant Afrotropical forests.

Janice Bossart

Southeastern Louisiana University, Hammond, Louisiana, United States

In Ghana, West Africa, forest destruction has been pervasive. Existing forest cover is estimated to constitute only 15-25% of its original extent and what remains is highly fragmented and isolated. In 2001, I initiated systematic surveys of five small sacred forest groves and two larger forest reserves in the Ashanti Region of Ghana to investigate the impact of forest fragmentation on forest fruit-feeding butterfly species. Two to three, edge-to-interior transects were established in each forest and sampled regularly over a two year period (June 2001- July 2002 and August 2005 – May 2006). Sites were sampled from 27-58 times, resulting in ~16,000 specimens from more than 120 species. The largest forest reserve supported the highest diversity, although combined diversity across sacred groves was comparable to that of a much larger reserve. Smaller communities were also found to be nested subsets of larger communities, indicating that species loss from forest patches is non random. Although there were notable exceptions, species trapped only in the forest reserves were generally those associated with high quality forest, whereas those trapped only in the sacred groves were generally those tolerant of forest degradation. Although forest edges were found to significantly impact butterfly community diversity, species considered vulnerable to forest degradation were notably not restricted to forest interior habitat. Analysis of species' abundance patterns across fragments established that the *Bebearia*, *Euriphene*, and *Euphaedra* will be the biggest losers in terms of species persistence versus extinction in this fragmented landscape.

Mid-Southern USA regional evaluation of insecticide seed treatments on soybeans

Kelly Tindall[1], Angus Catchot[2], Scott Stewart[3], Roger Leonard[4], Gus Lorenz[5]

[1]University of Missouri, Portageville, MO, United States, [2]Mississippi State University, Mississippi State, MS, United States, [3]University of Tennessee, Jackson, TN, United States, [4]Louisiana State University, AgCenter, Winnsboro, LA, United States, [5]University of Arkansas, Lonoke, AR, United States

The adoption rate of seed treatments has increased over the last several years. In soybeans, the most common treatments are Cruiser and Gaucho. Treatments costs range from $6-8 per acre depending upon the product and rate used, and they are effective in controlling/suppressing some early season insect pests (i.e., thrips, bean leaf beetle, three cornered alfalfa hopper, grape colaspis, white grubs, wireworms, seedcorn maggot and others). Data have shown that the seed treatments at least pay for themselves 71-85% of the time and yields can be increased as much as 10+ bushels per acre but average around a three bushel per acre. What is not understood is the point at which profits result from seed treatment. Therefore, a regional effort involving five Mid-Southern states was made to investigate planting dates and tillage practices to determine if there are systems that are more prone to have yield increases as opposed to 'breaking even'.

Juvenile hormone and sexual maturation in migratory and non migratory populations of the true armyworm, *Pseudaletia unipuncta*

Jeremy McNeil

The University of Western Ontario, London, ON, Canada

Sexual maturation and migratory flight both require juvenile hormone (JH), yet most insects that undertake migration in response to habitat deterioration do so as sexually immature adults. To explain this apparent paradox, Rankin and Riddiford proposed that the levels of JH production, and the subsequent behavioural responses observed, would be modulated by external cues that provided reliable information with respect to habitat quality. Under conditions indicative of habitat decline (e.g. short days, low temperature) JH titres would remain low, resulting in the expression of migratory flight behaviour by sexually immature individauals. In contrast, conditions reflecting good habitat quality (e.g. long days. warm temperatures) would result in high JH titres leading to the onset of reproduction in the current habitat. Studies on a number of different migratory species have provided support for the general model, with a number of variations being observed that related to species specific life history traits.

We have been using the true armyworm, *Pseudaletia unipuncta* (Lepidoptera: Noctuidae) as a model species to investigate the underlying physiology related to both sexual maturation (including pheromone production) and seasonal migration. In recent years we have been carrying out studies, comparing migratory populations from North America with non-migratory ones found in the Azores, a volcanic archipelago in the Atlantic Ocean. There are significant differences in morphology and reproductive output (females from the Azores being smaller but with a higher total fecundity). Furthermore, there are marked differences in the temporal patterns of sexual maturation, as well as the rates of JH biosynthesis and JH haemolymph titres, when reared under identical temperature and photoperiod conditions . Results will be presented and the implications related to the costs associated with migration and reproductive success will be discussed.

Floral rewards for bats subsidize pollination, herbivory and biodiversity in an aridlands hawkmoth community

Jeffrey Riffell, Ruben Alarcon, Leif Abrell, Goggy Davidowitz, Judith Bronstein, John Hildebrand

University of Arizona, Tucson, Arizona, United States

Hawkmoths (Sphingidae, Lepidoptera) are nocturnal pollinators that typically visit fragrant, showy flowers with concealed nectar. In the arid grasslands and foothills of southern Arizona, USA, the presence of adult moths and the flowering of hawkmoth-adapted plants only partially coincide; furthermore, hawkmoth flowers are relatively scarce for the large hawkmoth populations. Analysis of pollen removed from the probosces of >500 individual hawkmoths attracted to blacklights at the base of the Santa Rita Mountains over two years indicate that 8 of 11 hawkmoth species heavily visit *Agave palmeri* (Agavaceae), a common species morphologically and chemically adapted for bat pollination. Behavioral experiments with both naïve and experienced *Manduca sexta* reveal that these hawkmoths learn to feed from *Agave* through olfactory conditioning, but readily switch to the hawkmoth-adapted flowers of *Datura wrightii* (Solanaceae) based on an innate odor preference. We show that these species emit similar concentrations of floral odor, but *Agave* provides six times more chemical energy per flower and scent composition, nectar chemistry, and flower reflectance are distinct. Pollen-load data indicate that the shift to the *Datura* occurs when this species is at its peak bloom. *Datura wrightii* is *M. sexta*'s nearly exclusive host plant in these habitats; *M. sexta* is simultaneously *D. wrightii*'s primary pollinator. Our results suggest that *Agave* populations subsidize both the mutualistic and antagonistic components of the *Datura/ Manduca* interaction, and are likely facilitating the persistence of the hawkmoth community as a whole in this desert grassland habitat.

Fire ants and native ants: A cautionary tale

Walter R. Tschinkel

Florida State University, Tallahassee, FL, United States

Community ecologists, especially those working on ants, have long believed that interspecific competition structures communities. Consequently, for half a century the dogma has been that the Argentinean fire ant, *Solenopsis invicta*, suppresses populations of native ants in its adopted home in North America (where it arrived around 1935). This belief was not based on experiments, but on negative correlations between fire ant populations and native ant populations, baiting studies and relative abundance data. Careful reanalysis of the data suggested that native ant populations were suppressed by habitat disturbance, whereas *S. invicta*, a disturbed-habitat specialist, was independently favored by the same disturbance. We removed *S. invicta* from pastures for 3 years, and found that removal had no effect on the abundance or species richness of other ants, suggesting this community is not structured by competition. We also subjected plots in a habitat normally devoid of *S. invicta* to disturbance (mowing, plowing, control), and combined these treatments with the transplantation of mature fire ant colonies and appropriate controls. Plowing greatly reduced native ant populations, but mowing had little effect. Transplantation of mature fire ant colonies, although very successful, had little effect on native ants. Therefore, even in this native habitat, the ant community is structured by the habitat rather than by competition, and disturbance is the cause of native ant suppression. We emphasize that competition cannot be inferred without experimentation, a caution for community ecologists. The degree to which our findings apply to other ant communities remains to be tested.

New technologies for tackling major challenges in border diagnostics.

Karen Armstrong[1], Shelley Ball[1], Alan Flynn[2]

[1]Lincoln University, Canterbury, New Zealand, [2]MAF Biosecurity New Zealand, Auckland, New Zealand

The accurate identification of exotic insect species detected at the border provides fundamental information on which to base subsequent biosecurity decisions; it is a critical component of any front-line defence against the potentially harmful invasion into economic or native ecosystems. However for many taxa there are barriers to their effective identification by traditional morphological means. This places a burden on the biosecurity system, and can result in conservative actions being taken with potentially social, economic or trading-partner consequences. Diagnostic barriers may be taxonomic in nature, such as the unavailability of appropriate expertise, or of keys for distinguishing immature life stages, closely related siblings or strains. Non-taxonomic barriers may reflect difficulties in confirming the vector status within a species or the viability of sessile forms, or confirming the geographic origin of an interception following an eradication to verify it as a new incursion rather than evidence of a remnant population. Research into new technologies that may alleviate each of these barriers is underway. An example is drawn from the development and implementation of DNA barcodes for species identification. Originally developed for high risk dipteran and lepidopteran species, subsequent research aims to build the DNA barcode dataset as a predictive tool, targeting 'taxonomic gaps' associated with actual border-intercepted material. It has also been used in an integrative taxonomy approach to resolve systematic complications revealed during such research. This method is now proposed as the basis of a sustainable diagnostic resource, to supplement both traditional and novel morphological technologies used at the border in the coming decades.

Does atmospheric oxygen limit insect size? Effects of oxygen on insect growth and tracheal morphology

Jon Harrison, C Jaco Klok, John VandenBrooks, Alex Kaiser, Jake Socha, Wah-Keat Lee

[1]Arizona State University, Tempe, Arizona, United States, [2]Midwestern University, Glendale, Arizona, United States, [3]Argonne National Laboratory, Argonne, IL, United States

Atmospheric oxygen has varied through the earth's history, and can vary in availability in different habitats. Rearing insects in atmospheres with different oxygen levels has revealed substantial diversity in responses among species; however, most insects are smaller when reared in hypoxic conditions. Moderate hyperoxia increases the size of some species, but extreme hyperoxia reduces size. In fruitflies, all life stages are sensitive to oxygen. The mechanism of oxygen effects on size are unclear and may be diverse, but are often at least partially mediated by affects on cell size. Multigenerational studies with fruitflies indicate that these insects evolve larger size in higher oxygen levels. However, when fruitflies are selected for large size, body sizes were similar whether the atmospheric oxygen level was 21% or 40% oxygen. Fruitflies selected for large size in 10% were smaller than those in higher oxygen levels, indicating that hypoxia does restrict body size in flies; when these flies are returned to 21%, their body sizes are similar to those raised at higher oxygen levels, confirming the constraining, plastic effect of hypoxia on size. Dimensions of larval longitudinal and adult leg tracheae are inverse to rearing oxygen levels, but adult abdominal and pupal "snorkel" tracheae do not seem to respond to atmospheric oxygen levels in flies. Comparative studies with beetles and ontogenetic studies with grasshoppers indicate that larger species have proportionally larger tracheae, especially in the legs. This trend could limit insect size via spatial limitations on tracheae or other tissues. Thus multiple lines of evidence suggest that atmospheric oxygen and tracheal oxygen delivery are important for determining the size of insects, and these experiments generally support the hypothesis that Paleozoic hyperoxia could have enabled insect gigantism. Supported by NSF IBN 0419704 to JFH.

Beauveria bassiana – lessons learnt regarding a fungal insecticide in a commercial environment.

Sias Leipoldt

Biological Control Products SA (Pty) Ltd., Pinetown, KwaZulu Natal, South Africa

Biological pest control makes use of the natural ability of certain organisms to parasitize and destroy others. A major advantage of this approach is the minimal effect of these agents on the environment as a result of their limited host range. In addition, the absence of mammalian toxicity, the non-invasive and non-systemic nature of the biological agents and the lack of necessity for any withholding period, allow their use on crops for immediate sale and also on crops intended for sale to regions and countries where pesticide residue regulations are very strict.

Beauveria bassiana is a soilborne fungus and is found worldwide. Efficacy does vary between different *Beauveria bassiana* strains, but this fungus is effective against a wide range of target pests. Although the BCP commercialised strain has not been registered against every target organism, it has been found effective against the following in laboratory and field trials. The list includes various ant species, army worm, African bollworm, various aphid species, crickets, cockroaches, diamond back moth, fleas, locusts, mealy bug, sugar cane borer, thrips, ticks, termites, weevils and white fly.

If used correctly, this organism can be highly effective in reducing a variety of target pests. This presentation will focus on the mode of action of *Beauveria bassiana*, how it should be applied and what to expect.

Initiation and scheduling of an innate behavioral sequence by central peptidergic ensembles

Young-Joon Kim[1], Dusan Zitnan[2], C. Giovanni Galizia[3], Kook-Ho Cho[2], Michael Adams[1]

[1]University of California, Riverside, Riverside, CA 92521, United States, [2]Slovak Academy of Sciences, Bratislava, Slovakia, [3]University of Konstanz, Konstanz, Germany

Introduction: Molting in insects is terminated by shedding of the old cuticle. This is accomplished by performance of the ecdysis behavioral sequence, an innate behavior under the control of steroid and peptide hormones. Sequential behaviors consisting of pre-ecdysis, ecdysis, and post-ecdysis are initiated and scheduled by neuropeptide signaling cascades in the CNS under the control of ecdysis triggering hormones (ETHs).

Methods: Primary neural targets of ETH in the CNS are identified by expression of ETH receptor (ETHR) transcripts. In *Drosophila*, ETHR neuron activity is monitored by calcium imaging. Necessary roles of these neurons are examined by cell ablation, overexpression of ETHR, or RNA silencing of ETHR.

Results: ETHR is expressed predominantly in "peptidergic ensembles", groups of neurons that release FMRFamides, eclosion hormone, kinins, CCAP, MIPs, and bursicon both centrally and peripherally. FMRFamide neurons are activated during all phases of the behavioral sequence. Eclosion hormone, CCAP and CCAP/MIP neurons become active prior to ecdysis, and activity of CCAP/MIP/bursicon neurons coincides with post-ecdysis. Ablation of kinin neurons causes variable defects in pre-ecdysis behaviors. Ablation of subsets of CCAP/MIP/bursicon neurons leads to defects in ecdysis and postecdysis. Overexpression or knockdown of ETH receptors alters scheduling of behavioral steps. For instance, overexpression of ETHR in CCAP/MIP neurons accelerates ecdysis onset, while ETHR knockdown in the same neurons delays ecdysis onset.

Conclusions: These findings offer insights into how innate behaviors are assembled and executed by central peptidergic ensembles. Supported by NIH grant GM067310.

Frequent habitat changes in Saprininae as revealed from a cladistic analysis.

Tomas Lackner

Hokkaido University, Sapporo/Hokkaido, Japan

Saprininae (Coleoptera: Histeridae), with approximately 700 species worldwide, are the second largest subfamily (after Histerinae) of the beetle family Histeridae. In the Palaearctic region, Saprininae comprises about 34 genera and subgenera, members of which are mostly found on carrion and in dung, where they prey on the larvae of other arthropods, especially cyclorrhapan flies. However, many genera are highly specialized and are inquilinous in the nests of birds, or in the burrows of rodents or even ants.

After scoring 68 morphological characters for 33 ingroup and 3 outgroup taxa, we performed a phylogenetic analysis and obtained surprising results. The following morphological characters proved to be phylogenetically most informative:

1) Male genitalia

2) Mouthparts

3) Reichardt's organ (specialized sensory organ of antenna)

Although our study dealt only with Palaearctic genera and subgenera, given the present phylogenetic hypothesis, it is tempting to make several inferences on the evolution of the subfamily Saprininae. It seems likely that Saprininae are the sister group to Dendrophilinae, whose members are likewise mostly inquilinous. Inquilinous taxa within Saprininae comprise the most basal 'grade,' suggesting that Saprininae evolved inside the nests of warm-blooded animals and have been a part of this biocenosis for a very long time. They probably subsequently entered open spaces, where they found ample food, speciated, and adapted to many stressful habitats such as deserts. This scenario contrasts with the most parsimonious evolutionary pathway, which should go the other way – from generalized to specialized. Unfortunately, there is little information on the life history, ecology, and distribution of many taxa. Further research on the subfamily worldwide will likely bring many interesting results and remains a high priority in my research.

Clearing the clutter: a life table analysis of the strain of *Anagyrus* sp. (near) *pseudococci* (Hymenoptera: Encyrtidae) found in vineyards of the Western Cape province, South African, and subsequent successful taxonomic specimen identification

Martin Wohlfarter[1], Jeanne De Waal[1], Carel Van Heerden[2], Pia Addison[1]

[1]University of Stellenbosch Deparment of ConsEnt, Stellenbosch, South Africa, [2]University of Stellenbosch, Department of Genetics, Stellenbosch, South Africa

Introduction: The potential of using the polyphagous parasitoid *Anagyrus pseudococci* (Girault) for the biological control of the vine mealybug, *Planococcus ficus* (Signoret) in South African vineyards is dependant on several factors. The objective of this study was to investigate the influence of temperature on the developmental time and fecundity of the strain *A. pseudococci* found in local vineyards and to furthermore ensure the correct taxonomic identification of the biological control agent, as these factors are essential to the success of the biological control programme.

Methods: A life table analysis of the wild type *Anagyrus* sp. isolated from vineyards throughout the Western Cape, South Africa, was carried out at five temperature intervals, 14, 21, 27, 32 and 34°C, with relative humidity below 60%. Specimens from this laboratory colony were identified to species level using both morphological keys and molecular methods.

Results: Laboratory temperature-trials indicated that the strain of *A. pseudococci* found in vineyards in South Africa performed differently regarding developmental time and fecundity when compared to similar work done in California using the same species, which raised the issue of species identification. Morphologically the wild type specimens were identified as *Anagyrus* sp. (near) *pseudococci* and molecular identification show that the sequence obtained match 99% with the sequence of *Anagyrus* sp. nr. *pseudococci* from Italy (GenBank library accession number: DQ667740.1).

Conclusion: Life tables aid in determining the optimum time of *Anagyrus* sp (near) *pseudococci* mass field release. The need for a survey of the grapevine growing areas is however paramount to surpass the discrepancies of historic identification of *Anagyrus* sp. in South Africa.

A microarray platform for genome-wide expression studies in the spruce budworm, *Choristoneura fumiferana*

Dayu Zhang[1], Susan Bowman[1], Qili Feng[3], Tim Ladd[1], Cailing Liu[1], Peter Krell[2], Basil Arif[1], Daniel Doucet[1]

[1]Great Lakes Forestry Centre, Sault Ste. Marie, Ontario, Canada, [2]University of Guelph, Guelph, Ontario, Canada, [3]South China Normal University, Guangzhou, China

Microarrays, also known as DNA chips, are extremely useful tools for the study of gene expression in many organisms. Owing to the decreasing costs of gene sequencing, DNA synthesis and other associated costs, microarrays have become progressively more accessible to investigate gene expression in insect species not belonging to "model systems" (*e.g. Drosophila*, *Bombyx*). We have constructed a microarray for the moth *Choristoneura fumiferana* (the spruce budworm, sbw), an important pest of fir and spruce in North America. The array contains over 3000 unique sbw DNA sequences, obtained by spotting PCR products from a sbw EST clone collection. The sbw array has been used to support two projects: i) an analysis of gene expression profiles in larvae molting from 5th to 6th instar stages and ii) a study of the impact of infection by a naturally-occuring and a recombinant baculovirus on the sbw transcriptome.

Results from the first project will be presented. Genes represented by over 300 ESTs showed at least three-fold difference in the expression level between molting and intermolting larvae. These genes are involved in several biological processes such as cuticle synthesis and degradation, chitin synthesis and degradation, cuticle pigmentation, myogenesis, transcription and translation regulation and catabolic pathways. Results from the second study indicate that virus infection kinetics affect the expression of several uncharacterized genes. These might be involved in cellular stress reaction and/or a redirection of vital cellular processes benefiting virus replication and propagation.

Ecology of insect hosts and entomopathogens

Ann Hajek

Cornell University, Ithaca, NY York, United States

There are many components of the host/pathogen system that act together to support pathogen populations and these interactions are especially critical to obligate pathogens. Pathogens are successfully transmitted to new hosts in a number of different ways, must grow within hosts and reproduce and also survive in the environment when hosts are not present or conditions are unfavorable. We know that pathogens, being microorganisms, can be very sensitive to abiotic conditions, both when free-living as well as when inside of hosts. Biotic conditions can also influence the success of pathogens; hosts can behaviourally defend themselves from pathogens although, alternatively, some pathogens can change host behavior to enhance transmission. Although relatively few studies of community-level effects on insect pathogens have been conducted, we know that some pathogens are influenced by the plants that herbivorous hosts eat. When conditions are excellent for pathogens, infection prevalence can increase quickly and epizootics will develop. Understanding the conditions under which prevalence of infection can increase to create epizootics has been central to studies of the epizootiology of insect diseases. Today, we are also exploring the spatial aspects of epizootiology, asking to what extent pathogens are able to recolonize areas where they have not been able to persist.

Sterile insects for the control of perennial crop insect pests in a time of global change

Marc Vreysen, Jorge Hendrichs, Rui Cardoso Pereira

Insect Pest Control Sub-Programme, Joint FAO/IAEA Programme of Nuclear Techniques in Food and Agriculture, Department of Nuclear Applications, IAEA, Vienna, Austria

Concerns about pesticide residues in food commodities are increasing, as well as resistance to pesticides, contamination of the environment and outbreaks of secondary pests. The use of the species-specific sterile insect technique (SIT), applied as part of an area-wide integrated pest management approach (AW-IPM), is gradually increasing to help address the demands for efficient, more specific, and cleaner pest control methods, and to facilitate international trade by the establishment of low prevalence and pest free areas. In addition, with international trade and travel expanding rapidly, the risk of exotic species invading new territories is increasing manifold. The SIT is a control tactic well suited to deal with incursions of invasive species when the infested areas are still small and the pest population density is still low. The release of sterile insects is currently being used to eradicate incursions of the invasive painted apple moth in New Zealand, to contain the spread of the cactus moth in the USA, and to prevent outbreaks of the Mediterranean fruit fly in California and Florida. The SIT package is also being developed against major pests, which have not invaded new territories but pose serious threats in case of an accidental introduction, e.g. the false codling moth. A brief overview of ongoing SIT activities against pests of perennial crops will be presented, as well as of new technological developments in this area.

Feeding performance of two lepidopteran herbivores on chitinase transgenic birches (*Betula pendula*)

Liisa Vihervuori, Päivi Lyytikäinen-Saarenmaa, Hanna-Leena Pasonen

[1]University of Helsinki, Department of Forest Ecology, Helsinki, Finland, [2]University of Helsinki, Department of Applied Biology, Helsinki, Finland

Introduction: A previous field trial with the chitinase transgenic Silver birch (*Betula pendula*) was continued by insect feeding tests in laboratory conditions. The aim was to provide new information on the interactions between GM-birch and insect herbivores. The additional aim was to study the effect of the artificial herbivory on the performance of the larvae and on the regrowth ability of GM-trees compared to the control trees.

Methods: The studies were conducted in 2003 and 2007. Transgenic birches carrying a sugar beet chitinase gene were used. Birches from the field trial and greenhouse grown trees were used. Trees were grouped according to their chitinase expression levels (high, intermediate, low). Insect feeding tests were conducted with larvae of *Orgyia antiqua* and *Phalera bucephala*. Larvae groups consumed birch leaves during one week. The larval performance was measured as relative growth rate (RGR) and efficiency of conversation of ingested food (ECI).

Results: The growth rate of the larvae on transgenic leaves decreased compared to those on control leaves. The amount of consumed food and the proportion of digested food was lowest within the group on leaves of high transgene expression. Expression level affected amount of consumed and digested food. However, this was not clear. No impact of artificial insect herbivory on the performance of the larvae or on the regrowth of the trees was observed.

Conclusions: Based to these results, the chitinase transgene may have negative effects on herbivorous lepidopterans. The present study provides basic knowledge about the interaction of GM-trees with defoliators.

Plant litter-detritivore interactions: links between the green and the brown part of ecosystems?

Stephan Hattenschwiler

CNRS, Montpellier, France

Introduction: Plant leaf chemistry is a key factor in plant-insect interactions. The same plant material, but chemically modified during leaf senescence, provides the food and energy source for soil arthropods. However, litter chemistry control over macro invertebrates is poorly studied, despite its potential far ranging consequences for litter breakdown rates and nutrient cycling, which in turn has important feedback effects on plant growth.

Methods: Using data from a series of different experiments from mainly tropical and Mediterranean forest ecosystems, the following questions are explored: (1) how does food quality differ between green leaves and leaf litter, (2) how do litter feeding animals influence mass loss of litter mixtures, and (3) to what degree are the “herbivore-plant” and the “detritivore-litter” systems comparable and how might they be linked.

Results: Data from many tropical forest tree species show that C:N:P stoichiometry changes drastically in leaf litter compared to green foliage, but that other components of tissue quality such as lignin and polyphenols remain quite similar. Litter-feeding animals are selective in food choice and interact with litter diversity in a way that major ecosystem processes, such as carbon and nutrient dynamics are influenced.

Conclusions: The herbivore-plant and the detritivore-litter systems are in so far comparable that the general nutritional constraints for the animals, and plant tissue quality control are similar. Litter quality control over detritivores and more generally, over decomposition, suggests the possibility that certain plant traits might be selected for their “afterlife” effects and their feedback on plant performance.

Probing behaviour of *Diuraphis noxia* on near-isogenic wheat lines with resistance ex PI 137739 and PI 262660.

Vicki Tolmay[1], Freddy Tjallingii[2], Charl Van Deventer[3]

[1]ARC-Small Grain Institute, Bethlehem, Free State, South Africa, [2]Wageningen Agricultural University, Wageningen, Netherlands, [3]University of the Free State, Bloemfontein, Free State, South Africa

Introduction: In the summer rainfall region of South Africa the most damaging pest of cultivated wheat , *Triticum aestivum* , is the Russian wheat aphid (RWA), *Diuraphis noxia.*

Methods: The DC EPG technique was used to characterise probing behaviour of RWA on near-isogenic, susceptible and resistant South Africa wheat genotypes.

Results: Distinct differences exist between the two susceptible genotypes Betta and Tugela in terms of the number of path periods and the time needed to attain sustained phloem ingestion. The influence of resistance in 1684/Tugela *ex* SA 1684 [PI 137739 (Dn1)] and 2199/Tugela *ex* SA 2199 [PI 262660 (Dn2)] on the probing behaviour of *D. noxia* is different. While resistance in 1684/Tugela was reflected in a lower proportion of time spent in phloem ingestion after attaining sustained phloem feeding, the resistance in 2199/Tugela was associated with a high number of probes shorter than three minutes prior to the first phloem activity denoting some host recognition or epidermal factor involved in the resistance of this genotype which was not evident in 1684/Tugela. In addition resistance in 2199/Tugela was associated with a significantly higher percentage of time spent in phloem ingestion after the first sustained phloem feeding had been attained. The mechanisms of resistance for these genotypes as reported in a previous study are consistent with the data from this investigation.

Conclusions: EPG data collected for *D. noxia* on two susceptible and two resistant host genotypes reveals that the interaction between the aphid and each host genotype is unique.

Collaborative Screening for Russian wheat aphid (*Diuraphis noxia*) resistance

Vicki Tolmay[1], Gary Puturka[2], Cheryl Baker[2], Robbie Lindeque[1]

[1]ARC-Small Grain Institute, Bethlehem, Free State, South Africa, [2]United States Department of Agriculture - Agricultural Research Service, Stillwater, Oklahoma, United States

Introduction: Russian wheat aphid (RWA) is the most damaging pest of wheat in the summer rainfall production region of South Africa. It also occurs in the USA where it causes severe crop losses in the Western Great Plains wheat production areas but the biotypes that occur in the USA differ from those found in South Africa. Host plant resistance (HPR) has been found to be a viable and economically sound approach to controlling this pest. South African germplasm was screened in the USA with two RWA biotypes to proactively identify lines with effective resistance against biotypes that might occur in South Africa in future.

Methods: Using a split plot design with three replicates, seedlings of 288 lines were screened against USA biotypes RWA1 and RWA2 using a 1-10 (resistant – susceptible) damage rating scale, in the greenhouse. Resistant seedlings were selected and grown to maturity.

Results: Thirty percent of the lines were susceptible to the USA biotypes. Of the 200 resistant lines, 134 lines potentially contain resistance from more than one resistance donor accession and 74 showed resistance to both biotypes tested. In total 647 single plants were selected with 174 and 473 resistant to RWA1 and RWA2 respectively.

Conclusions: Collaborative screening, exploiting different RWA biotypes from different regions in the world, proved effective in identifying resistant lines against potential biotypes, thus strengthening HPR breeding programmes.

What can social parasites tell us about cooperation and conflict in insect societies?

David Nash

University of Copenhagen, Copenhagen, Denmark

Social parasites exploit the resources and organization of social insect colonies. There are at least two fundamentally different routes to social parasitism: Social parasites can arise via exploitation of conspecific (or congeneric) social insects, or distantly-related organisms can evolve strategies to exploit social insect colonies. Both types of social parasitism can provide useful insights into cooperation and conflict within insect societies. Closely related social parasites are essentially the outcome of the breakdown of cooperation and the realisation of conflict, and the unique features of their evolution can provide information on how cooperation is normally maintained in insect societies. Distantly related social parasites must evolve de novo exploitation strategies without the benefit of shared ancestry of social traits with their hosts, so that their evolution can be used to examine how cooperation can be exploited independent of these traits. In this presentation I will examine both types of social parasitism in detail, and provide some examples of the insights they can bring to the study of cooperation and conflict.

Towards a gene drive system in *Anopheles* mosquitoes using homing endonuclease genes

Philippos Papathanos, Nikolai Windbichler, Andrea Crisanti

Imperial College, London, United Kingdom

Mosquito species of the *Anopheles gambiae* complex represent the major vectors of human malaria and they pose an enormous burden on global health. Molecular advances have made it possible to express genes that can block the transmission of *Plasmodium* in model systems. However, the translation of such achievements in suitable control measures still represents a major scientific and technical challenge. A mechanism must be developed to spread the desired genetic modification from a few laboratory-reared mosquitoes to a large fraction of the vector population. Homing endonuclease genes (HEGs) are selfish genes that promote their movement from one allele to the other by creating a double-strand break at a specific target site in an allele lacking the HEG. Homologous DNA repair then copies the HEG to the cut chromosome. The observation that HEGs can be engineered to cleave novel DNA sequences offers a multitude of opportunities to utilize these elements for mosquito control. We have demonstrated that naturally-occurring homing endonucleases, including the well - characterised I-*Sce*I*,* are active in *Anopheles gambiae* cells and embryos leading to target specific cleavage followed by HEG-induced homologous repair. We have characterized and isolated a number of promoter elements suitable for driving pre-meiotic expression of HEGs in the germline of *Anopheles gambiae*. We have generated reporter constructs and transgenic mosquito lines using those novel putative promoter elements to confirm their ability to direct expression early in the development of the germline. We have also completed the construction of a reporter system to determine HEG homing and activity rates in transgenic mosquitoes. The output of this system is a measurement of the functional activity of I-*Sce*I, expressed during spermatogenesis, on a modified eGFP reporter gene, harbouring the I-*Sce*I recognition sequence. HEG activity is scored as a loss of neuron-specific eGFP expression. Transgenic lines harbouring these reporter constructs using the novel promoter elements are being generated. Evaluation of HEG activity in this reporter system should allow us to determine the feasibility of invasive HEG constructs in mosquito populations.

Phylogenetic approaches to delimit baculovirus species based on single gene and whole genome data

Elisabeth Herniou[1], Timothy Barraclough[1], Jennifer Cory[2]

[1]Division of Biology, Imperial College London, Ascot, United Kingdom, [2]Department of Biology, Algoma University College, Sault Ste. Marie, Canada

Baculoviruses are among the best known insect pathogens and yet we know little of their diversity. The nomenclature of baculoviruses, by using the juxtaposition of host name and virus morphology, has long had the advantage of being simple, but it introduces a lot of confusion for taxonomic purposes. The wealth of available baculovirus sequences provides an excellent framework to test a new phylogenetic method that delimits clusters of individual sequences into independently evolving groups or species. We have assembled 3 datasets: 2 based on single genes, 293 *polyhedrin* and 221 *lef-8* sequences, and one based on 43 complete genomes. We use molecular phylogenies to reveal the interrelationships of individual viral isolates. In addition, the branching patterns within trees give further information on the evolution of the viruses, which is reflected in part by changes in branching rates during the history of the group. We have developed a new method that detects the transition from between-species to within-population branching in phylogenies. One of the benefits of this approach is the definition of groups of individuals with shared evolutionary histories. These clusters of isolates can be interpreted as species groups. This method provides an objective way to delimit species without *a priori* assumptions of host use. By comparing the 3 types of datasets, we aim to validate the method for baculoviruses and determine the most appropriate data to use to describe new baculovirus isolates. This method has also been successfully tested on a number of invertebrate and plant taxa.

Variation in resistance in willow against a gall-forming cecidomyiid

Stig Larsson, Solveig Hoglund

Swedish University of Agricultural Sciences, Uppsala, Sweden

Large genotypic variation in resistance against the gall midge *Dasineura marginemtorquens* is found in *Salix viminalis*. On resistant genotypes, neonate larvae die within 48 hours after egg hatch (no gall induction). Resistance is associated with rapid cell death at the site of attack, production of phenolic compounds, and induction of hydrogen peroxide – events frequently linked with the syndrome of hypersensitivity response (HR). However, certain resistant willow genotypes do not show any sign of HR (no necrotic spots or production of hydrogen peroxide), and larval mortality is still as high as on genotypes expressing typical HR symptoms. The complexity in the expression of HR in this system may have implications for many plant-insect interactions where HR is claimed to be the resistance factor. This and other apparent contradictions in the interaction between the willow and the gall midge will be discussed in the talk.

Trichromatic colour vision and alightment of a psyllid

Alan Urban

Rhodes University, Grahamstown, E. Cape, South Africa

Introduction: A study was made of the influence of colour on the locomotory responses of a 'yellow-sensitive' African psyllid, *Trioza erytreae* (Del Guercio) (Hemiptera: Triozidae).

Methods and results: Phototaxis of test populations of psyllids was measured by their rate of walking towards light emitted by a monochromator, the radiant flux of which was measured using a vacuum thermopile. Their phototactic action spectrum (against wavelength) was trimodal, with peaks in the yellow-green (YG) at wavelength ca. 550 nm, blue (B) ca. 450 nm, and ultraviolet (UV) ca. 350 nm. Rate of phototaxis was proportional to the logarithm of light intensity over 6 orders of magnitude, and was not influenced by bandwidth. In a very simple flight chamber incorporating a target of coloured light, YG and UV light each independently stimulated alightment, and their effects were approximately additive. Different response threshold light intensities indicated that the YG and UV receptor systems were separate. Blue light alone did not stimulate alightment, and was strongly alightment-inhibitory in combination either with YG or with UV light. On the basis of these physiological/behavioural findings, a formula was derived for describing/predicting the apparent manner of alightment-determining integration of the spectral reflectance of a coloured surface. The relative alightment stimulus (RAS) of a coloured surface was given by RAS = YG + UV – B, where the colour terms refer to the 'receptor'-sensitivity-weighted logarithm of the quantum flux from the target in the wavebands: YG = 480-670 nm, UV = 300-390 nm, B = 390-480 nm, minus the logarithm of the relevant colour threshold. The frequency of alightment on some series of differently coloured surfaces correlated slightly better and more consistently with the new formula than with previously available colour parameters.

Conclusions: The relative frequency with which this psyllid alights, is the result of neural integration of stimuli received by its three colour receptor systems from the spectral reflectance of differently coloured surfaces. Indications were obtained that a new alightment prediction formula developed here may be applicable to various other 'homopteran' pests, such as aphids.

Trichromatic colour vision and alightment of a psyllid

Alan Urban

Rhodes University, Grahamstown, E. Cape, South Africa

Introduction: A study was made of the influence of colour on the locomotory responses of a 'yellow-sensitive' African psyllid, Trioza erytreae (Del Guercio) (Hemiptera: Triozidae).

Methods and results: Phototaxis of test populations of psyllids was measured by their rate of walking towards light emitted by a monochromator, the radiant flux of which was measured using a vacuum thermopile. Their phototactic action spectrum (against wavelength) was trimodal, with peaks in the yellow-green (YG) at wavelength ca. 550 nm, blue (B) ca. 450 nm, and ultraviolet (UV) ca. 350 nm. Rate of phototaxis was proportional to the logarithm of light intensity over 6 orders of magnitude, and was not influenced by bandwidth. In a very simple flight chamber incorporating a target of coloured light, YG and UV light each independently stimulated alightment, and their effects were approximately additive. Different response threshold light intensities indicated that the YG and UV receptor systems were separate. Blue light alone did not stimulate alightment, and was strongly alightment-inhibitory in combination either with YG or with UV light. On the basis of these physiological/behavioural findings, a formula was derived for describing/predicting the apparent manner of alightment-determining integration of the spectral reflectance of a coloured surface. The relative alightment stimulus (RAS) of a coloured surface was given by RAS = YG + UV – B, where the colour terms refer to the 'receptor'-sensitivity-weighted logarithm of the quantum flux from the target in the wavebands: YG = 480-670 nm, UV = 300-390 nm, B = 390-480 nm, minus the logarithm of the relevant colour threshold. The frequency of alightment on some series of differently coloured surfaces correlated slightly better and more consistently with the new formula than with previously available colour parameters.

Conclusions: The relative frequency with which this psyllid alights, is the result of neural integration of stimuli received by its three colour receptor systems from the spectral reflectance of differently coloured surfaces. Indications were obtained that a new alightment prediction formula developed here may be applicable to various other 'homopteran' pests, such as aphids.

Potential efficacy of a candidate agent, *Cornops aquaticum* Brüner (Orthoptera: Acrididae) for biological control of water hyacinth, *Eichhornia crassipes* Mart. Solms-Laubach (Pontederiaceae) as influenced by water nitrate and phosphate levels

Angela Bownes[1], Martin Hill[2], Marcus Byrne[3]

[1]Agricultural Research Council, Pretoria, South Africa, [2]Rhodes University, Grahamstown, South Africa, [3]University of the Witwatersrand, Johannesburg, South Africa

The South African biocontrol programme against water hyacinth has had variable success, despite having released more agents than any other country with water hyacinth biocontrol projects. Agent efficacy is assumed to be constrained under particular nutrient conditions prevailing in South Africa, therefore, additional agents were sought in South America, resulting in the introduction of the water hyacinth grasshopper, *Cornops aquaticum*, into quarantine as a potential agent. Pre-release testing to evaluate the potential of *C. aquaticum* to contribute to water hyacinth control as influenced by water nutrient levels showed that herbivory by the grasshoppers at a density of one per plant, significantly reduced ($F = 66.02$; $P = 0.0000$) biomass accumulation in plants grown in eutrophic, mesotrophic and oligotrophic nutrient conditions compared with control plants. Plant growth and reproductive parameters were also significantly reduced in the presence of grasshopper feeding, however a density of more than one per plant would be needed to significantly reduce infestations in eutrophied environments. Herbivory by *C. aquaticum* resulted in a 99% reduction in the plant's competitive ability, in high nutrient conditions. Fecundity as measured by the number of egg packets per female ($F = 26.06$; $P = 0.0000$) and number of eggs per egg packet ($F = 8.57$; $P = 0.0048$) were significantly affected by water nutrient levels and suggested that higher grasshopper population densities would be attained where plants are growing in eutrophic water bodies. These results suggest that the grasshopper will be a valuable introduction into the S.A. water hyacinth biocontrol programme.

Impacts of ants (Hymenoptera: Formicidae) on vine mealybug parasitoids *Anagyrus* sp. near *pseudococci* (Girault) and *Coccidoxenoides perminutus* (Timberlake) (Hymenoptera: Encyrtidae) under laboratory conditions.

Nyembezi Mgocheki, Pia Addison

Stellenbosch University, Stellenbosch, South Africa

Introduction: *A.* sp. near *pseudococci* and *C. perminutus* are potential parasitoids that can be used for the biological control of the vine mealybug, *Planococcus ficus* (Signoret), a key pest in vineyards. Three ant species, *Anoplolepis steingroeveri* (Forel), *Crematogaster peringueyi* Emery and *Linepithema humile* (Mayr) forage for honey-dew from the vine mealybug in vineyards and promote the latter's infestations to unacceptable levels.

Methods: Ants and parasitoids were allowed to forage on vine mealybug infested butternuts. The number of ants and parasitoids was recorded for a one minute period at ten minute intervals for two hours after which parasitoids were allowed to forage for 24 hours. Parasitoid mortality and vine mealybug parasitism by the two parasitoids were then recorded in the presence and absence of the three ant species. Data were analysed using a repeated measures generalized linear model (GEE) approach in SAS.

Results: The mean number of *C. peringueyi* on the mealybug-infested butternuts was significantly higher than that of *A.steingroeveri* and *L. humile* between time intervals and parasitoid species ($p<0.0001$ in all cases). The mean number of *C. perminutus* foraging on the mealybug infested butternut was significantly higher than that of A. sp.nr. *pseudococci* over the two hour period, between ant species, and time intervals ($p<0.0001$ in all cases). *C. peringueyi* and *L. humile* caused significantly higher mortality of both parasitoids ($p<0.001$) than *A. steingroeveri* during the 24-hour exposure period. *C. perminutus* parasitised significantly more vine mealybugs than *A.* sp. near *pseudococci* for all treatments ($p < 0.0001$).

Conclusion: Ant control is essential before release of parasitoids for optimum biological control of the vine mealybug in South Africa.

Co-radiation of gall-inducing scale insects and their myrtaceous hosts.

Lyn Cook[1], Penny Gullan[2]

[1]The University of Queensland, Brisbane, Qld, Australia, [2]University of California, Davis, CA, United States

There have been multiple origins of galling among Australian scale insects (Hemiptera: Coccoidea), with two large (> 100 species) radiations of gall-inducing scale insects on Myrtaceae. One of these, *Apiomorpha*, is restricted to *Eucalyptus* but the other clade comprises radiations on several speciose genera such as *Eucalyptus*, *Corymbia*, *Melaleuca* and *Leptospermum*. Phylogenies indicate that the gall-inducing scale insects form host-specific clades that might have co-radiated with their hosts. There has been some duplication of scale insects on the one host group (speciation in the scale without concomitant speciation in the host) but no host-switching between host plant genera despite broad co-distributions. The latter observation suggests strong evolutionary constraints that differ from those of many non-galling scale insects, in which host switching is inferred to have been considerably more frequent.

Pollen nutritional content: We know everything but what it means

T'ai Roulston

Blandy Experimental Farm/University of Virginia, Boyce, Virginia, United States

Pollen is the most nutrient-rich and complex of floral rewards, ranging widely in protein content (2.5 – 61%) and starch content (0 – 22%). It also varies in amino acid content, with some pollen lacking essential amino acids and making pollen mixing a requirement for complete nutrition. Despite an abundance of information on the range of nutrients in pollen, and their taxonomic distribution across plant species, there is little consensus regarding the evolutionary forces responsible for this distribution, the evolutionary forces responsible for pollen use patterns among pollen-consuming animals, or the ecological consequences for plant-animal interactions of having pollen that differs in nutritional characteristics.

It is clear that pollen traits can affect the digestibility of pollen and the development or performance of organisms that eat it, but experiments thus far carried out lead to little or no predictability for which pollens are actually consumed. Because pollen is a critical resource for many invertebrates, including many pollinators, our current lack of understanding of the evolutionary and ecological drivers for pollen traits reveals a broad lack of understanding of a major area of ecology. Experiments that intentionally vary pollen traits to test for preference and performance among floral visitors are difficult to carry out, but they are critical to move our understanding of pollen forward.

Dissection of community structure reveals neutrality among tropical arthropods

Farnon Ellwood, William Foster, Andrea Manica

University of Cambridge, Cambridge, United Kingdom

Species are distributed according to deterministic factors including habitat gradients, competitive advantages and dispersal ability. In species-rich habitats, dispersal is limited and competitive interactions are weaker, which generates stochastic forces, ecological equivalence and neutrality. Here we dissect the structure of local communities, separate the effects of deterministic factors, and reveal the existence of hidden stochastic forces. By performing manipulative experiments using arthropod decomposers in an epiphytic fern, we establish that species are distributed at random among local communities in undisturbed ferns in both the high and low canopy of a tropical forest in Borneo. However, when we introduced habitat gradients by pooling ferns from different heights, the structure of the communities became non-random. We also partitioned the deterministic effects of ecological succession to reveal the existence of stochastic forces at discrete points in time and space. Our results show that stochastic and deterministic forces coexist and the scale of the investigation determines which forces predominate. Our study illustrates the difficulties of analyzing community structure with an imperfect knowledge of the history of the assemblages, and underlines the importance of empirical data.

Variation in the susceptibility of *Helicoverpa armigera* larvae to different *Bacillus thuringiensis* Cry proteins

Hua Li, Gustav Bouwer

School of Molecular and Cell Biology, University of the Witwatersrand., Johannesburg, South Africa

Introduction: The susceptibility of the most important pest in South Africa, *Helicoverpa armigera* Hübner (Lepidoptera: Noctuidae), to *Bacillus thuringiensis* Cry proteins was investigated and a local benchmark for *B. thuringiensis* insecticidal Cry protein toxicity to this pest was established.

Methods: Cry proteins were produced in *Escherichia coli* BL21 cells that were transformed with plasmids containing one of the six Cry proteins used in the study. Bioassays were performed using whole BL21 cells, with the concentration of the Cry protein in the BL21 cells determined by Protein Analysis Chip (Biorad). The toxicity of each of the Cry proteins to *H. armigera* larvae was determined using two bioassay methods (surface treatment and droplet method). The median lethal dose (LD_{50}) and median effective dose (ED_{50}; weight stunting) for each of the proteins were determined.

Results: There was no significant difference in the toxicities of untransformed BL21 cells and water controls for neonates or second instars of *H. armigera*. Second instars were consistently less susceptible to Cry proteins than neonates. The relative toxicities of Cry proteins ranked differently between neonates and second instar larvae. On the basis of LD_{50} analysis, three Cry proteins were found to be highly toxic to both neonates and second instar larvae. Cry protein with the lowest LD_{50} also produced the lowest ED_{50} value.

Conclusions: This study highlighted the feasibility of using *E. coli* strains as Cry protein producing hosts in bioassay to establish an initial benchmark of Cry protein toxicity to *H. armigera*. The dose response for mortality and weight stunting demonstrated that both *H. armigera* neonates and second instar larvae were most sensitive to the same Cry protein.

The difficult transition from good science to good business – a decade in review of the key drivers and restrainers in BCP's quest to commercialise microbial control products

Ken Neethling

BCP, Durban, KZN, South Africa

Biological Control Products (Pty) Ltd was founded in 1995 with the vision of developing promising technology primarily for the agricultural industry, using bio-pesticides as a viable alternative to synthetic chemicals. Over a decade later, BCP has a stable of products catering to the needs of sustainable agriculture. A rise in prominence of organic, pesticide-free, fresh produce has helped fuel demand for these products.

However, many valuable lessons have been learnt along the way and good science has not always materialised into good business. By looking at a case study of arguably BCP's most successful bio-pesticide, Green Muscle™, as well as doing a post-mortem on some that didn't make it, some of these lessons are shared. These lessons include the pro's & cons of research collaborations, the hidden costs and benefits to obtaining registrations, the importance of the voice of the customer, the power of the brand and the place for science in the business model.

Infochemicals for the management of the banana weevil, *Cosmopoilites sordidus*

William Tinzaara, Eldad Karamura, Cliff Gold, Marcel Dicke, Arnold Van Huis, Caroline Nankinga

Bioversity International, Kampala, Uganda

Infochemicals (pheromones and kairomones) play an important role in the biology of many insect species. An understanding of their role in plant-herbivore-carnivore interactions can be used in the development of tools for the enhancement of environmentally benign alternatives to synthetic pesticides. Infochemicals may potentially be used for control of the banana weevil *Cosmopolites sordidus* (Germar) (Coleoptera: Curculionidae), which is a major pest of East African highland banana and plantains in most banana growing regions of the world. The weevil produces an aggregation pheromone that attracts both males and females. The pheromone has been identified and synthesized and is being recommended as an effective method of trapping and controlling the weevil. In this overview, the use of the aggregation pheromone and host-plant kairomones as components of an integrated management approach of the banana weevil is presented. The use of the aggregation pheromone in mass trapping, enhancement of the pheromone with host plant volatiles (kairomones), and integration of the pheromone with predators and entomopathogenic fungus, for the control of the banana weevil are discussed. Further research areas that can provide information for the development of an infochemical-based trapping system for the management of banana weevil are discussed.

Can polyphagy explain geographic distribution? A phylogenetic analysis on butterfly subfamily Nymphalinae

Jessica Slove, Niklas Janz

Stockholm University, Stockholm, Sweden

Insects, in particular phytophagous insects, are highly diverse. The oscillation hypothesis focuses on transitional polyphagy as a source of variation for an increased speciation rate. According to the hypothesis, the increase in host range should enable an increase in geographic range. The larger distribution in turn increases the likelihood of divergent selection for local differences and speciation. Here we test the assumption that polyphagy is correlated with geographic distribution.

Previous studies have looked at correlations on local to regional scales but these processes are more likely on a larger scale. Nymphalinae are globally distributed and therefore well suited for this study. Geographic range was calculated from worldwide distribution maps, and the correlation with host range was then analysed by independent contrasts.

Towards a better insecticide-treated target for controlling *Glossina fuscipes fuscipes*

Jenny Lindh[1], Steve Torr[2], Glyn Vale[2], Mike Lehane[1]

[1]Liverpool School of Tropical Medicine, Liverpool, United Kingdom, [2]Natural Resources Institute, University of Greenwich, Greenwich, United Kingdom

Introduction: Traps and insecticide-targets are used to control tsetse flies, the vectors of human and animal sleeping sickness. The performance of these catching devices can be improved by adding odour attractants and/or optimising their visual appearance. Here we focus on visual responses of *G. fuscipes*, a tsetse species for which the information on visual responses are scant.

Method: Studies were carried out on Chamaunga island in Lake Victoria, Western Kenya. Electric nets were used to estimate the numbers of tsetse attracted to and either captured or killed by a biconical trap or targets of various, colour, size, shape and height above ground.

Results: A biconical trap and a black target (1x1m) caught equal number of flies. However, catches from electric nets placed adjacent to the trap or target suggest that only 27% or 39% of tsetse attracted to the vicinity of the devices are captured or killed, respectively. Further experiments revealed that a blue-and-black target attracts up to 2x more tsetse than an all-black one. Moreover, increasing the height of the target from 0 to 1m above ground reduces the catch but increase the proportion of flies that land to 80%.

Conclusion: The above results suggest that a simple insecticide-treated target of blue-and-black flanked by a fine black netting panel would be 4x more effective than a biconical trap for half the price. Further studies of the visual responses of Palpalis group species of tsetse promise even greater improvements in the cost-effectiveness of using artificial baits to control sleeping sickness.

Diamondback moth choice in glucosinolate-containing plants, hosts and non-hosts

Francisco Badenes-Perez, Michael Reichelt, David Heckel

[1]Max Planck Institute for Chemical Ecology, Jena, Germany, [2]Max Planck Institute for Chemical Ecology, Jena, Germany, [3]Max Planck Institute for Chemical Ecology, Jena, Germany

Introduction: *Plutella xylostella* (L.) (Lepidoptera: Plutellidae) is a specialist of glucosinolate-containing cruciferous plants. Plants in the family Brassicaceae and other families containing a wide variety of glucosinolates (Caricaceae, Limnantheceae, Moringaceae, Phytolaccaceae, Resedaceae, and Tropaeolaceae) were studied as hosts for *P. xylostella*. Faba beans and peas (Fabaceae) were included as non-host plants. Three different strains of *P. xylostella* reared on artificial diet, cabbage, and peas were used to determine oviposition choices and survival on the different plants.

Methods: Ovipositional preference was studied in non-choice and two-choice tests. Larval survival on hosts was recorded. Glucosinolate and saponin contents in plants were determined with HLPC-UV and LC-MS, respectively.

Results and Discussion: Oviposition differences were often significant between plants of different genus, but not between species within the genus *Barbarea* despite qualitative and quantitative differences in glucosinolate and saponin composition and in absence/presence of trichomes. Oviposition and development also occurred in non-brassicaceous plants containing glucosinolates. Oviposition on non-hosts occurred in non-choice experiments. The role of glucosinolates and saponins in *P. xylostella* host choice is discussed.

Comparative genomic analysis of immunity-related genes in *Bombyx mori*

Hiromitsu Tanaka[1], Jun Ishibashi[1], Kosuke Fujita[1], Yoshiro Nakajima[1], Aki Sagisaka[1], Mikio Yoshiyama[1], kazuya Tomimoto[1], Yoichi Kaneko[2], Takashi Iwasaki[2], Tomoya Sunagawa[2], Ai Asaoka[1], kazuei Mita[1], Minoru Yamakawa[1]

[1]National Institute of Agrobiological Sciences, Tsukuba, Ibaraki, Japan, [2]University of Tsukuba, Tsukuba, Ibaraki, Japan

Comparative genome analysis of innate immunity-related genes was carried out using the lepidopteran insect, silkworm, *Bombyx mori*. Over 200 immunity-related genes were identified by searching genes encoding similar amino acids sequences to known defense proteins in *Drosophila melanogaster, Anopheles gambiae*, *Apis mellifera*, and *Tribolium castaneum*. *B. mori* had unique genes encoding antimicrobial peptides and a recognition protein, which was not present in other insects except for Lepidoptera, suggesting a lepidopteran specific gene evolution occurred in such genes. Our analysis also suggested that recognition, modulation and effectors mechanisms seemed not to be same between Lepidoptera and other insect species, because the similarity of the proteins involved in such mechanisms between *B. mori* and other insect species were not so high. On the other hand, the factors involved in the intracellular signal transduction pathways were well conserved, suggesting these immune signal transduction pathways were conserved between Lepidoptera and other insect species.

The emerald ash borer invasion of North America: how can a secondary pest threaten the existence of an entire tree genus?

Daniel Herms

The Ohio State University / OARDC, Wooster, OH, United States

Introduction: Emerald ash borer (EAB), *Agrilus planipennis*, has killed millions of ash (*Fraxinus* spp.) trees in the Midwestern United States since its accidental importation from Asia. Congeneric relatives endemic to North America only colonize stressed trees. However, EAB is killing healthy trees on high quality sites, creating a wood-borer outbreak of unprecedented intensity.

Methods: We have 99 forest plots to determine effects of community composition on susceptibility to invasion, and established a common garden to document interspecific variation in ash resistance to EAB.

Results: Once trees began to die in an infested stand, ash mortality progressed rapidly, increasing 30% per year. There was no relationship between ash mortality and ash density, ash basal area, total stand density, or any measure of biodiversity, suggesting that silvicultural approaches hold little potential for reducing ash mortality. In a common garden study, Manchurian ash, which is also native to Asia, was found to be much more resistant to EAB than North American green and white ash, perhaps by virtue of targeted defenses selected via its coevolutionary history with EAB. Phytochemical analysis of phloem revealed the presence of phenolic compounds unique to Manchurian ash that might represent mechanisms of resistance to EAB.

Conclusions: As EAB continues to spread, it clearly has the potential to decimate ash throughout North America with impacts reminiscent of chestnut blight and Dutch elm disease. A hybridization program has been initiated with the objective of breeding resistance genes into North American ash species.

Fitness costs associated with lab-selected Cry1Ac-resistance may help explain the lack of field-evolved resistance in *Helicoverpa zea* to Bt cotton

Konasale Anilkumar, William Moar

Auburn University, Auburn, Alabama, United States

A stable and highly resistant (>100-fold) population of *H. zea* to the *Bt* Cry 1Ac toxin has been established (AR) and maintained in the laboratory for 30 generations. While feeding on toxin-treated diet, AR had significant fitness costs (increased pupal mortality, male sex ratio and male mating costs resulting in a reduction in mating) compared to the unselected parental strain (SC). Similarly, on untreated diet, AR had lower larval and pupal weight, and increased larval, pupal mortality and larval and pupal duration compared to SC. Cry1Ac toxin resistance in AR was reduced significantly within a generation in the absence of selection. When tested for performance on Bt cotton, AR significantly outperformed SC in numbers of survivors, highest number of larval instar reached, and duration of larval survival; however, AR could not complete larval development on *Bt* cotton. Additionally, a significantly lower percentage of AR (25%) larvae reached pupation on non-Bt cotton compared to SC (31%). Therefore, this study demonstrates that fitness costs are strongly linked with selecting for Cry1Ac resistance in *H. zea* in the laboratory, and fitness costs remain, and in some cases, even increase, after selection pressure is removed. These results support the low percentage of success for selecting, and maintaining Cry1Ac-resistant populations of *H. zea* in the laboratory, and may help explain why field-evolved resistance has yet to be observed in this major pest of *Bt* cotton.

Using insects in an integrated, novel approach to land-use planning: A case study of bioenergy crops

Alison J. Haughton[1], David A. Bohan[1], Rufus Sage[2], Mark Mallott[1], Victoria Mallott[1], Mark Cunningham[2], Jon Finch[3], Martin Turner[4], Trudie Dockerty[5]

[1]Rothamsted Research, Harpenden, Hertfordshire, United Kingdom, [2]The Game and Wildlife Conservation Trust, Fordingbridge, Hampshire, United Kingdom, [3]Centre for Ecology and Hydrology, Benson Lane, Crowmarsh Gifford, Wallingford, Oxfordshire. OX10 8BB., United Kingdom, [4]University of Exeter, Amory Building, Rennes Drive, Exeter. Devon. EX4 4RJ, United Kingdom, [5]University of East Anglia, 5School of Environmental Sciences, Norwich, Norfolk. NR4 7TJ, United Kingdom

Introduction: EU and UK Government policies for reducing greenhouse gas emissions present challenging targets. Energy from crops is expected to contribute significantly to reducing CO_2 emissions and, in the UK, it has been predicted that energy crops will occupy some 1.1m ha by 2020. The area of land planted to perennial biomass crops is expected to expand considerably. This will constitute a major land use change since energy crops differ from the annual arable crops typical of UK and northern European farming landscapes. Increasing land-use under these crops could have wide implications for insect biodiversity and the public acceptance, amongst other things.

Methods: Our work in the RELU-Biomass project (www.relu-biomass.org.uk) uniquely integrates the natural and social sciences to aid sustainable land-use planning for energy crops and focuses on the use of insects as biodiversity indicators. We describe a novel approach to land-use planning where we identify and integrate appropriate entomological indicators with social and economic data from a bioenergy crop, *Miscanthus*, in a Sustainability Appraisal Framework (SAF). The SAF, which takes a long-term view of the expected impacts of a proposed plan, is a tool for policy makers. We illustrate how field and extrapolated regional scale entomological data will be used to produce large-scale integrated maps of sustainable biomass crop planting. Thus, we demonstrate how insects can enable i) optimisation of environmental benefits of the location of energy crops; ii) development of best environmental practice guidelines for planting energy crops; and, iii) improvement of SAF indicators used in decision-making.

Old and novel parasitoid-fruit flies association: physiological suitability consideration

Samira Mohamed[1], Sunday Ekesi[1], Rachid Hanna[2], Robert Wharton[3], Fritz Schulthess[1]

[1]International Centre of Insect Physiology and Ecology (ICIPE), Nairobi, Kenya, [2]International Institute of Tropical Agriculture (IITA), Cotonou, Benin, [3]Department of Entomology, Texas A&M University College Station, Texas, United States

Introduction: Africa is generally considered to be the home of the genera *Dacus* and *Ceratitis*. The latter includes, two notorious species: *Ceratitis capitata* (Wiedemann) (Diptera: Tephritidae), one of the most polyphagous, widespread and damaging fruit fly pests and *C. cosyra* (Walker). In addition to the plethora of native fruit fly pests in Africa, several members of the genus *Bactrocera* have also invaded the continent, including the most devastating species *B. invadens*. In an attempt to find a promising parasitoid candidate for biocontrol of these pests two introduced parasitoid species, *Fopius arisanus* (Sonan) (Hymenopera: Braconidae) and *Diachasmimorpha longicaudata* (Ashmead) (Hymenoptera: Braconidae) and one native parasitoid species *Tetrastichus giffardii* Silvestri (Hymenoptera: Eulophidae) were evaluated. Host acceptability for oviposition and suitability for development of two invasive and six native species were evaluated.

Methods: Host acceptability was assessed by exposing the suitable host stage to the parasitoid species. Then the exposed hosts were later dissected and the number of parasitoid host was recorded. Host suitability was evaluated by rearing the exposed hosts until flies and parasitoid emergence. Total number of parasitoid progeny, Sex ratio (proportion of female) and percent parasitism were recorded. Hosts that proved to be unsuitable were further examined for immunological reaction to three parasitoids species.

Results: Females of three parasitoid species accepted all host species tested though at varying degree. Host suitability was also influenced by host quality. With exception of *D. longicaudata*, sex ratio varied across host species. Eggs of the three parasitoids were encapsulated in at least three of the tested host species. The native parasitoid *T. giffardii* and the introduced *F. arisanus* performed best on their old associated hosts, *D. ciliatus* and *B. invadens*, respectively.

Prey location mechanisms in the snail-killing flies, *Dictya montana* and *Sepedon spinipes spinipes* (Diptera: Sciomyzidae)

Rory Mc Donnell[1], Timothy Paine[1], Mike Gormally[2]

[1]University of California, Riverside, United States, [2]National University of Ireland, Galway, Ireland

Introduction: The Family Sciomyzidae is unique amongst insects in that almost all species are exclusively malacophagous. Globally, this feeding behavior has made the family a target for the selection and assessment of biocontrol agents of snail intermediate hosts of trematode diseases and of gastropod pests of agricultural/horticultural systems. Although a wide range of information has been published on the life history of these flies, relatively little is known about prey location mechanisms.

Methods: In this study, the ability of neonate larvae of the aquatic sciomyzids, *Sepedon spinipes spinipes* and *Dictya montana*, to follow snail mucus trails was assessed using filter paper Y-mazes. Mucus from snails within the intermediate host genus, *Lymnaea*, were used for both species. The responses of neonates to fresh and aged (45 minutes) mucus trails was determined

Results: When fresh mucus trails were used, all of the neonates displayed a positive response and followed the mucus trail into the experimental arm. The stimulatory substance(s), however, appears to become inactive with time and after 45 minutes none of the tested larvae reached the trail end.

Conclusions: These results suggest that trail-following behaviour in Sciomyzidae is an innate response and that aquatic species may have the potential to forage for food in shoreline and semi-aquatic areas. Such plasticity in microhabitat specificity also has significance from a biocontrol point of view as released larvae may have the potential to attack aquatic host populations in addition to utilising fresh mucus trails to locate stranded or shoreline host snails.

Importance of male sex pheromones in sexual selection in the African butterfly *Bicyclus anynana*

Caroline Nieberding[1], Klaus Fischer[3], Helene de Vos[1], Maria Schneider[1], Jean-Marc Lassance[4], Natalia Estramil[1], Jimmy Andersson[5], Joaquim Bang[5], Erik Hedenstrom[5], Christer Lofstedt[4], Paul Brakefield[1]

[1]Institute of Biology, Leiden, Netherlands, [2]Zoogeographical Research Unit, Liege, Belgium, [3]Zoological Institute & Museum, Greifswald, Germany, [4]Chemical Ecology and Ecotoxicology, Lund, Sweden, [5]Chemistry laboratory, Sundsvall, Sweden

Introduction: Sex pheromones in female Lepidoptera ensure recognition between conspecific individuals, discrimination between sexes, and mate choice. As such they play key roles in *i)* the reproductive success within species; and *ii*) the reproductive isolation between species. Whilst interest has focused on female pheromones, male Lepidoptera also produce sex pheromones. The role of sex pheromones produced by males in reproductive success and isolation remains largely unknown in insects. Based on the model butterfly *Bicyclus anynana* (Butler, 1879), we aim to assess here experimentally the role of male sex pheromones in the process of sexual selection by females.

Results: We describe the courtship behaviour of male *B. anynana,* and highlight how androconia distribute pheromones during courtship. We identify by GC-MS and GC-EAD the three active male pheromone components. Competition experiments in a field-like environment show that the mating success of males depends on the presence of pheromones. We then quantified the level of pheromone variability and estimated the heritability level of the male pheromone blend and androconia size by a father-sons regression. Finally, the variation of pheromone titres and ratios was compared between outbred and inbred males, which had been shown previously to display a difference in male mating success.

Discussion and conclusions: Results together suggest that the male sex pheromone blend in *B. anynana* is used by the female as an indicator of its fitness or quality. Therefore, this study and model system will allow evaluate the importance of male sex pheromones in driving reproductive isolation through sexual selection.

Available genetic enhancements to the Sterile Insect Technique

Luke Alphey

Oxitec Ltd, Oxford, United Kingdom

The Sterile Insect Technique (SIT) is a species-specific, environmentally friendly method of pest control which depends on the mass-rearing, sterilization and release of large numbers of pest insects. These sterile insects mate with the wild population, thereby reducing its reproductive potential. If a sufficient number of sterile insects can be released for a sufficient period, the target population will decline and collapse. Large-scale SIT programs have been conducted around the world against a range of pest insects, notable the New World Screwworm (*Cochliomyia hominivorax*) and tephritid fruit flies especially the Mediterranean Fruit Fly (Medfly, *Ceratitis capitata*). Genetic methods have provided major improvements to the Sterile Insect Technique (SIT), for example through the introduction of genetic sexing strains. Recombinant DNA 'transgenic' methods have the potential to provide further improvements, with a wider variety of novel traits and on shorter timescales than by classical methods. Many potential uses for recombinant DNA methods have been suggested; I will focus on developments that have already been incorporated into pest insect strains. Specifically, the methods discussed will be those that have been developed and work well in the laboratory and are in various levels of field testing. These include:

i) a heritable, fluorescent genetic marker;

ii) genetic sexing systems, especially for species other than Medfly;

iii) 'genetic sterilization' methods to reduce or eliminate the need for irradiation; and

iv) 'genetic containment' methods to minimize the hazard from non-irradiated releases and thereby allow a wider range of rearing and distribution options.

Introduction of any or all of these improvements into field practice would improve the cost-effectiveness and/or safety of the SIT. We have developed strains incorporating some or all of these features for the mosquitoes *Aedes aegypti* and *Aedes albopictus*, Medfly (*Ceratitis capitata*), Mexfly (*Anastrepha ludens*), and pink bollworm (*Pectinophora gossypiella*). These are currently in trials in several countries, including an extensive series of field trials in the US for pink bollworm, which will be reported.

Geographic variation in phenotypic plasticity and genetic adaptation to climate in the Afrotropical butterfly *Bicyclus anynana*

Maaike de Jong, Paul Brakefield, Fanja Kesbeke, Bas Zwaan

Leiden University, Leiden, Netherlands

Introduction: The East-African butterfly *Bicyclus anynana* shows striking seasonal plasticity for wing patterns and life history traits, which functions as an adaptation to contrasting wet-dry seasonal environments. Temperature is the single most important climatic variable determining *B. anynana* seasonal phenotype for our well-studied population from Malawi, where temperature is highly correlated with rainfall and thus a reliable indicator for the correct seasonal form. However, patterns of temperature-rainfall correlation vary strongly throughout the distribution of *B. anynana,* and different regions therefore pose different selection pressures on the species' plastic responses to temperature. The outcome of past adaptation can be used as a proxy for the potential for future adaptation of this organism to climate change.

Methods: We explored the nature and extent of phenotypic plasticity and genetic adaptation to temperature by comparing two Malawian populations and a South African population at three temperatures in a family design. This set-up allowed for the quantification of the reaction norms and the broad sense genetic variation of traits. The traits analysed at this level were: larval, pupal, and total developmental time, pupal weight, fat content, and wing pattern elements. Moreover, the following adult life history traits were measured at the population level: resting metabolic rate and starvation resistance.

Results: The experiment was carried out successfully, and first analyses indicate that the role of phenotypic plasticity is more important than genetic differentiation in the populations' ability to cope with local climate conditions. We will discuss our results in the light of adaptation to climate change.

Management of Rice Brown Plant Hopper by different modules of pesticide application

Monilal Chatterjee

Bidhan Chandra Agril. University, Mohanpur,West Bengal, India

Introduction: Rice brown plant hopper (*Nilaparvata lugens*) is one of the major key pests in intensive rice growing areas. Farmers of all parts are extensively used various toxic chemicals for the control of brown plant hopper. But in many cases they are unable to control successfully due to frequent resurgence and resistance phenomenon occurs in BPH. Serious outbreaks of plant hoppers have been reported from many parts of India. Nymphs and adults of brown plant hopper suck the plant sap, devitalize the plants and as a result drying and yellowing of leaves results which is often referred to as 'hopper burn'[1, 2.]

Methods: To cope with ever challenging insect pest's problems in Rice, farmer needs to have the latest technological knowledge in pest management. To control brown plant hopper in rice efficiently, some new modules of pesticide combination with novel chemicals were selected. To determine the effectiveness of different modules of application compared with farmer's practice a field experiment was done on rice over two seasons. They compared seven modules of application belongs to the chemicals imidacloprid, clothianidin, novaluron, buprofezin, dadeci, acephate, dichlorvos fenobucarb, fenvalerate and azadirachtin at different intervals and combination. All the agronomic practices were followed and the application was done from mid tillering stage followed by different intervals in different modules.

Results: The results showed that in module-1 -where application of imidacloprid followed by dadeci and clothianidin at 35, 55 &70 days after transplanting - completely checked the BPH population up to harvesting time, that was closely followed by module- 4 (novaluron+acephate and fenobucarb)and module-2(fenobucarb, novaluron & fenobucarb) at same days interval. In module-5, farmers practice, (imidacloprid 2 times and mixed formulation fenvalerate+acephate 2 times) was also effective in reducing the population initially but some resurgence were noted after certain laps of time. The benzophenyl urea groups of insecticide – novaluron and buprofezin when mixed with other insecticide were highly effective in reducing the BPH population up to harvesting that was reflected in yield also. Azadirachtin was however, less effective against BPH compared to other treatments.

Conclusion: The new pesticides with novel modes of action and high selectivity were highly effective against rice brown plant hopper. They are safer to non-target organisms and quickly degrade to non-toxic products.

Novel roles for E75A and Broad during segmentation of the milkweed bug, *Oncopeltus fasciatus*.

Deniz Erezyilmaz, Hans Kelstrup, James Truman, Lynn Riddiford

[1]Princeton University, Princeton, NJ, United States, [2]Janelia Farm Research Campus, Howard Hughes Medical Institute, Ashburn, VA, United States

The E75A and Broad transcription factors play well-established roles during molting and metamorphosis of holometabolous insects. We have examined the role of these two genes during embryonic development of the hemimetabolous milkweed bug, *Oncopeltus fasciatus*. We find that although the postembryonic roles of these genes in the bug are reminiscent of their reported postembryonic functions in the Holometabola, their embryonic functions in this insect are entirely novel. The milkweed bug is described as an intermediate germ insect, since it patterns the anterior segments simultaneously during the blastoderm stage and then switches to an anterior-to posterior progressive mode to pattern the abdominal segments at the germ band stage. We find that *Of'br* is globally expressed at the transition between the blastoderm and germ band stages, and later appears during nymphal differentiation. Loss of *Of'br* through parental RNAi causes posterior truncations. These truncations range from deletions of a few posterior segments to the loss of all but the most anterior head segments. We suggest that *Of'br* is a permissive factor, required for the transition between the blastoderm and germ band stages. *Of'E75A* also plays a role during segmentation. In this case, however, *Of'E75A* is expressed with double segment periodicity in the blastoderm, and in a dynamic pattern in the growing abdomen. Loss of *Of'E75A* results in fusions between adjacent segments. We show that these fusions occur as odd-numbered parasegments are deleted, resulting in an imperfect pair-rule phenotype. The significance of these findings will be discussed. Supported by NSF and NIH.

Genetic control of mosquitoes

Luke Alphey

Oxitec Ltd, Oxford, United Kingdom

Methods for transforming mosquitoes have improved to the point where it is practical to consider using these methods to control mosquito populations and mosquito-borne diseases. The availability of genome sequences has further increased the range of potential genetic options and improved the timescale for delivering them. Much work has focused on the development of strains refractory to transmission of mosquito-borne pathogens, with some notable successes. We have instead focused on controlling mosquito numbers – population suppression rather than population replacement. Our preferred strategy is a variant of the Sterile Insect Technique (SIT) which we call RIDL, in essence a set of genetic improvements to SIT.

SIT is a species-specific, environmentally friendly method of pest control used with great success and on a very large scale against some agricultural pests. However trials in the 1970s and 1980s against various mosquito species were rather equivocal – some significant successes, for example against *Anopheles arabiensis* in El Salvador, but other trials where poor male performance, or inadequate isolation, led to disappointing results. RIDL potentially allows some of the technical difficulties with classical SIT for mosquitoes to be overcome, thereby providing an attractive and sustainable control tool.

We have developed some very promising RIDL strains for the dengue vector *Aedes aegypti*, which appears to be a suitable target for RIDL; our current progress in this area will be discussed.

Spinosad 45 SC-the novel pesticides for the management of chilli pests

Monilal Chatterjee

Department of Agricultural Entomology. Bidhan Chandra Krishi Viswavidyalaya (Agricultural University), West Bengal, India

Introduction: Chilli is an important vegetable as well as spices crop in Indian Agriculture. Though India ranks first in the world with reference to area and production of chilli, however the average productivity is very low in comparison to other countries. A major constraint in chilli production is direct damage to fruit by *Helicoverpa armigera* (H) and *Spodoptera litura* (F) and damage by thrips (*Scirtothrips dorsalis*) at vegetative growth of plants. As chilli is one of the most popular and profitable crop, farmers everywhere feel the need to protect such high value crops from any type of damage caused by insect pests. They often use synthetic insecticides indiscriminately, and insect resistance to insecticides and resurgence are very common in the tropics.

Methods: To control chilli thrips and fruit borers efficiently, a new organic pesticides Spinosad 45 SC with novel mode of action has been developed recently. To determine the effectiveness of this new pesticides at different doses compared with traditional chemicals effect on natural enemies and compatibility to other insecticides, fungicides and urea, two field experiments were done over two seasons. They compared five pesticides (Spinosad 45 Sc @ 45, 56 & 73 g a.i./ha, Imidacloprid 20SL @ 40 g a.i., Chlorpyrifos 20 EC @ 500 g a.i., Endosulfan 35 EC @ 525 g a.i. and Fipronil 5 Sc @ 40 g a.i./ha) with untreated control. All other agronomic practices were standard, and a blanket sprays to control mites was applied when necessary. First spraying was done with the appearance of thrips and thereafter three sprays at fortnightly interval were followed.

Results : The results showed that Spinosad 45 % SC at 56 and 73 gm a.i./ha gave best control of thrips up to 14 days in both seasons. It has also reflected in yield parameter. Similarly the fruit borer infestation was sharply reduced in Spinosad treated plot that was closely followed by Fipronil. In another observations Spinosad showed less hazard to natural enemies viz. *Menochillus* sp., *Syrphus* sp. And *Chrysoperla* sp. at different doses compared to untreated control. The compatibility of Spinosad with Quinalphos, Carbendazim and Urea was well and no phytotoxicity was noted at any stages of the crop growth .

Conclusions :Spinosad is a naturally derived insecticide produced by fermentation of bacterium, *Saccharopolyspora spinosa* and consists of a mixture of related Spinosyn toxins, principally Spinosyn-A and D. It acts as contact and stomach poison (Dow, 1997, Salgado, 1997; Thompson *et al.* 2000). It has novel mode of action, disrupts the functions of GABA receptors of small neurons in the central nervous system. Spinosad is considered to be 'fast-acting' insecticide provides 7 to 14 days of control have practically no odor, moderately strong soil absorption and degrades rapidly in the environment. It offers excellent selectivity to beneficial organisms with low environmental risk to human beings and has potential use in Integrated Pest Management (IPM) systems.

Globins in *Drosophila*: Oxygen carrier, ROS detoxifier or else?

Thomas Hankeln[1], Eva Gleixner[1], Stefan Zimmerling[1], Thorsten Burmester[2]

[1]University of Mainz, Mainz, Germany, [2]University of Hamburg, Hamburg, Germany

Introduction: Respiratory proteins have been considered unnecessary in most insects, which do not dwell in hypoxic habitats. However, our survey has revealed that globins are a natural constituent of the insect gene repertoire. In *Drosophila*, three globin genes of unknown function have been identified.

Methods: Expression patterns of globin genes have been studied by in situ-hybridization and quantitative realtime RT-PCR. Gene expression levels have also been experimentally modified by RNAi and transgenic overexpression to elucidate functional consequences.

Results: *glob1* is the most prominently expressed Drosophila globin, found in the tracheal system and fat body in embryos, larvae and adults. After experimental hypoxia, *glob1* mRNA levels do not change in adult *D. melanogaster*, but are diminished by 50 % in embryos. Increased *glob 1* expression was observed in larvae after hypoxia/normoxia cycles and after hypERoxia. RNAi-induced downregulation of *glob1* leads to elongations in developmental time. In situ hybridization analysis of the phylogenetically closely related *globins 2* and *3* reveals preferential, but weak expression exclusively in the testes.

Conclusions: Gene regulation data suggest that *glob1* preferentially fulfils a role in supplying O_2 or detoxifying reactive oxygen species, or both. Expression patterns for *glob 2* and *3* suggest a redundant function of the duplicates associated with spermatogenesis.

The role of Allee effects in gypsy moth invasions

Patrick C. Tobin and Andrew M. Liebhold

Forest Service, United States Department of Agriculture, Northern Research Station, 180 Canfield Street, Morgantown, WV USA 26505

Allee effects have been historically applied in efforts to understand the low-density population dynamics of rare and endangered species. Many biological invasions likewise experience the phenomenon of decreasing population growth rates at low population densities, mainly because most founding populations of introduced non-native species occur at low densities. In established species, range expansion occurs when new colonies are introduced outside of the organism's current range, and also can be at low densities and thus subject to Allee dynamics. There has been consistent empirical and theoretical evidence demonstrating, and in some cases quantifying, the role of Allee dynamics in the gypsy moth, *Lymantria dispar* (L.), invasion of North America. In this paper, we will examine the potential causes of an Allee effect in the gypsy moth to highlight the importance of mate-finding failure as the primary mechanism behind an Allee effect. We then explore the role of Allee effects in the establishment and spread dynamics of the gypsy moth, which can serve as an appropriate model system for understanding how Allee effects manifest themselves in the dynamics of other biological invasions.

Comparative and functional genomics of disease vector mosquitoes

Geoge Christophides

Imperial College London, London, United Kingdom

Introduction: Mosquitoes are vectors of parasitic and viral diseases of immense importance for global health. Genome sequencing and comparative genomics studies laid down the basis for the establishment of conceptual and technological frameworks towards understanding of the mosquito responses to the various pathogens which could accommodate the observed diversity between different transmission systems.

Results: Comparative genomics analyses revealed a fascinating picture when vector immune responses were disarticulated into sequential phases, beginning with recognition of microbial patterns, producing signals which may undergo modulation and/or transduction before activating effector mechanisms. Each phase is characterized by different evolutionary dynamics, which collectively account for high flexibility that enables adaptation to new challenges, such as malaria parasites or viruses. These findings, in conjunction with transcriptomics analyses and functional genomics, led us to identify numerous genes as involved in the mosquito responses to infection by the malaria parasite *Plasmodium* and disease viruses. Several of these genes are often highly divergent and have no orthologs in other species. Genetics and population genomics data demonstrated that these genes are likely to have played a key role in the vectorial capacity of mosquitoes to transmit human malaria.

Conclusions: Mosquito response to invasion by human pathogens largely determines their competence for disease transmission. This innate capacity of mosquitoes to kill pathogens could be utilized in future integrated efforts to control and ultimately eradicate human diseases.

Influence of landscape features on the establishment and spread of mountain pine beetle populations

Brian Aukema, Honey-Marie Giroday

Canadian Forest Service at University of Northern British Columbia, Prince George, British Columbia, Canada

The current outbreak of mountain pine beetle in western Canada now covers an area approaching 10 million hectares. In the past few years, several aeolian dispersal events have transported large numbers of insects from central British Columbia over the Rocky Mountains into areas without similar historic beetle pressure, including northeastern British Columbia and northwestern Alberta. Many of these dispersal events have deposited sufficient numbers of insects to colonize and kill live trees, raising concern of eventual movement of mountain pine beetle throughout the boreal forests of northern Canadian within jack pine hosts. In this paper, we present recent research on the settlement patterns of new populations in relation to landscape features, the persistence of new populations, and spatial rates of change that may provide insight into the dominance of local vs. long distance dispersal in establishment events.

Physiological adaptations enable American dog tick adults to survive temperature extremes

Glen Needham, Kai-Lun Hwang

The Ohio State University, Columbus, Ohio, United States

Introduction: Physiologically and behaviorally ticks survive adverse environmental conditions for considerable periods of time. Water balance and metabolism have received considerable attention but studies on specific physiological adaptations that facilitate survival at extreme high or low temperatures are few. We report on one of the most important human disease vectors in North American, the American dog tick *Dermacentor variabilis*.

Methods: Adult ticks were exposed to various temperature regimens to determine their physiological responses including survival, and expression of heat shock proteins and polyol production.

Results: Rapid heat and rapid cold hardening provided significant protection from exposure to high and low temperature extremes in the laboratory. Two partial clones of heat-shock 70 proteins (Hsp70) were identified and characterized (one long Hsp70L at 1727 base pairs; one short Hsp70S at 1540), with differences in the 3' ends, 81% nucleic acid identity and 87% amino acid similarity with an Hsp70 of *Ixodes scapularis*, the deer tick. Hsp70S was expressed at a much higher level than Hsp70L in response to high temperature exposure using a Northern blot analysis. Glycerol and sorbitol concentrations increased with rapid hardening (brief exposure to a temperature extreme). Glycerol appears to protect adult ticks from both high and low temperature injury.

Conclusions: Collectively these adaptations of expressing Hsp70 and increasing polyol concentrations augment survival of this ixodid tick and may play a role in the widespread distribution of this species in North America.

Reconstructing social evolution in halictine bees

Sean Brady[1], Bryan Danforth[2]

[1]Smithsonian Institution, Washington, DC, United States, [2]Cornell University, Ithaca, NY, United States

Introduction: Accurately reconstructing the historical patterns of eusocial gains and losses is critical to understanding general processes of social evolution. We investigated this issue in halictine bees (sweat bees) that show a pattern of multiples gains and loses of primitive eusociality.

Methods: We obtained sequence data from multiple gene fragments for a wide range of halictine social and nonsocial taxa, and conducted phylogenetic analyses using parsimony, likelihood, and Bayesian methods. The timing of social evolution was reconstructed using fossil-calibrated, relaxed molecular clock techniques under both penalized likelihood and Bayesian criteria. The pattern of gains and losses of sociality was inferred using both parsimony and model-based likelihood and Bayesian methods for ancestral state reconstruction.

Results: Our molecular data provided robust resolution for most major lineages of halictine bees. Eusociality in halictine bees evolved as recently as 20 million years ago in three independent lineages. These recent origins are consistent with the high levels of social variation observed within this group. We evaluated alternative scenarios for the pattern of social gains and losses in each of the three social halictine lineages.

Conclusions: Phylogenetics provides crucial insights into the timing and patterns of social evolution in halictine bees. We discuss our results within the context of the age of social origins in other eusocial taxa, and especially consider the impact of our results toward hypotheses regarding the canalization of eusocial traits over time.

Cat fleas, dust mites and mold mites are susceptible to a brief exposure of ultraviolet light

Glen Needham[1], Roman Denallo[1], John Needham[1], Leon Fourie[2]

[1]The Ohio State University, Columbus, Ohio, United States, [2]ClinVet International, Bloemfontein,

Introduction: Ultraviolet (UV) exposure is lethal to an array of organisms by damaging nucleic acids. UV-C sterilizes surfaces in air ducts, laboratories and other settings where micro-organisms were the target. The potential for this non-chemical tactic to kill household arthropods such as cat fleas (*Ctenocephalides felis*), American house dust mites (HDM, *Dermatophagoides farinae*) and mold mites (*Tyrophagus putrescentiae*) has received little or no attention. We report that these organisms are very sensitive to UV-C.

Methods: Embryonic and postembryonic life stages of these three arthropods were exposed to a bulb chamber (35 Watts, 11mW/cm^2 of UV-C irradiance, Halo Technologies) for brief periods but generally less than 5 secs then kept at constant RH and temperature that optimize their survival. In some cases food was provided *ad libitum*. Survival was monitored and recorded.

Results: The embryonic (egg) stage for all three species was very sensitive to UV-C exposure, usually 1 sec was sufficient to cause 100% mortality. Flea larvae (L1 & L3) were sensitive to UV-C and their behavior/physiology was impacted (reduced feeding, mobility changed, delayed molting). Dust mites and mold mites perished several days post-exposure, female mites laid fewer eggs, and feeding activity was diminished, thus reducing allergen production.

Conclusions: With pesticide resistance and exposure to non-target organisms always a concern, novel methods are needed for insect and mite control, especially in very sensitive indoor environments. UV-C offers an alternative especially as an adjunct to vacuuming (Halo Technologies).

Probabilistic methods for assessing the risk of the evolution of resistance to transgenic crops

Michael Caprio[1], C. D. Parker[1], Ryan Kurtz[2]

[1]Mississippi State University, Mississippi State, MS, United States, [2]Syngenta Biotechnology Incorporated, Research Triangle Park, NC, United States

We examine methods to incorporate variation due to both stochastic features and parameter uncertainty into spatially-explicit stochastic models. There is always uncertainty involved in estimation of parameters for both simple and complex models. The conventional methods of risk analysis place this uncertainty between different scenarios with little guidance for users to determine the relative likelihood of the scenarios. Probabilistic risk assessment incorporates uncertainty into a probabilistic framework. By using probability functions for uncertain parameters and running thousands of simulations using random draws from those functions, a probability distribution of time to resistance is obtained that incorporates demographic variation as well as variation due to uncertainty in parameters. The more certain one is in model parameters, the less the variance in the final probability distribution. We examine two case scenarios, the removal of mandated refuges for 2-gene cotton and the impact of reducing requirements for non-Bt corn refuges from 50% to 20% in the Mid-southern USA.

Analyses of diversity and composition of the arthropod fauna associated with bromeliads

Anne Zillikens[1], Nivaldo Peroni[2], Josefina Steiner[2]

[1]University of Tuebingen, Tuebingen, Germany, [2]Federal University of Santa Catarina, Florianópolis, SC, Brazil

Introduction: Tank bromeliads provide aquatic and terrestrial microhabitats suitable for a wide array of invertebrates. The purpose of our study was to compare the species richness and composition of the associated fauna between bromeliad species and habitats.

Methods: In Santa Catarina State, southern Brazil, the arthropods of four species of terrestrial and one species of epiphytic bromeliads were collected in Atlantic rain forests, identified to the lowest taxonomic level possible or assigned to morphospecies. For each bromeliad species sample rarefaction curves were plotted and non-parametric species richness estimators were calculated. The arthropod assemblages of were described using Correspondence analyses (CA).

Results: Highest species richness was observed in *Nidularium innocentii*. For this species and for *Aechmea lindenii* rarefaction curves reached a plateau whereas for *Canistrum lindenii* and *A. nudicaulis* they tended to increase. CA demonstrated similarity of the faunal communities between *A. nudicaulis* and *A. lindenii*, and *C. lindenii* and *N. innocentii*, respectively, whereas that of *Vriesea vagans,* the only epiphytic species among the bromeliads studied, was more different from all other species. Detrended CA revealed a good differentiation between the faunal communities of bromeliads from secondary versus primary forest.

Conclusions: Our study documented a high species richness of the bromeliad associated fauna which differed according to bromeliad species. Factors like similar habit, as in the two *Aechmea* species, or the same microhabitat, as in *C. lindenii* and *N. innocentii,* probably contributed to more similar arthropod faunas. Forest type also strongly influenced the arthropod community.

Progress report on the Lepidoptera Tree-of-Life (LepTree) – 2.5 years of facilitating lepidopteran research globally

Jerome C. Regier[1], Joaquin Baxieras-Almela[2], John W. Brown[3], Soowon Cho[4], Michael P. Cummings[5], Donald R. Davis[6], Akito Y. Kawahara[7], Conrad C. Labandeira[8], Charles Mitter[7], Cynthia S. Parr[9], Amanda D. Roe[10], Jae-Cheon Sohn[7], Susan J. Weller[10], Andreas Zwick[1]

[1]University of Maryland Biotehnology Institute, Center for Biosystems Research, University of Maryland, College Park, MD, United States, [2]Universitat de Valencia, Valencia, Spain, [3]USDA Systematic Entomology Laboratory, c/o National Museum of Natural History, Smithsonian Institution, Washington, DC, United States, [4]Department of Plant Medicine, Chungbuk National University, Cheongju, Republic of Korea, [5]Center for Bioinformatics and Computational Biology, University of Maryland, College Park, MD, United States, [6]National Museum of Natural History, Department of Entomology, Smithsonian Institution, Washington, DC, United States, [7]Department of Entomology, University of Maryland, College Park, MD, United States, [8]National Museum of Natural History, Department of Paleobiology, Smithsonian Institution, Washington, DC, United States, [9]Institute for Advanced Computer Studies, University of Maryland, College Park, MD, United States, [10]Department of Entomology, University of Minnesota, Saint Paul, MN, United States

The Lepidoptera Tree-of-Life Project, or LepTree, is an international community collaboration which seeks to advance progress on lepidopteran phylogeny. We review our project goals and highlight three areas of accomplishments after 2.5 years of funding: 1. informatics structure (Leptree.net), 2. morphology and molecular workshops, and 3. molecular project progress. Within the first year, the interactive website Leptree.net was launched, and the LepTree Knowledge Project template is now available for community use. Several morphology and molecular workshops have facilitated exchange of ideas and techniques among lepidopterists, and more are planned. A fossil data base is being constructed for dating divergence times. Nearly all superfamilies and many families have been sequenced for several genes, and we present preliminary phylogenetic results.

Progress report on the Lepidoptera Tree-of-Life (LepTree) – 2.5 years of facilitating lepidopteran research globally

Jerome C. Regier[1], Joaquin Baxieras-Almela[2], John W. Brown[3], Soowon Cho[4], Michael P. Cummings[5], Donald R. Davis[6], Akito Y. Kawahara[7], Conrad C. Labandeira[8], Charles Mitter[7], Cynthia S. Parr[9], Amanda D. Roe[10], Jae-Cheon Sohn[7], Susan J. Weller[10], Andreas Zwick[1]

[1]University of Maryland Biotehnology Institute, Center for Biosystems Research, University of Maryland, College Park, MD, United States, [2]Universitat de Valencia, Valencia, [3]Spain, USDA Systematic Entomology Laboratory, c/o National Museum of Natural History, Smithsonian Institution, Washington, DC, United States, [4]Department of Plant Medicine, Chungbuk National University, Cheongju, Korea, [5]Republic of, Center for Bioinformatics and Computational Biology, University of Maryland, College Park, MD, United States, [6]National Museum of Natural History, Department of Entomology, Smithsonian Institution, Washington, DC, United States, [7]Department of Entomology, University of Maryland, College Park, MD, United States, [8]National Museum of Natural History, Department of Paleobiology, Smithsonian Institution, Washington, DC, United States, [9]Institute for Advanced Computer Studies, University of Maryland, College Park, MD, United States, [10]Department of Entomology, University of Minnesota, Saint Paul, MN, United States

The Lepidoptera Tree-of-Life Project, or LepTree, is an international community collaboration which seeks to advance progress on lepidopteran phylogeny. We review our project goals and highlight three areas of accomplishments after 2.5 years of funding: 1. informatics structure (Leptree.net), 2. morphology and molecular workshops, and 3. molecular project progress. Within the first year, the interactive website Leptree.net was launched, and the LepTree Knowledge Project template is now available for community use. Several morphology and molecular workshops have facilitated exchange of ideas and techniques among lepidopterists, and more are planned. A fossil data base is being constructed for dating divergence times. Nearly all superfamilies and many families have been sequenced for several genes, and we present preliminary phylogenetic results.

Agromyzidae (Diptera) leafminer fly-parasitoid relationships in potato agroecosystems of the Peruvian coast

Norma Mujica[1], Jürgen Kroschel[4]

[1]International Potato Center, Lima, Peru [2]Sociedad Peruana de Entomología, Lima, Peru, [3]IOBC-Neotropical Regional Section, Lavras, Brazil [4]University of Hohenheim, Stuttgart, Germany

Introduction: *Liriomyza huidobrensis* is an important potato pest at the coast of Peru, which is mainly controlled by the use of insecticides. *Liriomyza* species are known to have many natural enemies, particularly in the New World. The aim of our study was to assess in potato agroecosystems leafminer fly-parasitoid relationships in arable weeds that could serve as important reservoirs for the augmentation of parasitoids for the natural control of *L. huidobrensis*.

Methods: In field surveys leave of arable weeds around potato fields and infested by leaf miners were collected and flies and parasitoids reared, recorded and identified. Seven samples were made during the potato-growing season from May to October, during the Peruvian winter.

Results: Agromyzidae flies mined 22 weeds belonging to 14 plant families. *L. sabaziae* was the dominant species (58.7%), followed by *L. huidobrensis* (13.6%). *Galinsoga parviflora* (Asteraceae), *Malva parviflora* (Malvaceae) and *Commelina fasciculata* (Commelinaceae) hosted only non-Agromyzidae potato pests and the highest number of common parasitoids with *L. huidobrensis.* Parasitism from collected weed leaves was 48.9% compared to 21.5% in potato. Fifty hymenoptera parasitoids were recorded with *Chrysocharis caribea*, *C. flacilla*, *Halticoptera arduine*, *Diglyphus begini* and *D. websteri* as the most important. The Shannon index showed higher leafminer fly and parasitoid species diversity around potato fields.

Conclusions: Most weeds proved to provide reservoirs for non-economically important Agromyzidae leafminer flies and are important resources for common parasitoids of *L. huidobrensis*. A rational management of arable weeds associated with potato could support the augmentation of parasitoids and the natural control of *L. huidobrensis*.

Functional genomic analysis of appendage development in the red flour beetle, *Tribolium castaneum*

David Angelini, Moto Kikuchi, Elizabeth Jockusch

University of Connecticut, Storrs, CT, United States

We are studying the relationships between changes in developmental regulatory genes, genetic networks, and the evolution of morphology in the context of adult appendage patterning in cosmopolitan pest beetles closely related to the genetic model *Tribolium castaneum* (Coleoptera, Tenebrionidae). Antennae of *Tribolium* possess an annulated flagellum of nine segments divided into two morphologically distinct regions, the funicle and club. The number of funicle vs. club segments varies across species. We used RNA interference to characterize the function of 23 candidate genes hypothesized to play a role in antennal growth or patterning. Our data suggest that the *Tribolium* antenna is patterned in a "gap"-like manner. The club and the funicle require specific genes, while another group of genes functions throughout the antenna. Novel developmental roles were found for several genes in the specification of regions of the flagellum. Relatively few of these genes had conserved functions, compared to *D. melanogaster*. Genes such *Notch* are conserved in the formation of joints, while *spineless* is required for antenna identity in both species. Preliminary data from morphologically distinct species of *Tribolium* suggest that changes in the regulation of *dachshund* and/or the function of *odd-skipped*-like genes may have been involved in evolution of antenna morphology. We are currently constructing *piggyBac* reporters to test these hypotheses of molecular evolution and to identify region-specific drivers for use in future experiments.

Response of two mosquito heat shock proteins to environmental stress

Joshua Benoit, Giancarlo Lopez-Martinez, David Denlinger

Ohio State University, Columbus, Ohio, United States

Heat shock proteins (Hsps) play a vital role in stress survival, but few such studies have focused on mosquitoes. In this study, we will provide a detailed view of the upregulation and downregulation of genes encoding Hsp70 and Hsp90 when the mosquitoes are subjected to various stresses. The primary stresses tested were heat, cold, and desiccation, both individually or combined. To determine if the response varies between mosquito species we tested *Culex pipiens*, *Anopheles gambiae*, and *Aedes aegypti*. We cloned both Hsps from all three species and found high amino acid homology for the portions of the genes used for northern blot hybridization. Overall, we have determined that *Hsp70* and *Hsp90* respond differentially to different stress, but the three mosquitoes respond in much the same way. Our goal is to provide a comprehensive description of how heat shock proteins are regulated in mosquitoes.

Disease resistance and viral epizootics in western tent caterpillars

Judith Myers[1], Jenny Cory[2]

[1]University of British Columbia, Vancouver, BC, Canada, [2]Algoma University, Sault Ste. Marie, Canada

Western tent caterpillars, *Malacosoma californicum pluviale* demonstrate regular population cycles over their range in western North America. An observed relationship between epizootics of nucleopolyhedrovirus and a subsequent reduction in fecundity of tent caterpillar populations led to the formulation of the disease defense hypothesis. This predicts that viral epizootics select for more resistant moths with reduced fecundity reflecting a cost of disease resistance. To test this, we measured variation in larval resistance to NPV infection for families from four spatially distinct populations of western tent caterpillars over years of peak and declining host densities. Susceptibility to disease varied considerably among families and populations, but was not related to egg mass size. Thus we reject the disease defense hypothesis. In 2003 a population that had previously experienced a less intense NPV epizootic over the last outbreak period in 1997 was significantly more susceptible to NPV than 3 other populations for which epizootics had been more severe. In 2004 the single population that experienced an NPV epizootic the previous year was significantly more resistant to virus suggesting that selection for resistance could have occurred. Although viral epizootics are a characteristic of outbreak populations, mortality of larvae from other causes increased in both the years of peak and early decline and indicated a major deterioration in the quality of field populations. Sublethal and covert viral infection may reduce the fecundity of moths in the decline and also be related to the deterioration in overall quality and increased susceptibility of populations to other diseases.

The evolution and development of integrated phenotypes

Goggy Davidowitz[1], Elizabeth Jockusch[2], Lisa Nagy[1]

[1]University of Arizona, Tucson, AZ, United States, [2]University of Connecticut, Storrs, CT, United States

Phenotypic integration - the ability of a large number of genetic, developmental, physiological and functional morphological characters to generate a functional organism, often under different environmental conditions - is an essential attribute of organisms. Without integration, development would lead to functional multicellular organisms less frequently than it does and the potential for evolutionary change would be severely impaired. Without integration, changes in body size would be constrained, as would developmental plasticity.

We discuss the question of how development is structured to produce integrated phenotypes in relation to both morphological and physiological traits. The best examples of phenotypic integration at the morphological level arise from the study of modularity. Modules are identified as sets of traits within which there is a high level of correlation and between which there is a lower level of correlation. We evaluate examples of modularity from arthropod systems, including segmentation, wing patterns, wing shape and appendage morphology. At the physiological level we compare examples from the study of the regulation of body size and development time as well as endocrine regulation of insect polymorphisms. Finally, we analyze how advances in methodology allow for novel approaches to understand how the environment regulates gene expression through the neuroendocrine axis of the organism.

Phylogeny of the fungus-growing ants and the major evolutionary transitions in their symbiosis with fungi

Sean Brady, Ted Schultz

Smithsonian Institution, Washington, D.C., United States

Introduction: All fungus-growing ants (tribe Attini) depend obligately on the cultivation of fungus for food. We present the first fossil-calibrated comprehensive molecular phylogeny of attine ants in order to illuminate the coevolutionary history between the ants and their fungal cultivars.

Methods: We generated data from four nuclear genes from 65 attine taxa incorporating the full range of taxonomic diversity within the group, with special attention given to rarely collected and potentially paraphyletic groups. Phylogenetic analyses were conducted using parsimony, likelihood, and Bayesian methods. We used fossil-calibrated divergence dating to date the origins of the symbiotic systems using penalized likelihood and Bayesian relaxed clock approaches.

Results: The symbiotic relationship between ants and their fungal cultivars originated in the Neotropics a single time ~50 million years ago. Three known additional symbiotic systems (yeast agriculture, coral fungus agriculture, and higher agriculture) have separately evolved from this original symbiosis during the past 30 million years. The attine genera *Cyphomyrmex* and *Trachymyrmex* are both nonmonophyletic, results with important implications regarding the origin and diversification of the higher agricultural symbiosis. Leaf-cutting ants that practice a highly specialized form of higher agriculture evolved remarkably recently, 8-12 million years ago.

Conclusions: We reconstructed the broad evolutionary history between ants and their fungal cultivars. Our results identify species occupying phylogenetic positions that are transitional between these major fungal symbiotic systems. Future study of these key species may help clarify the accretion of behavioural and ecological characteristics that produced these symbioses.

Pre-breeding for resistance to Russian wheat aphid, *Diuraphis noxia*, in wheat and barley in Australia: germplasm characterization against multiple biotypes

[1]Mehmet Cakir, Janine Vitou[2], Scott Haley[3], Owain Edwards[4], Frank Peairs[3], Dolores Mornhinweg[5], Jacob Lage[6], Haydn Kuchel[7], Bertus Jacobs[8], Iain Barclay[9], Ana Maria Castro[10], Joyce Malinga[11]

[1]Murdoch University, Murdoch, WA, Australia, [2]CSIRO European Laboratory, Montpellier, France, [3]Colorado State University, Fort Collins, CO, United States, [4]CSIRO Entomology-Perth, Floreat Park, WA, Australia, [5]USDA, ARS, Western Stillwater, OK, United States, [6]CIMMYT, Mexico, [7]Australian Grain Technologies, Roseworthy, SA, Australia, [8]LongReach, Marleston, SA, Australia, [9]Department of Agriculture and Food WA, South Perth, WA, Australia, [10]University of La Plata, 1900-La Plata, Argentina, [11]KARI-Njoro, Njoro, Kenya

Russian Wheat Aphid (RWA), *Diuraphis noxia*, has been reported to be one of the most damaging pests for wheat and barley. This aphid is not yet present in Australia though the risk of introduction in the future is high. Since the use of resistant varieties, as opposed to using insecticides, has been found to be most economical method of managing this pest, the Australian Cereal Industry has decided to invest in a pre-breeding project that is highly collaborative with other RWA workers around the world. The objectives of the project are to: 1) characterize available RWA resistant germplasm accessions against available RWA biotypes in France, USA and elsewhere 2) identify closely linked molecular markers to resistance genes and validate them in Australian wheat and barley backgrounds, and 3) introgress RWA resistance into Australian wheat and barley backgrounds.

To date, a number of wheat lines that are known to be resistant to USA RWA biotypes 1 and 2 were tested in Montpellier, France, against four RWA biotypes collected from Mexico, Hungary, South Africa, and France. The aphid infestation was conducted at the seedling stage with infestation six days after planting. Leaf chlorosis and biomass was measured at 21 days after planting. Four lines tested thus far have shown good resistance to biotypes from France, Mexico and South Africa. Results from the testing of these lines with RWA biotypes from Kenya, Argentina, and a second biotype from South Africa, and the screening of 99 barley lines from Oklahoma-USA will also be discussed.

Pre-breeding for resistance to Russian wheat aphid, *Diuraphis noxia*, in wheat and barley in Australia: germplasm characterization against multiple biotypes

[1]Mehmet Cakir, Janine Vitou[2], Scott Haley[3], Owain Edwards[4], Frank Peairs[3], Dolores Mornhinweg[5], Jacob Lage[6], Haydn Kuchel[7], Bertus Jacobs[8], Iain Barclay[9], Ana Maria Castro[10], Joyce Malinga[11]

[1]Murdoch University, Murdoch, WA, Australia, [2]CSIRO European Laboratory, Montpellier, France, [3]Colorado State University, Fort Collins, CO, United States, [4]CSIRO Entomology-Perth, Floreat Park, WA, Australia, [5]USDA, ARS, Western Stillwater, OK, United States, [6]CIMMYT, Mexico, [7]Australian Grain Technologies, Roseworthy, SA, Australia, [8]LongReach, Marleston, SA, Australia, [9]Department of Agriculture and Food WA, South Perth, WA, Australia, [10]University of La Plata, 1900-La Plata, Argentina, [11]KARI-Njoro, NJORO

Russian Wheat Aphid (RWA), *Diuraphis noxia*, has been reported to be one of the most damaging pests for wheat and barley. This aphid is not yet present in Australia though the risk of introduction in the future is high. Since the use of resistant varieties, as opposed to using insecticides, has been found to be most economical method of managing this pest, the Australian Cereal Industry has decided to invest in a pre-breeding project that is highly collaborative with other RWA workers around the world. The objectives of the project are to: 1) characterize available RWA resistant germplasm accessions against available RWA biotypes in France, USA and elsewhere 2) identify closely linked molecular markers to resistance genes and validate them in Australian wheat and barley backgrounds, and 3) introgress RWA resistance into Australian wheat and barley backgrounds.

To date, a number of wheat lines that are known to be resistant to USA RWA biotypes 1 and 2 were tested in Montpellier, France, against four RWA biotypes collected from Mexico, Hungary, South Africa, and France. The aphid infestation was conducted at the seedling stage with infestation six days after planting. Leaf chlorosis and biomass was measured at 21 days after planting. Four lines tested thus far have shown good resistance to biotypes from France, Mexico and South Africa. Results from the testing of these lines with RWA biotypes from Kenya, Argentina, and a second biotype from South Africa, and the screening of 99 barley lines from Oklahoma-USA will also be discussed.

Release of alarm pheromone components during feeding increases bed bug encounters with their host and decreases traumatic insemination

Joshua Benoit[1], M. Robert Michaud[1], Jay Yoder[2], David Denlinger[1]

[1]Ohio State University, Columbus, Ohio, United States, [2]Wittenberg University, Springfield, Ohio, United States

Alarm behavior was elicited in nonfed bed bugs *Cimex lectularius* in response to bugs that were feeding or had recently fed. GC/MS analysis of headspace volatiles captured on absorbents indicated that feeding dramatically boosted secretion of (E)-2-hexenal and (E)-2-octenal, two chemicals previously reported as active components of the bed bug alarm pheromone. When nonfed bugs were exposed to extracts from fed individuals, (E)-2-hexenal, (E)-2-octenal, or a mixture of these two chemicals, the time required for the bugs to locate a feeding site was reduced nearly 50%. The amount of fluid consumed during feeding was not affected, suggesting that, once feeding was initiated, there was no stimulatory effect elicited by the feeding of neighboring bugs. These same two chemicals previously implicated in the alarm response and in aggregation (when present in low concentrations) appear to increase the likelihood of host location. Additionally, we documented that traumatic insemination was significantly reduced when exposed to the high levels of alarm pheromones, indicating one purpose of (E)-2-hexenal and (E)-2-octenal release is to repel males from fully engorged females to prevent damage during insemination. We propose that (E)-2-hexenal and (E)-2-octenal, when present in high concentrations, function as general excitants that modify bed bug behavior by stimulating them to increase movement that leads to shorter periods needed to discover a host and may prevent traumatic insemination immediately after feeding.

Differential gene expression due to diet quality during caste determination in honey bees

Diana Wheeler[1], Jay Evans[2]

[1]University of Arizona, Tucson, Arizona, United States, [2]USDA Bee Research Laboratory, Beltsville, Maryland, United States

Introduction: Worker honey bees determine the caste fate of larvae by controlling their diet. Developing queens are fed rich royal jelly and developing workers receive poorer quality worker jelly.

Methods: We studied larvae 16-88 hours old, ages that span determination and early differentiation. Some larvae were exposed to normal queen and worker diets, and others were transferred from one diet to the other. We examined expression patterns of candidate genes involved in the insulin and TOR signaling pathways, in juvenile hormone synthesis and metabolism, and in management of nutrient supplies and stores.

Results: JH titers are known to begin rising in queen larvae after about 48 hours. The mechanism that triggers this rise would need to be activated prior to that time. In larvae 40 hours past hatching, presumptive queens showed higher expression than workers for ILP1, insulin receptor, TOR and TSC1 genes, suggesting that these signaling pathways could link nutrition and JH titers. Response to transfer varied with gene and caste. ILP1, insulin receptor, and Rheb gene expression directly tracked nutritional quality. Decreased diet quality was followed by dramatic upregulation of gene expression of numerous genes relevant to caste determination and differentiation. In stark contrast, the switch to a poorer quality diet provoked little deviation from normal worker patterns of expression.

Conclusion: Numerous genes known or suspected of being involved in caste determination show a pattern of expression that may represent canalization of the effect of diet on caste.

Insect-pathogenic nematodes and their potential for citrus pest control in the Sonoran Desert

S. Patricia Stock

Department of entomology. University of Arizona, Tucson, Arizona, United States

Citrus production in southwestern USA is limited to areas that are relatively frost-free and where sufficient inexpensive water is available. Climate changes and urban expansion have contributed to changes in this crop's insect and pathogen complex. One of the most debilitating pests is the citrus nematode, *Tylenchulus semipenetrans.* At present, 90% of citrus grown in Arizona are infected by this nematode. Given the current lack of successful control measures and the increasing awareness of the detrimental health and environmental effects due to chemical pesticides, new alternatives are deeply needed for management of this nematode. In this respect, one of the choices for substitution of chemical nematicides is the consideration of biological control agents such as entomopathogenic nematodes (EPN). In this study, two commercially available EPN, *Steinernema riobrave* (Biovector) and *Heterorhabditis bacteriophora* (Nemasys) were assessed for their efficacy against the citrus nematode in laboratory assays. Two-month-old rough lemon seedlings were grown in cone-tainers, at 25℃ and 30% humidity. *Tylenchulus semipenetrans*-infected seedlings were inoculated at a concentration of 12,000 J2/seedling. Citrus nematode (J2) root penetration rate and female egg production were assessed in relation to: 1) EPN application time (i.e., simultaneous [EPN simultaneously applied with citrus nematode], after [EPN applied after citrus nematode establishment in the citrus seedlings]), and 2) EPN application method (i.e., aqueous suspension, EPN-infected cadavers). A completely randomized design with two replications (12 citrus-seedlings/treatment) for each evaluated parameter was considered. Data were subjected to analysis of variance (ANOVA). Results from these studies will be presented and discussed. Assessment of this information is critical for understanding EPN-citrus nematode interactions and in making predictions of the various impacts of EPN application for the control of this nematode.

Analysis of the relationship between Pgm (Phosphoglucomutase) heterozygosity and fitness in honeybee, *Apis mellifera* L.

Meral Kence, Zerrin Gulduren

Middle East Technical University, Ankara, Turkey.

Introduction: In honeybee populations of three different geographical regions each representing different subspecies, combination of the long-term analysis of genetic variation at Pgm locus with the characterization of biochemical and functional correlates of this enzyme polymorphism have revealed that seasonal allele and genotype frequency changes have adaptive value.

Methods: Pgm genotypes were determined by starch-gel electrophoresis. Enzyme activity and glycogen content of worker bees measured spectrophotometrically. Goodness-of-fit (G^2), unpaired, two-side *t*-tests, and Spearman correlation tests were used in analyses of the data where appropriate.

Results: Frequency of Pgm-75/100 heterozygotes were significantly high ($P<0.001$) among winter bees. Analysis of enzyme activity of *Pgm-75/100* and *Pgm-75/75* genotypes revealed that enzyme activity is higher in heterozygotes ($P<0.0001$), the mean PGM activity measured as 1.943 and 3.187 units/mg protein in homozygotes and heterozygotes respectively. Summer and winter bees differed also in their glycogen content ($P<0.0001$) being higher in heterozygotes. Strong correlation (Spearman $r = 0.8410$, $P<0.0001$) detected between enzyme activity and glycogen content.

Conclusions: The observation that *Pgm* heterozygotes that predominate in winter colonies independent of geographical location, have both high levels of PGM activity and glycogen content may be the underlying mechanism to the increased life span during winter because increased PGM activity may provide efficient utilization of the glycogen reserves compared to homozygotes.Therefore increased heterozygosity at *Pgm* locus in winter can be an important physiological mechanism that contributes to efficient use of the glycogen for heat production during thermoregulation and longevity of the bees which is important for the winter survival of the colony.

Pest management in organic hazelnut growing in Turkey

Sebahat K. Ozman-Sullivan, Gregory Thomas Sullivan

Ondokuz Mayis University, Samsun, Turkey

Introduction: Organic hazelnut growing has great potential in Turkey, but pest management strategies need further development.

Methods: The demographics, attitudes, behaviours and practices of 50 organic growers were surveyed in the Black Sea region in 2008. Factors such as education level, avenues of learning, reasons for adopting organic growing, pest species and control methods were elucidated. A review of alternative organic pest control techniques was also undertaken to identify additional low-cost strategies to assist growers to more effectively manage a wide spectrum of pests.

Results: Most organic growers were members of grower cooperatives. Growers' ability to identify pests, predators, parasites and entomopathogens was low. They employed a small range of approved chemical, physical, cultural and mechanical treatments. Mixtures of ash, lime and sulphur were used to control the major pests, the hazelnut weevil *Curculio nucum* L. and big bud mites *Phytoptus avellanae* Nal. and *Cecidophyopsis vermiformis* Nal. Sulphur was also used to control the big bud mites. Removal of big buds in winter was one of the mechanical treatments. Red sticky traps were used to control the bark beetles *Xyleborus dispar* (Fabricius) and *Lymantor coryli* (Perris). Cultural practices such as pruning were also employed.

Conclusions: Growers used a limited array of organic methods to control pests. The majority were not aware of the spectrum of options available for improving their pest management.

Plant-mediated effects in insect-virus interactions

Jenny Cory

Algoma University College, Sault Ste. Marie, Canada

Inter and intra-specific differences in plant chemistry and structure can have significant influences on the interactions between insects and their pathogens. This is particularly the case with pathogens, such as baculoviruses, that produce occlusion bodies that are able to persist away from the insect host on the plant surface and are ingested when the insects feed. There is a trade-off between the effect of plant phytochemicals on the insect and the pathogen; insect performance will be reduced on a poor quality host, making it more susceptible to entomopathogens, whereas, plant allelochemicals might also reduce the effectiveness of the virus. Outcomes of these interactions are hard to predict. Whether it is possible for plants to manipulate insect pathogens as 'bodyguards' to increase their own fitness is a possibility, but has yet to be shown. However, it is becoming increasingly clear that plant-mediated effects could have an important role, not only in the efficacy of baculoviruses as insecticides, but also in the ecology and evolution of insect-pathogen relationships.

Genomic approaches in forest entomology – implications for insect ecology and pest control

Jenny Cory

Algoma University College, Sault Ste. Marie, Canada

Genomics and post genomic technologies have tremendous potential in forest entomology, from providing the tools for unravelling the intricacies of insect-plant and insect-pathogen relationships, to exploring the impact of multi-trophic interactions, and investigating the effects of environmental change on trees, insects and their natural enemies at the genomic level. Through these means we can not only provide insight into the mechanisms that underlie the ecology and evolution of these interactions, but also find ways of overcoming potential pest problems through the creation of novel pest control strategies and the selection or manipulation of crop traits. While these insights may move us towards more environmentally sustainable pest control, the potential consequences of any alterations to ecosystem components must also be considered from a risk assessment perspective.

The determination of some behaviours of the Anatolian honeybee and the local honeybee on *Rhododendron luteum* Sweet, a native plant in Turkey

Ulkem Taniker[1], Sebahat K. Ozman-Sullivan[2]

[1]Black Sea Agricultural Research Institute, Samsun, Turkey, [2] Ondokuz Mayis University, Samsun, Turkey

Introduction: Turkey is the world's third highest honey producer. *Rhododendron luteum* Sweet is a common native plant of the Black Sea region of Turkey used by local honeybees. The Anatolian honeybee, *Apis mellifera anatoliaca* Maa has the best characteristics and is the common species in most parts of Turkey.

Methods: Certain behavioral characteristics of Anatolian and local honeybees were examined on the Korgan high plateau of Ordu in the Black Sea region, Turkey. Ten Anatolian and 10 local honeybee hives were brought to the experimental area during the rhododendron's flowering period from the Ankara-Beypazari district and the Ordu-Korgan high plateau, respectively. Aggression, mortality rate, flying activity and pollen collection were measured.

Results: The average aggressiveness scores of Anatolian and local honeybees were 8.04 stings/min. and 5.08 stings/min, respectively. The average number of dead workers for Anatolian honeybee was 11.17 colony/day and for the local honeybee was 6.69 colony/day. The average number of bees taking flight per minute for Anatolian and local honeybee colonies were 30.72 and 29.03, respectively. Average Anatolian honeybee pollen production was 44.51 g/colony/day from various plants and average local honeybee pollen production was 37.28 g/colony/day, predominantly from *R. luteum*.

Conclusions: Although the local honeybee fed on the dominant plant *R. luteum,* the Anatolian honey bee fed minimally on it and instead foraged on other plants. A hybrid of the local and Anatolian honeybee may have the capacity to better utilise the large quantities of nectar available from *R. luteum*.

Adding segments one by one: comparing the regulation of segmental growth between branchiopod crustaceans and insects

Terri Williams[1], Beata Blachuta[2], Thomas Hegna[1], Lisa Nagy[2]

[1]Yale University, New Haven, Connecticut, United States, [2]University of Arizona, Tucson, Arizona, United States

Introduction: Within arthropods, a taxon defined by their body segments, mechanisms of segmentation are well-described only in *Drosophila*. However, *Drosophila* produces segments simultaneously in the embryo, whereas the vast majority of arthropods add their segments sequentially, budding them one by one from an unsegmented posterior region called the "growth zone". It is clear this pattern is both ancestral and wide-spread. Nevertheless, we do not know whether sequential segment addition involves a variety of highly disparate mechanisms or, conversely, reflects a highly conserved set of mechanisms.

Methods: We use the branchiopods *Artemia franciscana*, *Triops longicaudatus* and *Thamnocephalus platurus***.** We inhibited cell division pharmacologically to examine the link between cell division and patterning. We also used chemical inhibition to examine the role of Notch signaling in segmental growth.

Results: Our data in branchiopods show that segmentation diverges from *Drosophila* in two important ways. First, segment patterning within the growth zone of branchiopod crustaceans is causally linked to cell proliferation. Second, pharmacological inhibition of *Notch* signaling arrests or slows segmentation but has no consequence on the overall growth of the larva.

Conclusions: We hypothesize that the growth zone is not comprised of naïve, unspecified cells, but that cells undergo some degree of specification prior to exiting the growth zone. We further hypothesize that *Notch* function within the growth zone is essential for segment patterning and morphogenesis, but is not controlling proliferative growth.

Fipronil treatments for controlling the dectes stem borer in soybeans

Lawrent Buschman, Holly Davis, Terutaka Niide, Phillip Sloderbeck

Dept. Entomology, Kansas State University, Manhattan, United States

The Dectes stem borer, *Dectes texanus* LeConte, is a native North American insect that normally lives on composite weed hosts such as ragweed, *Ambrosia artemisifolia*. However, it is now becoming an important pest of soybean, *Glycine max*, and sunflower, *Helianthus annuus*, in some parts of the United States. Management is difficult because the eggs are laid in the pith of the soybean plant and larvae tunnel in the pith and thus they are not controlled by standard foliar insecticide treatments. We tested 12 systemic insecticides as foliar treatments and 11 as soil treatments at cultivation for control of the Dectes stem borer in soybean. Only one insecticide, fipronil, clearly controlled the Dectes stem borer, either as a soil treatment or as a foliar treatment. In 2006 and 2007 we tested fipronil as a foliar treatment and also as a seed treatment. Foliar treatments gave 55 to 95% control, depending on the insect pressure at three locations. At the low rate (25mg/100kg) seed treatments gave 45 to 92% control, but at the high rate (100 mg/100kg) seed treatments gave 88 to 100% control depending on insect pressure at three locations. Although we observed excellent insect control we were not able to show a clear yield advantage to controlling Dectes stem borer infestations if harvest occurs before the larvae girdle the stems which cause the plants to lodge. This can cause serious crop losses.

The evolution of novel abdominal appendages in sepsid flies: a role for HOX genes?

Julia Bowsher, Lisa Nagy

University of Arizona, Tucson, Arizona, United States

How do evolutionary changes in the molecular processes of development result in changes in morphology? Abdominal appendages in the male sepsid fly *Themira biloba* (Diptera, Sepsidae) are complex novel structures on the fourth abdominal segment that are used during courtship and mating. This family is the only group of insects to have evolved a complex and well-articulated extra-genitalic abdominal appendage. Given the current phylogeny of Sepsidae, abdominal appendages appear to have evolved in a relatively short time period and in more than one instance within the clade. Determining the molecular processes underlying abdominal appendage development will elucidate how complex novel structure can evolve in a relatively short time period. Previous work has established that the abdominal appendages develop during pupation from imaginal histoblast cells on the fourth abdominal segment. We are investigating to what degree the genetic module known to specify thoracic limb development in Drosophila has been co-opted into the regulation of the sepsid abdominal appendages and to what degree their development is controlled by novel gene interactions. Although the appendages develop during pupation, the specification of fourth segment as the location for appendage development occurs earlier. We investigated when the abdominal appendages are first specified by examining the expression of the HOX genes in the Bithorax complex that are known to determine the identities of each abdominal segment.

Conservation biological control to manage pests of crop plants

Stephen Wratten, J Tompkins

Lincoln University, Lincoln, New Zealand

Introduction: Classical biological control has had dramatic successes but also some spectacular failures. Conservation biological control uses "ecological engineering" approaches to enhance efficacy of biological control agents already in the crop. This paper presents results outlining recent successes in this area, including their economic benefits.

Methods: Work in three agricultural sectors involves planting native New Zealand species as well as non-native within or around crops.

Results: A hierarchy of success has been demonstrated, ranging from aggregation of natural enemies on flowers to widespread adoption by growers.

Conclusion: Conservation biocontrol technologies, supported by sound ecological science, are being adopted throughout Australasia. They significantly reduce variable costs and provide novel marketing opportunities.

Insects and ecosystem services: introduction

Stephen Wratten[1], Harpinder Sandhu[2], John Porter[3,] M Jonsson

[1]Lincoln University, Lincoln, New Zealand, [2]CSIRO, Adelaide, Australia, [3]Copenhagen University, Copenhagen, Denmark

Introduction: From the work of Costanza, Daily, Sandhu, among others we know something of the economic value of insects as ecosystem service providers. For the service of biological control, for instance, Costanza *et al.* (1997) estimated it to be worth US$c500 billion per annum worldwide. However, E.O. Wilson points out that current biodiversity loss is at a rate of between 1,000 and 10,000 times higher than all past such events. This impacts on the ability of biodiversity to provide ecosystem function which, when expressed in monetary terms, is called ecosystem services. This presentation will review insects as ecosystem service providers, give examples of their economic value derived from value-transfer and experimental techniques.

Conclusion: Further significant biodiversity loss will increase reliance on "substitution agriculture", which is largely oil-based, with obvious consequences for energy and food security. This session reviews the vital role that insects play in minimising the dependence on substitution agriculture as well as in ecosystem function in non-crop environments.

Impact of selected pesticides on canopy-dwelling predatory guilds on eastern hemlock, *Tsuga canadensis*

Jerome Grant[1], Abdul Hakeem[1], Paris Lambdin[1], Frank Hale[2], James Rhea[3]

[1]University of Tennessee, Knoxville, Tennessee, United States, [2]University of Tennessee, Nashville, Tennessee, United States, [3]USDA Forest Service, Asheville, North Carolina, United States

Introduction: Hemlock woolly adelgid (HWA), *Adelges tsugae*, native to Asia, is found in the eastern United States, where is has caused tremendous losses to eastern hemlock, *Tsuga canadensis*. This tree is an ecologically important component of eastern forests. In the Great Smoky Mountains National Park, ca. 50% of hemlocks have died since this pest was first found in 2002. Insecticides, the primary means of protecting hemlock, are effective at managing HWA in forests; however, little is known about their impact on non-target predators.

Methods: A two-year study was conducted on the Cherokee National Forest in Tennessee. Thirty trees were grouped in three blocks in a 2x5 split plot design (two treatment times: Fall and Spring; and five treatments: horticultural oil, imidacloprid as soil injection/as soil drench/as tree injection, and untreated [control]). Trees were sampled monthly with beat sheets, malaise traps, and direct observations. A bucket truck was used to assess vertical distribution of predators.

Results: Spiders comprised more than 60% of all predators (n=4,917). More predators were collected from control and horticultural oil-treated trees than from any imidacloprid treatments. Predator numbers rebounded 1-1 ½ years after imidacloprid treatment. Treatment time did not affect predator densities.

Conclusions: Predators were distributed throughout the tree canopy regardless of treatment. Imidacloprid, regardless of application method or treatment time, decreased predators in each strata (top, middle and bottom). Further studies are necessary to assess long-term effects of pesticides on predators on hemlock to enable forest managers to better understand these pesticide management tools.

Does successful biological weed control by an insect herbivore improve the plant community?

Judith Myers, Andrea Stephens, Pam Kranitz

University of British Columbia, Vancouver, BC, Canada

The success of biological control of weeds is usually judged by the decline in the density or biomass of the target weed. An important consideration however is whether successful biological control is followed by restoration of the habitat following the decline of the weed. Recently a serious rangeland weed of western North America, diffuse knapweed, *Centaurea diffusa*, has been successfully controlled at many sites following the establishment and spread of an introduced weevil, *Larinus minutus*. Surveys taken over the period of knapweed decline indicate that another introduced weed, Cheat grass, *Bromus tectorum*, has increased in density. I will discuss the biological control program for knapweed which involved the release of 12 insect species, the impacts of knapweed decline on the diversity of the plant community at rangeland sites, and the success biological weed control for rangeland restoration.

Chemical ecology of *Xylosandrus crassiuculus* (Motschulsky) (Coleoptera: Curculionidae) in the southern USA

Eric Ott, Brian Sullivan, Kier Klepzig

University of Montana, Missoula, MT, United States

Introduction: To date no research has used semiochemical analysis in an attempt to develop novel management techniques for angiosperm-infesting ambrosia beetles, despite increasing concern of these non-indigenous beetles in the United States. A novel technique of flooding host trees stimulated ambrosia beetle attacks while quantifying host compounds and behavioral responses.

Methods: *In-situ* host volatile sampling from bole and leaf were collected on Porapak-Q. Gas chromatography mass spectrometry (GC-MS) analysis of these compounds tested for differences in the compounds, amounts, and area of release (leaf or bole) being emitted by the flooded and unflooded trees. Coupled gas chromatography electroantennographic detection aided in testing antennal responses to these aerations. Field trapping assays tested the behavioral responses of the most promising compounds.

Results: Ambrosia beetle attraction to drowning white oak trees peaked on day 4 of flooding and varied by species. Significant differences in the compounds, amounts, and area of release (leaf or bole) being emitted by the flooded and unflooded trees were found using GC-MS. Coupled gas chromatography electroantennographic detection revealed response to 29 host compounds and 12 nonhost compounds, including known bark beetle pheromones. Field trapping assays with these compounds displayed that ethanol and eugenol in combination showed a mean increase in the number of *Xylosandrus crassiusculus* caught over the current standard trapping bait, ethanol.

Conclusion: A novel technique of flooding angiosperm trees was used in combination with semiochemical techniques in bait development. The antennal and behavioral responses to host and nonhost volatiles suggest a complex semiochemical system.

Is decreased generalized immunity a cost of Bt-resistance in cabbage loopers *Trichoplusia ni*?

Jerry Ericsson[1], Alida Janmaat[2], Judith Myers[3]

[1]Simon Fraser University, Burnaby, BC, Canada, [2]University-College of the Fraser Valley, Abbotsford, BC, Canada, [3]University of British Columbia, Vancouver, BC, Canada

Cabbage loopers, *Trichoplusia ni*, are pests in vegetable greenhouses in British Columbia Canada. Heavy use of the microbial control *Bacillus thuringiensis kurstaki, Btk* has resulted in selection for resistance in these moths. We have studied the immune responses following exposure to a low dose of *Btk* in a resistant population derived originally from a greenhouse and compared this to a susceptible strain. To test if a cost of systematic resistance is a reduced ability of the resistant strain to respond to a disease challenge, we measured the levels of resistance following a low dose of *Btk*, the expression profiles of hemolymph proteins, hemolymph phenoloxidase activity, and the differential number of circulating hemocytes. Exposure to *Btk* or injections with *E. coli* increased the hemocyte counts of susceptible larvae but not of resistant larvae. The hemolymph protein composition of larvae varied between populations and treatments. Phenoloxidase activity was not significantly different following challenge in either line, whereas protein levels only declined significantly in the hemolymph of susceptible larvae continually exposed to *Btk*. The data suggest that phenoloxidase is not involved in constitutive resistance to *Btk*. These results suggest that constitutive resistance may reduce the inducible immune responses of cabbage loopers.

Top-down and bottom-up forces shape the evolution of prey alarm signalling

Wolfgang Weisser

Friedrich-Schiller-University, Jena, Germany

Recent advances in chemical ecology have unravelled a vast array of chemical signals in plant-plant, plant-herbivore, herbivore-predator and plant-predator interactions. While most of these infochemicals are investigated in the context of a specific interaction between two particular species, the evolution of such a signal takes place in a network of biotic interactions. Consequently, the same chemical compound can have different roles depending on the organisms involved. The relative costs and benefits of the signal in its different roles will affect not only whether the signal may evolve at all, but will also influence the quantities emitted and its chemical identity.

Using the example of aphid alarm pheromone I will investigate how top-down and and bottom-up forces affect the evolution of this intraspecific signal. When attacked by a predator or parasitoid aphids may emit this alarm pheromone, in most cases (E)- β-Farnesene (EBF), to warn conspecifics of the presence of a natural enemy. In addition to this function as a pheromone, EBF may be perceived by a variety of natural enemies. I will present evidence that the costs associated with EBF's role as a kairomone may be substantial. EBF also alerts ants, and may act as kairomone or synomone depending on the interaction between aphid and ant. Finally, there is increasing evidence that aphids have to counter-act attempts of manipulation by the host plant. Thus, in the network of interactions between plants, aphids, natural enemies and ants, EBF can take all roles as pheromone, allomone, synomone and kairomone which has consequences for alarm pheromone evolution and emission dynamics.

Harmonising approaches to pest risk assessment in Europe: The EFSA Plant Health Panel

Sharon Cheek[1], Jan Schans[2], Elzbieta Ceglarska[1], Giuseppe Stancanelli[1]

[1]EFSA, Parma, Italy, [2]Ministry of Agriculture, Nature Management and Fisheries, Wageningen, Netherlands

The Plant Health (PLH) Panel of the European Food Safety Authority provides independent scientific advice on the risks posed by plant pests which threaten the safety and security of the food chain and the wider environment in the EU. The aim of the Panel is to contribute to development of a harmonised approach for pest risk assessment in the EU, in cooperation with EU Member States and international organizations. The Panel, which started its activity in June 2006, is composed of 21 Members with expertise in various fields of risk analysis and plant health. It operates with the support of the EFSA PLH secretariat and includes a permanent working group on arthropods. Since its start, it has published six scientific opinions on the risk posed by invasive plants, weeds, a citrus bacterial disease and a citrus insect pest. Most recently, it evaluated thirty pest risk assessments, for the French overseas departments of Martinique, Guadeloupe, French Guiana and Réunion, with the aim of harmonizing their phytosanitary rules with EU plant health legislation. Seven of these opinions relate to insect pests of banana and citrus.

The particular challenges faced by the PLH Panel faces include dealing with uncertainties relating to entry pathways and impacts, and developing a harmonised approach to the evaluation of risk assessments in the EU.

Fruit fly pests of horticultural crops in tropical Africa: present knowledge and prospects for management

Rachid Hanna[1], Sunday Ekesi[2], Desire Gnanvossou[1]

[1]International Institute of Tropical Agriculture, Cotonou, Benin, [2]International Centre for Insect Physiology and Ecology, Nairobi, Kenya

Introduction: Tropical Africa is home to at least 10 fruit fly species that are severe pests of fruit-bearing horticultural crops. Successive invasions of 4 Asian *Bactrocera* species have considerably exacerbated exiting fruit fly problems. Until recently detailed knowledge of factors affecting distribution and abundance of fruit flies infesting horticultural crops, and much less the effectiveness of management options developed and used elsewhere, has been minimal. We illustrate these challenges with examples from cucurbits and mango.

Materials and Methods: We reviewed available knowledge on species composition, distribution, temporal dynamics and host-crop/variety-specific levels of fruit fly infestations and natural control with predators and parasitoids. We compared the effectiveness of male lures and female attractants for population monitoring and potential for use in fruit fly control, and tested the effectiveness of GF-120 as bait spray. We also examined the potential of classical biological control against exotic species, and the enhancement of biological control of native fruit fly pests with native and introduced natural enemies.

Results: Generally**,** *Dacus ciliatus*, *D. vertebratus* and *Bactrocera cucurbitae* are the most common species infesting cucurbits, while *Ceratitis cosyra* and *B. invadens* are the dominant species infesting mango. Fruit fly infestations in both crops can reach 75%, depending on geography, season and varieties, with the large majority of fruits being infested by a single species while the rest by two and rarely by more species. Torula yeast was in general most attractive to the spectrum of fruit flies attacking cucurbits and mango, followed by NuLure, waste yeast from local breweries and BioLure – the latter being least attractive to *Dacus* and *Bactrocera* species. Bait sprays of GF-120 was ineffective for cucurbit flies but appear promising for mango-infesting flies. Parasitism rates on native species were low, but classical biological control of the exotic species such as *Bactrocera invadens* with the braconid *Fopius arisanu*s is promising, as are soil and bait applications of *Metarhizium anisopliae* as components of fruit fly IPM in cucurbits and mango.

Conclusions: Future work should determine the feasibility of, and to test and promote the use of multiple tactics and area-wide approach for fruit fly management in horticultural crops in tropical Africa.

Diversity and role of termites in West African savannas: case studies in Burkina Faso and Côte d'Ivoire

Souleymane Konaté, Dorkas Kaiser, Kanvaly Dosso, Eduard K. Linsenmair

[1]University of Abobo-Adjamé, Abidjan, Cote D'Ivoire, [2]University of Würzburg, Würzburg, Germany

Introduction: African savannas are important and very extended ecosystems of great significance for biodiversity and as a human economic area. Termites represent a very important component of soil biodiversity in West African savannas, delivering essential ecosystem services (by e.g. improving soil water content, soil fertility and carbon sequestration). This study aims to analyse the diversity and functional roles of the termites along a climatic and anthropogenic gradient in West African savannas, with two case studies in Burkina Faso and Côte d'Ivoire.

Methods: Rapid assessment protocol of biodiversity, based on standardized transects, was use to record the termite diversity. Termite biogenic structure and soil physico chemical properties were analyses to access their influence on soil water and nutrient dynamics.

Results: Termites species richness and functional diversity broadly decrease with the increasing aridity (from moist savannas to dry savannas) and with the land use intensification. The fungus growing termite of the genus *Odontotermes* plays a key role, as ecosystem engineer, in the dry savannas as well as in the moist one; where they impact the vegetation structure and dynamic. This they achieve in first line by modifying soil physico chemical properties and soil water content.

Conclusions: In West African savannas, the diversity of termite change with the amount of rainfall and the land use type. Fungus growing termite are playing a key role in soil functioning and performs some essential ecosystems services like soil restoration (in arid savannas) and carbon dynamic (in moist savannas).

Diversity and role of termites in West African savannas: case studies in Burkina Faso and Côte d'Ivoire

Souleymane Konaté, Dorkas Kaiser, Kanvaly Dosso, Eduard K. Linsenmair

[1]University of Abobo-Adjamé, Abidjan, Cote D'Ivoire, [2]University of Würzburg, Würzburg, Germany

Introduction: African savannas are important and very extended ecosystems of great significance for biodiversity and as a human economic area. Termites represent a very important component of soil biodiversity in West African savannas, delivering essential ecosystem services (by e.g. improving soil water content, soil fertility and carbon sequestration). This study aims to analyse the diversity and functional roles of the termites along a climatic and anthropogenic gradient in West African savannas, with two case studies in Burkina Faso and Côte d'Ivoire.

Methods: Rapid assessment protocol of biodiversity, based on standardized transects, was use to record the termite diversity. Termite biogenic structure and soil physico chemical properties were analyses to access their influence on soil water and nutrient dynamics.

Results: Termites species richness and functional diversity broadly decrease with the increasing aridity (from moist savannas to dry savannas) and with the land use intensification. The fungus growing termite of the genus *Odontotermes* plays a key role, as ecosystem engineer, in the dry savannas as well as in the moist one; where they impact the vegetation structure and dynamic. This they achieve in first line by modifying soil physico chemical properties and soil water content.

Conclusions: In West African savannas, the diversity of termite change with the amount of rainfall and the land use type. Fungus growing termite are playing a key role in soil functioning and performs some essential ecosystems services like soil restoration (in arid savannas) and carbon dynamic (in moist savannas).

Effect of hurricanes Katrina and Rita on the ant fauna of South Louisiana, USA

Linda Hooper-Bui, Beverly Wiltz, Kaitlin Baudier, Rachel Strecker

Dept. Entomology, Louisiana State University, Baton Rouge, La, United States

In August of 2005, Hurricane Katrina inundated southeast Louisiana with storm surge and flood waters; three weeks later Hurricane Rita similarly inundated southwest and portions of southeast Louisiana. More than 80% of New Orleans and the surrounding area were flooded for a few days to several weeks. Initial surveys indicated that most ant populations, including those that are flood adapted, were decimated by the salty storm surge. Only islands of ant populations remained in high areas or in areas with trees where some ants dwell. In laboratory experiments, we demonstrated that flood adapted *Solenopsis invicta* are unable to maintain in salt water (3.5%) the characteristic floating raft that colonies typically form in water. In some flooded areas, all ant populations were eradicated for nearly a year. For three years we have monitored the repopulation of the affected area with ants. In most flooded areas, three invasive ants, *Solenopsis invicta*, *Cardiocondyla venustula*, and *Brachymyrmex patagonicus* are the only ants that reinvaded or remain, except for areas where tree-dwelling species survived because they were high in trees. Presently, these invasive ants are present in extremely high numbers, and in many cases have reached pestiferous levels for returning residents. It is possible that high populations of these invasive ants will suppress the natural succession of native ants in this newly disturbed ecosystem.

The weight of predatory mirids in whitefly control

Paolo Casula[1], Paolo Casula[2], Mauro Nannini[3]

[1]Division of Biology, Imperial College London, Ascot, Berkshire, United Kingdom, [2]Ente Foreste della Sardegna, Cagliari, Sardinia, Italy, [3]Agris Sardegna, Cagliari, Sardinia

Introduction: *Nesidiocoris tenuis* and *Macrolophus* spp. are important whitefly predators in Mediterranean crops. In Sardinia, these mirids are among the most abundant enemies present in summer pole tomato fields, where they may become extremely abundant during late summer. When mirids reach adequate numbers whiteflies are generally kept well below damaging densities. However, to what extent mirids affect whitefly population dynamics?

Methodology: to follow population trends in relation to insecticide applications we sampled mirid, whitefly, and other natural enemy populations in 10 and 9 tomato fields, for two consecutive years. Suction samples were collected monthly, from May to September. We also developed a set of models of whitefly-predator-insecticide interactions to understand predator-prey dynamics and determinants of whitefly resurgence. By means of model selection approaches based on information criteria we evaluated a set of hypotheses related to whitefly abundance variations, with particular focus on the role of predatory mirids in whitefly control.

Results: models specifying a direct link between predator abundance and whitefly control had strong support, showing the importance of mirids as effective whitefly biocontrol agents. Moreover, it was evidenced a relation among insecticide applications, decrease of mirid population and whitefly growth, which could explain whitefly resurgence and occasional outbreaks. Also, spiders appeared to be important in whitefly control, whereas parasitoids did not seem to play a relevant role in it.

Conclusion: The models developed and the model selection approaches appear to be valid tools for understanding complex predator-prey population dynamics, weighting the role of mirids in whitefly control.

Developing sanitary and phytosanitary (SPS) capacity in Africa

Marianna Theyse

Department of Agriculture, Pretoria, Gauteng, South Africa

African regulatory institutions are entrusted to facilitate safe agricultural trade with its international trade partners. The development and effective implementation of sanitary and phytosanitary measures, as non-tariff barriers to trade in important export markets and the local market have the potential to put agricultural imports and exports at risk.

The World Trade Organisation Agreement on the Application of Sanitary and Phytosanitary Measures (WTO SPS) concerns itself with the application of SPS measures. It is imperative for WTO members to develop and implement national systems and capacities to ensure effective implementation of the WTO SPS and its standard setting bodies i.e. International Plant Protection Convention (IPPC), International office of Epizootics (OIE) and Codex Alimentarius Commission.

The IPPC has developed a Phytosanitary Capacity Evaluation (PCE) Tool to assist a country to assess its specific capacity needs in relation to its implementation of the IPPC. The PCE tool is a significant component of the Strategic Direction No 4 (The development of the phytosanitary capacity of members by promoting the provision of technical assistance) and Article XX of the IPPC New Revised Text.

Culture-independent identification of gut bacteria in fourth-instar red imported fire ant, *Solenopsis invicta* Buren, larvae

Albert Lee, Linda Hooper-Bui, Claudia Husseneder

Department of Entomology, Louisiana State University, Baton Rouge, La, United States

Solenopsis invicta Buren, are omnivorous medical, urban, and agricultural pests from South America. Fourth-instar larvae are used by the colony to digest solid food and then regurgitate it for consumption by workers and queens. Larvae are an ideal source of investigations of endosymbiotic bacteria possibly involved in nutrient distributions. Obligate endosymbionts have been found in omnivorous carpenter ants, *Camponotus*, so we searched omnivorous fire ant guts for similar symbionts. Our study utilized 16S rDNA sequencing to describe the composition of the bacterial community in fourth-instar ant larvae in order to identify possible endosymbiotic bacteria present therein. The 16S rRNA gene was directly amplified from mixed-population DNA of whole fire ant larval guts and cloned into *Escherichia coli*. Bacterial communities from three geographically separated RIFA colonies were examined. Sequenced bacterial clones from guts were determined to be 66 species predominantly from the phylum *Proteobacteria* and the family *Enterobacteriaceae*. Our results did not detect the presence of endosymbiotic bacteria in the guts of RIFA larvae among the colonies. In addition, minimal species overlap was found when bacterial inventories were compared among colonies. Thus, bacteria coadapted with red imported fire ant larvae were not detected. Identified bacteria were not closely affiliated with endosymbiotic bacteria common in other insect species. Bacteria communities appeared to be unique to each geographical location and were determined by the foods consumed by the ants. It is possible that Camponotus are lacking nutrients that are provided by the obligate symbionts because they act as herbivores in their community because they often feed exclusively on honey dew from Homopterans; whereas fire ants are truly omnivorous in their dietary habits, which offers complete nutrition, and thus *S. invicta* has no need for obligate symbionts in the gut.

A real world examination of Sulfuryl Fluoride as a replacement for Methyl Bromide in midwestern US flour mills

Wan-Tien Tsai, Linda Mason, Klien Ileleji

Purdue University, West Lafayette, IN, United States

As a result of the Montreal Protocol, methyl bromide, a major fumigant for the food industry, is facing a mandatory 100% production and import phase out. Millers, food processors and fumigators are seeking replacements. Sulfuryl fluoride is one replacement strategy that was recently labeled for the food market. This paper summarizes research that is underway to compare the effectiveness of methyl bromide and sulfuryl fluoride under real world conditions. Since 2005, five methyl bromide and nine sulfuryl fluoride fumigations have been completed in four U.S. flour mills. All life stages (eggs, larvae, pupae, and adults) of two major pest species, Indianmeal moth, *Plodia interpunctella* (L) and red flour beetle, *Tribolium castaneum* (Herbst) were used in bioassays exposed during fumigations. Insect monitoring (moth flight traps and flour beetle dome traps) was conducted before and after the fumigations to determine the existing pests population and rebound rates. Bioassay results indicate 100% mortality of larval and adult stages of both species for both fumigants. More than 99% of RFB and 100% of IMM pupae died when exposed to either fumigant. Of the few exposed eggs that hatched, the majority died before the adult stage. Insect populations were usually significantly lower right after fumigation but could increase to pre-population level within 2-8 weeks depending on the facility, sanitation, and population pressure.

Impact of mattress rotation and vacuuming on allergen levels and dust mite populations

Giancarlo Lopez-Martinez, Glen Needham

The Ohio State University, Columbus, Ohio, USA

Introduction: House dust mites (HDM, *Dermatophagoides sp*) are considered to be the most important allergen producer indoors, thus making them the primary target of prevention and remediation efforts for asthmatics and allergic rhinitis sufferers. Novel methods for making the indoor environment safer without use of acaricides are desirable. Mattresses are a key allergen exposure sites. This study examined the impact of mattress rotation and flipping on dust mite populations and allergen production with the rationale being that these acarines require intermittent high relative humidity to thrive. Moving the allergens away from the sensitive individual has added benefits.

Methods: Mini-mattresses were inoculated with mating pairs of American HDM, *D. farinae*. Food was added and the relative humidity and temperature modulated to simulate human occupation. At various intervals mites and allergen were sampled before and after rotation and flipping of the mattresses. In addition mattresses were sampled to determine where mites matriculated over time. Vacuuming was evaluated as an effective means of allergen removal.

Results: Rotation/flipping reduced mite numbers and allergen levels by approximately 50%. After 25 wks most mites were in the polyester layer just beneath the mattress ticking. A HEPA vacuum removed 75% of the dust mites and allergen levels were reduced signficantly.

Conclusions: A combination of mattress vacuuming and rotation/flipping may have a major impact on dust mite and allergen levels, thus reducing exposure to allergens.

Within farm use of GIS technology for spatial management of blueberry insects: the case for blueberry maggot

Dean Polk, Cesar Rodriguez-Saona, Peter Oudemans, Marilyn Hughes

Rutgers University, New Brunswick, NJ, United States

Blueberry maggot (*Rhagoletis mendax*) has a “0” tolerance in fresh market blueberries. While easy to control with labeled insecticides, seasonal treatment for this insect represents the single greatest effort needed for insect control in terms of the number of applications, total amount of active ingredient (a.i.), costs of labor and equipment use, and effort made in observing pre-harvest and re-entry spray intervals. Fruit destined for export is required to undergo a strict spray program, either by a calendar method, or as dictated by trapping. Management practices have led to overuse of insecticides, time and resources, and do not fit well with resistance management practices, especially since some of the most effective insecticides continue to be the older organophosphates and carbamates, and reduced risk materials such as imidacloprid have limits on total use. Key blueberry pests often reside on alternate hosts in bordering woods prior to dispersal into cultivated fields. Objectives of this project are: Identify locations and high-risk areas of BBM activity on a whole farm basis; Demonstrate that these areas can be spatially recognized and individually managed; and Reduce Costs and Insecticide Use. Five growers participated with 737ha, using 1 trap for every 1.1ha. The majority of traps had a “0” capture, and most positive traps were near field edges. Spatial management led to fewer insecticide applications and less active ingredient applied per ha. Spatially managed farms had a total insecticide use ranging from about 70 to 30% of that on grower standard farms.

Progress towards engineering resistance to weevil in sweetpotato in East Africa using Bt gene technology

William Moar[1], Robert Mwanga[2], Benson Odongo[2], Moses Ekobu[3], Maureen Solera[3], Samuel Kyamanywa[3], Marc Ghislain[4]

[1]Auburn University, Auburn, AL, United States, [2]National Crop Resources Research Institute, Namulonge, Uganda, [3]Makerere University, Kampala, Uganda, [4]International Potato Center, Lima, Peru

Introduction: Sweetpotato is grown in Sub-Saharan Africa (SSA) as a staple food for the urban and rural poor. Major producing countries include Uganda, Nigeria, Rwanda, Burundi, Kenya, and Tanzania. Sweetpotato weevils (*Cylas* spp.) constitute the most important threat to crop productivity and sustainability with losses reaching 60% to 100%. Conventional integrated pest management practices are difficult to apply to production throughout the year by small-scale subsistence farmers. Instead, host plant resistance by expression of multiple *Bacillus thuringiensis* (Bt) proteins represents a new strategy for achieving sustainable control of weevils under African conditions.

Results: First, we developed a diet incorporation methodology to test Bt toxicity against weevil larvae. Of the eight Cry toxins test against *C. puncticollis* and *C. brunneus* using this artificial diet, three Cry toxins had LC_{50}'s below 1 ppm; Cry7Aa1, Cry3Ca1, and ET33/34. Therefore, Cry7Aa1, Cry3Ca1, and ET33/34 gene constructs were developed considering reduced cross resistance concerns, sweetpotato codon usage, avoidance of contractual restrictions and property rights, storage root expression and wound-inducible promoters, and combinations of two selection marker genes and Bt genes. A total of 10 Bt gene constructs have been developed and are now available for direct gene transfer into relevant African sweetpotato varieties. Regeneration and genetic transformation protocols were applied to two African cultivars, Tanzania and Wagabolige, and two non-African cultivars, Jewel and Huachano, Transformation and possible toxicity results of transformed plants will be discussed.

Mass spectral analysis of expressed versus predicted peptides (AKHs, PRLamides, FLRF-amides, NVP-like peptide) in the corpus cardiacum of beetles and moths: evolutionary relationships and functional significance

Robert Weaver[1], Heather Marco[2], Neil Audsley[1], Gerd Gaede[2]

[1]Environmental Biology Group, Central Science Laboratory, York, United Kingdom, [2]Zoology Department, University of Cape Town, Rondebosch, South Africa

Introduction: Mass spectrometry, together with genomic and cDNA sequence information, allows predictions to be made in relation to expressed peptides of the corpora cardiaca (CC).

Methods: Pairs of CC or extracts are analysed using MALDI-TOF or ESI mass spectrometry.

Results: Two AKHs (Trica-AKH, Pyrap-AKH) predicted from the genome of the red flour beetle, *Tribolium castaneum*, are confirmed, but an AKH-like peptide was not found. In contrast, *Tribolium brevicornis* and *Tenebrio molitor* contain only one AKH, which differs from the AKHs of *T. castaneum,* and is the same in both species. Other peptides from the CC of *T. brevicornis* (e.g. pyrokinins) also match the complement in *T. molitor*, but differ from those in *T. castaneum*.

Two peptides are always present in the lepidopterans; these are FLRF-amide-I and Arg^7-corazonin. The silk moth, *Bombyx mori* expresses Bommo-AKH (pELTFTPGWGQ-amide) as a newly identified second peptide to Manse-AKH. In comparison, the fall armyworm, *Spodoptera frugiperda* contains two cDNA-predicted AKHs , but a third predicted AKH (pELTFSSGW-amide) and an AKH-L were not present. Two other noctuid species contain a Gly-extended amidated peptide (pELTFTSSWGG-amide) as a potential third AKH. In the lepidopterans, there are similarities and differences between the peptides derived from the PBAN/diapause hormone precursor, including a new analog of Helze-PGN-8 / Bommo-γ-SNP, (Lacol-PK; NMNFSPRL-amide), which is found in the tomato moth, *Lacanobia oleracea.*

Conclusions: The tenebrionid *T. brevicornis* appears more closely related to *T. molitor* than to *T. castaneum*. Similarly, peptidomics of the lepidopteran CC may provide insight into functionality and relatedness within the noctuidae.

Criteria for determining field-evolved resistance in Bt cotton

William Moar

Auburn University, Auburn, AL, United States

Although monitoring for field-evolved resistance by target pests in Bt crops is widely accepted and practiced, the actual procedures involved with monitoring and interpreting results are not standardized in all cases, and reports arising from non-official monitoring have also been used to interpret field-evolved resistance. This presentation will discuss the US monitoring program for Bt cotton and bollworm (*Helicoverpa zea*) addressing specific topics such as deciding on: 1) the appropriate definition(s) of Bt resistance to use for determining field-evolved resistance, 2) the appropriate plants to collect *H. zea* from for use in laboratory bioassays; 3) whether to use discriminating concentrations vs. LC_{50}'s for determining susceptibility; 4) whether to include failure to molt to second instar in the definition of mortality; 5) the appropriate laboratory colony to be used for comparing susceptibilities of field populations and 6) the appropriate form of Bt protein to use for bioassays. Regardless of the conclusions, agreement of a standardized protocol for monitoring for field-evolved resistance should reduce the likelihood for confusion and controversy when reports of putative resistance to Bt crops by target pests occur.

How does alpine moth, *Syngrapha ottolenguii* adapt their life cycle and flight activity rhythm to severe Alpine environment?

Masami Sasaki, Satoshi Yamamura

Tamagawa University, Machida, Tokyo, Japan

Introduction: *Syngrapha ottolenguii* (Noctuidae: Plusiinae) is a typical Japanese alpine moth with adults appearing from mid to late summer. How does the noctuid moth adapt their life cycle and flight activity rhythm to severe Alpine environment?

Method: Both field surveys at Mt. Zao etc. (1800-2600 m asl) and laboratory studies using actographs were done from 2003-2007.

Results and Discussion: The moth was found to have a univoltine life cycle in 1 year, although one generation can be completed as short as 60 days at 16L-8D and 20℃.

We found two strategies—short-day-induced prolongation of 2nd and 3rd instar larval stages for winter, and long-day-induced arrestment of reproductive maturation in adults for summer to enable the life cycle without obligatory diapause. As a result, oviposition is delayed into autumn, and the late-hatched, cold-tolerant larvae overwinter under deep snow. Larvae before and after overwintering develop very slowly due to their unique behavior of hiding from the sun's radiant heat.

It has been known that the adults take flight and visit alpine flowers during day time even in nocturnal moth. We found the evidence from actograph studies that they (especially in mated female) weakened or lost their circadian activity rhythm to get ready to visit flowers at any favorable time under cold, severe alpine weather.

Stochastic spread of *Wolbachia*: drifting through the threshold

H. Charles J. Godfray[1], Vincent A.A Jansen[2], Michael Turelli[3]

[1]University of Oxford, Dept. of Zoology, Oxford, United Kingdom, [2]University of London, Royal Holloway, School of Biological Sciences, Surrey, United Kingdom, [3]University of California, Section of Evolution and Ecology, California, United States

Most *Wolbachia* that cause cytoplasmic incompatibility (CI) only spread when their frequency is higher than a threshold determined by their detailed biology. In finite populations, *Wolbachia* at frequencies lower than this threshold may become fixed through random events, and similarly infections above the threshold may become extinct by chance. We describe the probability of spread as a function of current frequency, population size, and *Wolbachia* biology. The probability of fixation of a near neutral *Wolbachia* with CI scales with the reciprocal of the root of population size (N) which is much higher than a neutral allele where fixation scales with 1/N. We discuss the implication of these results for *Wolbachia* spread in natural populations, and its use in pest and vector management.

Moth migration patterns over the past 40 years: how are they changing and how is climate influencing this change?

Duncan Sivell, Jason Chapman, Ian Woiwod

Rothamsted Research, Harpenden, United Kingdom

A number of moth species employ migration strategies to track the shifting availability of resources across seasons and continents. The UK receives immigrants from continental Europe and Africa each year, but the degree of influx can vary greatly and for some species in certain years may lead to pest outbreaks. To try to explain this variation and understand these migration patterns we examine a long-term dataset provided by the Rothamsted Light Trap Network, a moth monitoring scheme which has been running in the UK for more than four decades. These data hold spatial as well as temporal information on moth abundance and enable us to compare species with different migration strategies and investigate the relationship between migration events and climate. Migration events are obviously mediated by environmental conditions at their source and along their route, but as our moth data is limited to the UK we are lacking information on migrant species when they are abroad. However, historic climate data are available for the probable source areas of migation and these are assessed to speculate on how migrants fare in the other parts of their migratory range.

Mechanisms of host defense and the geography of galling insects

G Wilson Fernandes, Marco A.A Carneiro

Universidade Federal de Minas Gerais, Ecologia Evolutiva & Biodiversidade/DBG, Belo Horizonte, Brazil

Galling species richness increases with decreasing elevation, is higher under more stressful habitats, reaches a peak in habitats or regions dominated by sclerophyllous vegetation, and natural enemies and plant resistance play a major role in their geography. A tight physiological interaction between the galling organism and the host plant is crucial to the success of the galling habit in more nutrient-stressed, harsh, and sclerophyllous environments. Furthermore, the gall inducing organism success is also shaped by the interaction with the community of natural enemies via habitat. We argue that under higher temperatures and water and nutrient deficiency in harsher habitats, such as those found in the latitudes between 25 and 40 degrees and at the canopy of tropical rain forests, induced defenses are weaker, thus favoring the galling habit. Although plants living in dry and warm habitats may respond more slowly to gall initiation, their induced defenses, such as hypersensitivity, may not be efficient and/or quick enough to impair cell and tissue taken over by the inducing larva, therefore increasing the probability of gall development. Weak selective pressure caused by predators, parasites, pathogens, and plant resistance on galling insects in habitats where sclerophyllous plants are abundant, reinforces the pattern of high richness of galling insect species in this vegetation type. We postule that the geography of galling species and their biodiversity may be driven plant nutritional quality and ability to resist to galling, by leaf sclerophylly and consequent effects on meristem dynamics and natural enemies, all mediated by habitat intrinsic quality.

Mechanisms of host defense and the geography of galling insects

G Wilson Fernandes, Marco A.A Carneiro

Universidade Federal de Minas Gerais, Ecologia Evolutiva & Biodiversidade/DBG, Belo Horizonte, Brazil

Galling species richness increases with decreasing elevation, is higher under more stressful habitats, reaches a peak in habitats or regions dominated by sclerophyllous vegetation, and natural enemies and plant resistance play a major role in their geography. A tight physiological interaction between the galling organism and the host plant is crucial to the success of the galling habit in more nutrient-stressed, harsh, and sclerophyllous environments. Furthermore, the gall inducing organism success is also shaped by the interaction with the community of natural enemies via habitat. We argue that under higher temperatures and water and nutrient deficiency in harsher habitats, such as those found in the latitudes between 25 and 40 degrees and at the canopy of tropical rain forests, induced defenses are weaker, thus favoring the galling habit. Although plants living in dry and warm habitats may respond more slowly to gall initiation, their induced defenses, such as hypersensitivity, may not be efficient and/or quick enough to impair cell and tissue taken over by the inducing larva, therefore increasing the probability of gall development. Weak selective pressure caused by predators, parasites, pathogens, and plant resistance on galling insects in habitats where sclerophyllous plants are abundant, reinforces the pattern of high richness of galling insect species in this vegetation type. We postule that the geography of galling species and their biodiversity may be driven plant nutritional quality and ability to resist to galling, by leaf sclerophylly and consequent effects on meristem dynamics and natural enemies, all mediated by habitat intrinsic quality.

Ants on your plants: a meta-analysis of the role of ants as plant biotic defenses

Tatiana Cornelissen, Newton Barbosa, Livia Diniz, Frederico Neves, Yumi Oki, Flavia Pezzini, Felix Rosumek, Fernando Silveira, G W Fernandes

Universidade Federal de Minas Gerais, Ecologia Evolutiva & Biodiversidade, Belo Horizonte, Brazil

We reviewed the evidence for the effects of ants as plant biotic defenses, by conducting separate meta-analyses for the effects of experimental removal of ants on plant herbivory and fitness with data from 86 studies that generated 294 independent comparisons. Effects reviewed were mainly plant herbivory, herbivore abundance, homoptera abundance, predator abundance, plant biomass and reproduction in studies where ants were experimentally removed (90.5%) and studied where there was natural variation in ant presence among individual plants (9.5%). Ant removal exhibited strong effects on herbivory rates, as plants without ants suffered twice more damage than plants with ants and exhibited 70% more herbivores. Ants also influenced several parameters of plant fitness, as plant without ants suffered a reduction in biomass of (-19.8%), leaf production (-48.9%) and reproduction (-20.5%). Effects were much stronger for tropical regions compared to temperate ones as tropical plants suffered almost three-fold higher herbivore damage than plants from temperate regions (Q_B=37.08, P<0.0001) and exhibited almost five times more herbivores (Q_B=12.9, P=0.0003). In relationship to plant reproduction, reduction in the production of flowers, fruits and seeds were much more pronounced in tropical compared to temperate regions. In tropical regions, ant removal resulted in a reduction of plant fitness of about 59% (E++=-0.593, CI=-0.69 to –0.50), whereas in temperate regions this reduction was not statistically significant (E++=-0.012, CI= -0.08 to 0.05) (Q_B=108.8, P<0.0001). Altogether, these results suggest that ants do act as plant biotic defenses, but the effect of their presence is more pronounced in tropical systems.

Hormonal regulation of sequential insect oocyte development

Johannes Leuchtweis, Hans J. Ferenz

Martin-Luther-University, Halle, Germany

Insects sequentially mature a hierarchy of eggs with the terminal oocyte massively storing yolk reserves and the subsequent subterminal oocytes remaining much less developed. In our model insect *Locusta migratoria* terminal oocytes of all ovarioles grow synchronously while development of the subterminal oocytes is arrested at an early previtellogenic stage and induced only after the current terminal oocyte has completed its development. Although it is likely that the terminal oocyte directly or indirectly controls the developmental arrest of the subterminal oocytes proof for such control is lacking. In our locust model system we are examining cellular and molecular events sequentially up- or down-regulated by endocrines in subterminal oocytes and their follicle cells. Previtellogenic oocytes appear to be prepared and equipped for endocytosis of yolk material. However, the vitellogenic arrest is predominantly caused by the lack of patency in the follicle cell sheath. Thus the follicle cells of subterminal oocytes are the target of so far unidentified stimulating or inhibiting endocrine factors. We are studying such regulatory factors possibly induced by ovulation (neural and neurohormonal signals) or originating from follicle cells of terminal oocytes.

This presentation gives an overview on known mechanisms, discusses results of the locust system and outlines research perspectives.

The state and status of studies of insect learning

Brian H Smith

Arizona State University, Tempe, AZ, United States

With the pioneering work of Karl von Frisch over 100 years ago, insects broke through the traditional boundary between vertebrates and invertebrates in studies of learning. Until then, it was thought that learning, in particular, as well as sophisticated sensory processing, was limited to the realm of large brains. Since then a variety of insects, especially fruit flies, have been used in basic research on the neural and molecular bases of learning and sensory processing. The studies have proliferated because of the relatively smaller size and accessibility of insect nervous systems. Furthermore, in the last decade there has been increasing availability of genomic information as well as the ability to manipulate gene expression to test hypotheses about the relationships among between genetic pathways, neural networks and learning. These studies have been invaluable for what they have revealed of fundamental molecular, neural and behavioral mechanisms that underlie these processes in many animal species. There have also been many studies of learning in insects under more natural conditions. Recently these types of studies have begun to apply an understanding of learning to more applied problems in agriculture, medical entomology and bioterrorism. Because of the breadth and importance of all of these studies for basic and applied problems, insects are central to research on learning and memory. Therefore, entomologists who study learning now have an opportunity integrate these areas and make significant interdisciplinary contributions to many different fields of research.

Australian gall-inducing Eulophidae as globally invasive pests

John La Salle

CSIRO Entomology, Canberra, ACT, Australia

Within Australia, a phytophagous radiation from within the mainly parasitoid family Eulophidae is the dominant group of gall inducing organisms on Eucalyptus trees. A number of these gall inducers have achieved invasive pest status on Eucalyptus trees in many regions of the world. The biology, taxonomy, and pest status of these wasps is summarized. Classical biological control options are summarized, with particular reference to currently ongoing programs.

The Atlas of Living Australia

John La Salle, Donald Hobern

CSIRO Entomology, Canberra, ACT, Australia

The *Atlas of Living Australia* is an ambitious initiative to create a single seamless web interface providing access to integrated biodiversity information for the entire Australian biota. Progress on this project will be reported, along with the planned next steps. Path to impact will be discussed, and how the *Atlas* intends to deliver data in such a manner that it can underpin national initiatives towards sustainable bio-management, improved biosecurity, and increased use of Australian biodiversity for biodiscovery

Modelling temperatures and insect succession on cadavers inside a vehicle environment

Ian Dadour, Sasha Voss, Neville Fowkes

University of Western Australia, Western Australia, Australia

Introduction: (1)Differences in rate of decomposition and insect succession between exposed carcasses on the soil surface and those enclosed within a vehicle following carbon monoxide (CO) poisoning was examined. (2)Temperatures inside vehicles were also modelled.

Methods: (1)Nine 45kg pigs were used as models for human decomposition. Animals were sacrificed by CO gas, half were placed within the driver's side of separate enclosed vehicles and half were placed under scavenger proof cages on the soil surface. (2) Vehicles were placed in open areas in a east/west orientation. Temperatures were measured for 10 days inside the vehicle, inside the trunk and the metal skin surface temperature. These parameters were compared with prevailing climatic conditions.

Results: Progression through the physical stages of decomposition was 3-4 days faster in the enclosed vehicle due to higher temperatures inside the vehicle compared to external ambient temperatures. Patterns of insect succession also differed between vehicle and surface treatments. The pattern of insect succession and rate of decomposition was similar between surface carcasses within trials regardless of the mode of death

Conclusion: This study provides baseline data outlining the decomposition patterns of a carcass enclosed within a vehicle following carbon monoxide poisoning in Western Australia. Understanding how variation in decomposition situations impact on the rate of decomposition and patterns of insect succession is essential to obtaining an accurate estimate of post-mortem interval (PMI). How temperatures change inside a vehicle over time has ramifications for not only cadaver decomposition but also the deaths of children and pets, a consequence of negligence by vehicle operators.

Temperature and humidity facilitates competition between native ants and *Pheidole megacephala* (Hymenoptera:Formicidae) on Fraser Island, Australia.

Wayne Robinson

University of the Sunshine Coast, Queenlsand, Australia

Pheidole megacephala is one of the worlds worst invasive ants and can be common in urban areas in coastal Australia and occasionally in native bushland. Anecdotally, there appears to be a few native species that are consistently able to coexist with *P. megacephala*, and this research investigates the mechanisms of their success. I performed a small scale field experiment on Fraser Island, Queensland, Australia where shade cloth was used to adjust the temperature and humidity on a series of baits that were monitored through a 72 hour period. The experiment was fully crossed between areas with low and high native vegetation cover and areas where *P. megacephala* invasions were long established or at the invasion front. *Iridomyrmex bicknelli* and *Monomorium sydneyensis* were able to exist in *P. megacephala* infestations by partitioning foraging to suitable temperature and humidity conditions. *P. megacephala* were dominant however and displace the native ants when environmental conditions suit their foraging. Without shade *P. megacephala* could not forage above 40oC (Ground temperature) or below 20 % humidity. Vegetation that offers more shade and moister conditions can be readily invaded by *P. megacephala*. However *P. megacephala* will forage at cooler times of the day when invading hotter drier areas and hence can still invade or at least cross drier habitats readily. I also present details of a large scale experiment currently in progress that manipulates environmental factors and native ant communities to further investigate the role of biotic resistance in *P. megacephala* invasions.

Insulin signaling and growth control in *Drosophila*

Ernst Hafen, Hugo Stocker

ETH Zurich, Zurich, Switzeralnd

The control of cell and organ size is important for the developing organism. The discovery of the Drosophila homolog of the vertebrate IRS1–4 (CHICO) has shown that manipulating the Drosophila insulin signaling pathway leads to alterations in cell size, proliferation, and cellular metabolism. Systematic genetic screens relying on a tissue-specific recombination system or over-expression led to the identification of new genes whose products are dedicated to the control of cell and organ growth. Some of them constitute components of the insulin signaling pathway (PKB, PDK1, PTEN) and the dTOR pathway. These two pathways are not only important for the regulation of growth during normal development, they are also the target of environmental influences such as nutrients, oxidative stress, and hypoxia all of which regulate growth. Several of the genes whose products connect environmental stress to the regulation of the insulin and TOR pathways are dispensable under normal culture conditions and mutations were only detected in the overexpression screen. I will provide an overview of our recent results from these genetic screens and describe we combine genetic and proteomic analyses towards an understanding of growth control at the systems biology level.

Experiences of a South African company

Mike Morris[1], Mark Laing[2]

[1]Plant Health Products (Pty) Ltd, Nottingham Road Village, South Africa, [2]University of KwaZulu-Natal, Pietermaritzburg, South Africa

Plant Health Products (Pty) Ltd was started 9 years ago, initially to commercialize some research coming out of the University of KwaZulu-Natal, but it has now grown beyond that. During this time some harsh realities have been experienced. The background of key personnel (research versus business or marketing) influenced decision-making and direction during the early years. The early need for a high level of research inputs and capital puts a huge budgetary strain on a small, start-up company. But outside loans or investments need to be very cautiously approached due to the, often slow, returns to investors. The registration process and delays of several years for each new product in each and every country where markets are opened up is a huge constraint that has to be overcome. Other factors that will be discussed include the importance of market research, production scale up constraints, the damage in the marketplace caused by poorly researched, unregistered products and the importance of product quality and formulation development.

The Bt cowpea project – the long road to field trials

Larry L. Murdock

Purdue University, W. Lafayette, IN, United States

The recipe for creating a public-sector project to develop a genetically-modified crop for Africa requires that the cooks start with a mild case of insanity and have skin so thick that the slings and arrows of skeptics, which are legion, bounce off of it. The Bt cowpea project started this way at Purdue University, in 1987. It involved would-be cooks who should have known better, and should have foreseen that it would take enormous energy and time, more than twenty years, plus plenty of money. Much was learned in the still-ongoing project, thanks to errors of commission and omission, but the ultimate lesson is that a band of individuals with dogged determination and patience can achieve things that only well-funded biotechnology companies otherwise could ever achieve. Some of those lessons are: (1) A biotechnology project should focus on a problem that can not be solved any other way; (2) Private sector help must be accessed, for that is where indispensible experience – and intellectual property – reside; (3) A public-sector project depends on volunteers; (4) There is enormous power in people to do big and unselfish things – if you can find ways to unshackle that power; (5) Institutions each have their own personalities, vanities and agendas, but if you grin and bear it they can be indispensible allies; (6) Even short of success and along the way, the rewards are great and there is joy in it all.

Parasitic wasps: succession, development and forensic importance as PMI indicators.

Sasha Voss[1], Helen Spafford[2], Ian Dadour[1]

[1]Centre for Forensic Science, University of Western Australia, Perth, Australia, [2]School of Animal Biology, University of Western Australia, Perth, Australia

Introduction: The presence of parasitic wasp larvae within insect hosts such as fly pupae can be used to provide and extended estimate of time since death. Use of parasitic wasps as tools in criminal investigations requires; baseline data on the temperature-dependant development of both the host and parasitoid species; knowledge of the development stage at which the female wasp parasitizes the host; and an understanding of the factors involved in host location within a decomposition habitat. Currently, there is a paucity of relevant reference data and the research that is available is either geographically specific or is focused on parasitoid species used as biological control agents of filth flies rather than in a forensic context.

Methods: In this study, the species and biology of parasitic wasps associated with decomposing remains in Western Australia and their relevant host species were investigated. A monthly survey of relevant insect fauna frequenting decomposing remains was conducted. Domestic guinea pig carcasses (*Cavea porcellus*) were used as an attractant.

Results: The stage of decomposition at which the observed parasitoid species attended carcasses, species seasonality and rates of parasitization in the field were identified. Base-line reference data on the temperature-dependant development of two important parasitoid species were also established under laboratory conditions.

Conclusions: The biological and developmental data presented will improve the accuracy of PMI estimations in cases where decomposition has advanced beyond the life cycle of flies, the traditional indicators of time since death.

Insect-Wolbachia-WO phage tripartite symbiotic interaction: exploring the role of phage

Panagiotis Sapountzis[1], Haralabia Boleti[2], Seth Bordenstein[3], Kostas Bourtzis[1]

[1]Department of Environmental and Natural Resources Management, University of Ioannina, Agrinio, Greece, [2]Molecular Parasitoloty Unit & Light Microscopy Unit, Hellenic Pasteur Institute, Athens, Greece, [3]Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, The Marine Biological Laboratory, Woods Hole, United States

Wolbachia is a group of obligatory intracellular and maternally transmitted a-Proteobacteria that infect a number of invertebrate species, including mites, spiders, crustaceans, filarial nematodes, and especially insects. This bacterial group has been extremely successful in establishing symbiotic associations ranging from reproductive parasitism to mutualistic symbiosis. Several *Wolbachia* strains carry prophage elements in their genome. Bacteriophages are responsible for the transfer of new functions to a bacterial cell and are recognized as important agents in bacterial evolution. The molecular mechanisms that mediate host-*Wolbachia*-phage symbiotic interactions are currently unknown.

In the present study, we cloned part of the orf7 gene encoding the minor capsid protein of WO-B bacteriophage located in the genome of the *wMe*l strain of *Wolbachia*. The cloned region of the orf7 gene, which is conserved among different Wolbachia strains of the A and B supergroup, was expressed in *E. coli* as recombinant protein and used to produce rabbit polyclonal anti-sera. Expression of the WO-B bacteriophage capsid protein was confirmed in different insect-*Wolbachia* symbiotic associations by Western Blot and in *Wolbachia*-infected *Drosophila* testes and ovaries by immunofluorescence confocal microscopy. Interestingly, sex specific differences were observed.

Malaria vector control : will insecticide resistance be our downfall?

Maureen Coetzee

[1]NRF Chair in Medical Entomology & Vector Control, Schoo of Pathology, University of the Witwatersrand, Johannesburg, South Africa, [2]Vector Control Reference Unit, National Institute for Communicable Diseases, NHLS, Johannesburg, South Africa

Introduction: Since 1911 when Giemsa first discovered that pyrethrum killed flies, the use of chemicals has been the mainstay of both agricultural and public health control of insect pests. Early research in South Africa, published in 1936, demonstrated that: 1) malaria vector mosquitoes like to rest inside human habitations while waiting for their eggs to develop, and 2) weekly administration of pyrethrum space spraying markedly impacted on the mosquito populations, dramatically reducing malaria transmission. This information led directly to the WHO Eradication Campaign of the 1950's when DDT's residual properties made house spraying a feasible option.

The appearance of insecticide resistance: The discovery of DDT and dieldrin, with their highly insecticidal, long-lasting effects, lead to the enthusiastic adoption of wide-scale application of these insecticides to fight every pest that plagued the human population. As a result, it was not long before insecticide resistance appeared, first in fly populations in Italy and Sardinia in 1947 and in African malaria vector mosquitoes in 1956.

The situation today: All three major malaria vector species in Africa now exhibit insecticide resistance over some parts of their distribution. The extent and spread of the resistance, however, is by no means uniform. With the current global efforts directed at malaria vector control, it is imperative that baseline entomological surveys be carried out prior to implementation of control interventions, followed by regular monitoring so that control strategies can changed to protect the use of insecticides for the future. If the resistance is not managed properly through integrated control measures, then indeed, we may well see the current efforts fail with fatal consequences.

The Brazilian experience in the resistance monitoring and control of *Aedes aegypti*

Denise Valle[1], José Lima[1], Isabela Montella[2], Priscila Viana-Medeiros[1], Thiago Belinato[1], Nathalia Giglio[1], Ima Braga[3]

[1]Fundacao Oswaldo Cruz, Rio de Janeiro, Brazil, [2]Instituto de Biologia do Exército, Rio de Janeiro, Brazil, [3]Secretaria de Vigilância em Saúde, Ministério da Saúde, Brasília, Brazil

Introduction: In Brazil, dengue is a major public health concern. Brazilian Dengue Control Program coordinates the *Aedes aegypti* Insecticide Resistance Monitoring Network (MoReNAa). This network is also implicated in defining sentinel municipalities, testing alternative insecticides and recommending novel control strategies.

Methods: Epidemiological parameters, including the dengue historical series of cases in each one of the 5,564 Brazilian municipalities, were used to define localities to be continuously monitored. Resistance monitoring includes larvae and adults bioassays and biochemical tests to unravel resistance mechanisms. Alternative insecticides, mainly Insect Growth Regulators (IGR), are tested in laboratory, simulated field and field conditions. Their potential to induce cross resistance in Brazilian mosquito populations is also evaluated.

Results: One-hundred strategic and sentinel municipalities were chosen to be continuously followed. Novel population classification criteria, based on the Brazilian resistance monitoring experience, were defined. These criteria are at the basis of MoReNAa control strategies recommendations to the Brazilian Dengue Control Program. Biochemical assays point to a strong metabolic resistance component in Brazilian *Aedes* populations. The IGRs tested in laboratory conditions were effective against field mosquito populations resistant to chemical insecticides. Potential relation between IGR tolerance and organophosphate resistance is not general. Persistence in the field of some IGRs, mainly chitin synthesis inhibitors, is consistent with the Brazilian dengue control routine.

Conclusions: In Brazil, dengue is a complex problem that transcends health questions. Although we are far from eliminating dengue from the country, the Brazilian experience is a strong example of integrated work between research and public health services.

Assessing the impact of Bt maize pollen on adult green lacewings

Yunhe Li, Michael Meissle, Jörg Romeis

Agroscope Reckenholz-Tänikon Research Station ART, Zurich, Switzerland

Although the application of *Bt* plants can largely reduce the need for conventional insecticides and benefit the environment and human health, concerns about potential effects of *Bt* crops on non-target organisms have been raised due to the high and consistent expression of *Bt* toxin in most plant parts throughout the whole growth period.

Adults of the green lacewing *Chrysoperla carnea* (Stephens) (Neuroptera: Chrysopidae) are prevalent pollen-consumers in maize field. They are therefore exposed to insecticidal proteins expressed in the pollen from certain *Bt* maize events. Laboratory experiments were conducted to evaluate the impact of transgenic *Bt* maize pollen on adult *C. carnea*.

Adult *C. carnea* were fed with pollen from transgenic maize events Event 176 or Mon 88017 (expressing Cry1Ab or Cry3Bb1, respectively) or from their corresponding non-transformed maize varieties together with sucrose solution. Over a period of four weeks, different life-table parameters (fecundity, fertility, survival) were recorded. The results revealed no negative effects on adult *C. carnea*. To confirm that adult lacewings are not sensitive to Cry1Ab or Cry3Bb1, additional studies were conducted where the insects were fed with an elevated dose of the two purified Cry proteins incorporated into artificial diet. The toxin dose was approximately 10 times higher that in the transgenic pollen. Again no effects on the recorded life-table parameters were detected.

This study shows that adult *C. carnea* are not sensitive to Cry1Ab and Cry3Bb1 and that the consumption of *Bt* maize pollen does not pose a risk to this important non-target species.

Modelling the bait control of tsetse flies (*Glossina* spp) in heterogeneous areas of operation

G.A Vale[1], S.J Torr[2]

[1]Southern African Centre for Epidemiological Modelling and Analysis, University of Stellenbosch, Stellenbosch, South Africa, [2]Natural Resources Institute, University of Greenwich, Greenwich, United Kingdom

A deterministic model simulated the bait control of tsetse in operational areas 32km wide, with good and poor habitat, adjacent to an invasion source of good habitat. In good habitat there were 2500 males and 5000 females/km^2. The population expired due to mating-finding difficulties when the male density was <0.1/km^2, associated with female densities of about 1/km^2. Daily displacement averaged 249m for males and 367m for females. Baits were placed in all or parts of the operational. With good habitat near the invasion front, evenly spaced baits killing 2.5% of the population per day reduced the female density to <1/km^2 at 22km from the front after 18 months; compared to 3km after 2 months with a 40% kill. Gaps of 2-3km between bait placements were inconsequential provided the average kill rate was maintained. Gaps 7km wide delayed effective control within the whole operational area by 11 years. Campaign costs were only 30% greater using the 40% kill, as against the 2.5% -- costs offset by the speedier and more extensive opportunities for tsetse-free farming. The annual cost of progressive control can be double that of the static, but involves the prospect of widespread clearance to natural barriers against invasion. The need for vigilance in maintaining invasion barriers is stressed.

Modelling the bait control of tsetse flies (*Glossina* spp) in heterogeneous areas of operation

G.A Vale[1], S.J Torr[2]

[1]Southern African Centre for Epidemiological Modelling and Analysis, University of Stellenbosch, Stellenbosch, South Africa, [2]Natural Resources Institute, University of Greenwich, Greenwich, United Kingdom

A deterministic model simulated the bait control of tsetse in operational areas 32km wide, with good and poor habitat, adjacent to an invasion source of good habitat. In good habitat there were 2500 males and 5000 females/km^2. The population expired due to mating-finding difficulties when the male density was <0.1/km^2, associated with female densities of about 1/km^2. Daily displacement averaged 249m for males and 367m for females. Baits were placed in all or parts of the operational. With good habitat near the invasion front, evenly spaced baits killing 2.5% of the population per day reduced the female density to <1/km^2 at 22km from the front after 18 months; compared to 3km after 2 months with a 40% kill. Gaps of 2-3km between bait placements were inconsequential provided the average kill rate was maintained. Gaps 7km wide delayed effective control within the whole operational area by 11 years. Campaign costs were only 30% greater using the 40% kill, as against the 2.5% -- costs offset by the speedier and more extensive opportunities for tsetse-free farming. The annual cost of progressive control can be double that of the static, but involves the prospect of widespread clearance to natural barriers against invasion. The need for vigilance in maintaining invasion barriers is stressed.

Interventions for control of beetle pests of staple food crops in Pacific island countries

Sada N Lal

Secretariat of the Pacific Community, Land Resources Division, Suva, Fiji

The beetle pests, rhinoceros beetle (*Oryctes rhinoceros*) and taro beetles (*Papuana* spp.) are a menace to coconut (*Cocos nucifera*) and taro (*Colocasia esculenta*), which are major staple, cash and culturally important crops in the Secretariat of the Pacific Community region.

The first biocontrol attempts for the rhinoceros beetle were in the 1930's, shortly after arrival of the pest, with introduction of several predators and parasitoids from Asia and Africa, but with limited effect. The first pathogen to be introduced, the fungus *Metarhizium anisopliae* (*Ma*), was released in Samoa in 1939 for use in the breeding sites. Most effective biocontrol was achieved after the *Oryctes virus* was introduced to the region in 1967. Within 3 years of the virus release, beetle damage fell from levels of 70% to 90% of palms infected down to 5% to 15%. The beetle populations reappeared after a decade and the virus was re-released to overcome the damage. Regular releases of virus have continued, but in Samoa and some other countries beetle damage has once again increased and the virus releases no longer appear to reduce the damage levels.

Taro beetles have no effective biocontrol agents although several pathogens are present in its centre of origin, the Papuan region. *Oryctes virus* is very infective to taro beetle, but unlike use for control of rhinoceros beetle its use in the field is limited due to lack of transmission. *Ma* on its own does not give required field control of taro beetles, but is a useful organism as it can be used in synergy with low doses of insecticides such as imidacloprid and provide sufficient control of the beetle to yield over 90% of marketable corms.

Comparative approaches to the evolution of a blood-feeding lifestyle in ticks

Ben Mans

[1]Onderstepoort Veterinary Institute, Pretoria, South Africa, [2]National Institutes of Health, Rockville, United States

Introduction: The vector-host interface is a focus area for the understanding of the evolution of blood-feeding behavior in ticks. Hard (long-feeders) and soft (fast-feeders) ticks evolved different strategies to regulate host defences such as the immune and hemostatic systems. Characterization of these strategies in regard to conservation across tick lineages allows us to reconstruct past adaptations to the blood-feeding niche.

Methods: Comparative biochemical, molecular biological and bio-informatical methodologies are employed to determine conserved functions across various tick genera.

Results: Hard and soft ticks possess similar salivary gland protein family repertoires. Few orthologs are, however, shared between hard and soft ticks or even within the major lineages found within the Ixodidae (prostriate and metastriate). Rather, multi-member protein families show lineage specific expansions. In contrast, a wide diversity of conserved functions is present within the Argasidae.

Conclusions: Conservation of function in the Argasidae suggests that these functions existed in the ancestral lineage of the soft ticks. The lack of conservation found within the Ixodidae suggests that their specific lifestyle (prolonged exposure to the host's defences) had a significant impact on their adaptation to a blood-feeding lifestyle.

Insect-plant interactions in a multitrophic world

Louise E.M. Vet

Netherlands Institute of Ecology (NIOO-KNAW), Maarssen, Netherlands

Insects and plants live in a world of love and hate. To fully understand their interactions a multitrophic approach is crucial since relationships between successive trophic levels can be influenced by other trophic levels. Research on multitrophic interactions (MTI) aims at identifying the molecular, physiological, and behavioural mechanisms involved and how these affect higher-level processes such as the structure, dynamics, functioning and evolution of multitrophic communities. Insight in the functioning of ecological communities is more crucial than ever due to the rapid global changes that our planet is experiencing.

MTI research is flourishing and studies are becoming increasingly interdisciplinary, which is also a general development in ecology. Plant defence is central to multitrophic theory. Plants can defend themselves directly against herbivores, but also indirectly by emitting volatiles upon herbivore damage that attract natural enemies. In addition, plant defence links above- and belowground interactions. Rhizosphere processes can thus have significant consequences for interactions between aboveground herbivores and their natural enemies such as parasitoids, as well as for their fitness. Since insect parasitoids are major players in many terrestrial food webs, not only as enemies of herbivores but also as friends of plants, research on MTI must address their responses to dynamical food web processes such as induced plant defence. For both plants and insects in MTI studies it is becoming imperative to connect different levels of biological organization, i.e. to address and link processes operating at levels from the gene to the community. New techniques such as genomics and metabolomics provide exciting opportunities to forward the field of insect plant-interactions. I will discuss some of these challenges and identify novel foci of MTI research.

Bio-diversity, conservation and priorities concerning some families of the orders Coleoptera, Hemiptera and Lepidoptera

Dolly Kumar, Bhumika Naidu

M.S.University of Baroda, Vadodara, Gujarat, India

Introduction: Insect diversity studies from India, are immense but reports on disappearing insect species and their families from the country are sparse. This is the first comprehensive report on the population studies and the reducing numbers of insect species from the families Scarabidae, Belostomatidae and lycaenidae from the western part of the Indian peninsula.

Methods: Study was undertaken for a period of 4 years from Jan. 2004 to Jan. 2008. Collections and sightings were made within the city area. Rank abundance, Species Diversity and percent composition calculations indicated decline in the entomofauna of the said families.

Results : Percentage composition of *Belostoma indica* declined from 36 % to 9 %. From the family Scarabidae *Gymnopleurus cyaneus* declined from 40% to 9.5%. Occurrence of the members of family Lycaenidae was also rare. Only one or two *Zizeeria otis* were sighted in the year 2007.

Discussion: Decline in the population of Belostomatids is due to the increase in the level of pollutants in the water bodies. Dung rollers are becoming rare as the cattle rearing landscapes are undergoing urbanization. The food plants of family Lycaenidae are being destroyed by humans. Caterpillars of *Freyeria trochilus*, thrives on the weed ,*Heliotropium* which is being killed by weedicides.

Over emphasis and excessive collection of insects by insect lovers is also responsible for their imperilled status.

Evolution and development of *Heliconius* wing patterns

Robert Reed

University of California, Irvine, Irvine, CA, United States

Introduction: Neotropical *Heliconius* butterflies are famous for their extreme geographic wing pattern variation and for the convergence of mimetic wing patterns between species within the genus. To better understand how mimetic polymorphism evolved in this group, we are working to identify the genes underlying mimetic wing pattern variation.

Methods: Our lab is part of a collaboration working to map and sequence regions of the *Heliconius erato* genome containing wing pattern variation genes. We are screening candidate genes identified from genomic sequences using a comparative expression approach. Specifically, by applying genomic tiling microarrays, quantitative RT-PCR, and *in situ* hybridization, we are assessing which candidate genes show color-pattern related expression differences during wing development.

Results: We have successfully sequenced across two different genomic intervals containing two respective color pattern genes. From these intervals we have identified several genes that are expressed during wing development. We will present our most recent results concerning the expression of these candidate genes in butterflies showing different mimetic phenotypes.

Conclusions: Through a combination of mapping, targeted genomic sequencing, and gene expression studies we are getting closer to identifying the specific genes that underlie wing pattern variation in *H. erato*. Identifying these genes will allow us to ask fundamental questions about the evolution and development of adaptive polymorphism and convergent evolution.

Impacts of some forest management practices on insects and other taxa in Europe

Allan Watt[1], Adam Vanbergen[1], Patrick Lavelle[2], Jari Niemelä[3], Paulo Sousa[4], Chris Van Swaay[5]

[1]Centre for Ecology and Hydrology, Edinburgh, United Kingdom, [2]Institut de Recherche pour le Développement, Paris, France, [3]University of Helsinki, Helsinki, Finland, [4]Universidade de Coimbra, Coimbra, Portugal, [5]Dutch Butterfly Conservation, Wageningen, Netherlands

Introduction: The BioAssess project considered the diversity of arthropods and other taxa in eight European countries. The main objectives were to quantify the impact of land use and management on a range of taxa and to identify suitable indicators of biodiversity. Managed and unmanaged forests were included in all countries.

Methods: Field sites were established in eight countries representing all the major biogeographic regions of Europe: Boreal – Finland; Atlantic – UK (Scotland) and Ireland; Continental – France; Pannonian – Hungary; Alpine – Switzerland; Mediterranean – Spain and Portugal. The abundance and diversity of soil macrofauna, soil Collembola, carabids, plants, lichens, butterflies and birds was quantified in each country along land-use intensity gradients from unmanaged forest to intensively managed arable sites. The impact of land use and management on each of these components of biodiversity was quantified and the potential of several indicators was evaluated.

Results: Forest management was found to have a marked impact on the diversity and species composition of all taxa but the impact of forest management varied between taxa and in some cases between regions.

Conclusions: The project highlighted the range of forest management practices in Europe and identified some of their impacts of insects and other taxa. The project also demonstrated that some taxa are better indicators of biodiversity than others. Butterflies, for example, predicted the species richness of birds, lichens and plants, but Carabidae (ground beetles) were found to be a poor indicator of other elements of biodiversity, only showing a weak correlation with soil macrofauna.

The evolution of "resin flowers" (Euphorbiaceae, Clusiaceae) and their bees (Apidae, Megachilidae): the roles of exaptation and natural selection in reward diversification

W. Scott Armbruster[1], Mats Gustafsson[2]

[1]University of Portsmouth, Portsmouth, Hants, United Kingdom, [2]University of Aarhus, Aarhus, Denmark

Flowers have evolved resin as a pollinator reward 3-6 times independently: once in the Euphorbiaceae (*Dalechampia*) and up to five times in the Clusiaceae (*Clusia*, *Tovomitopsis, Clusiella*). Resiniferous Clusiaceae appear to be exclusively neotropical, but resiniferous *Dalechampia* are found in the paleotropics as well as neotropics. Floral resins are collected by pollinating (and non-pollinating) bees (Apidae, Megachilidae) that use resin in nest construction. While resin is often brightly coloured, choice of *Dalechampia* blossoms by resin-collecting bees is usually based on the size of the involucral bracts, an honestly correlated advertisement. In the neotropics, resin lineages have given rise to nectar-reward lineages (*Clusia*), pollen-reward lineages (*Clusia, Dalechampia*), and fragrance-reward lineages (*Dalechampia*). While all *Dalechampia* in the continental paleotropics offer resin rewards, those in Madagascar have pollen rewards and are pollinated by pollen-feeding beetles, flies, and bees, or are "buzz" pollinated by bees. In addition to useful waterproofing and mechanical properties (*Dalechampia*), some floral resins have antibiotic properties (*Clusia*), which seem to be valued by bees. Reward resins probably arose by exaptation from floral-defence resin/latex, and reward resins may have, in turn, promoted the evolution of fruit and foliar defences.

Comparing apples and oranges: methodological challenges of temperate - tropical comparisons

Vojtech Novotny

Biology Center, Czech Academy of Sciences, University of South Bohemia, Czech Republic

Latitudinal gradient in species diversity represents one of the major challenges to ecological theory, as well as an excellent opportunity to study processes generating and maintaining species diversity. Rigorous comparisons between tropical and temperate ecosystems are however rare. Temperate and tropical communities tend to be studied by different sets of ecologists, each using distinct sampling protocols. This methodological bias is further complicated by large biological differences between temperate and tropical communities in their phylogenetic composition, species richness and niche structure. The present study analyses these challenges and suggests unified protocols for the study of insect communities and determinants of their species richness along global latitudinal gradients.

Wide area approach to control *Carpophilus* spp. (Coleoptera: Nitidulidae) in stone fruit in Australia

Mofakhar Hossain, David Williams, Mamun Hossain

Department of Primary Industries (DPI), Tatura, Victoria, Australia

A user-friendly Attract and kill (A&K) system using aggregation pheromone and synthetic co-attractant has been developed for control of *Carpophilus* spp without having to spray the orchard. The attract and kill system proved effective in small scale trial (1 ha block). Generally three attract and kill stations per ha were deployed at the up wind corner of each one ha block. We are currently assessing a wide area approach to reduce *Carpophilus* spp populations across a larger area in order to make the system more effective and sustainable. During the fruit growing season of 2005/06 and 2006/07, respectively 70 and 100 ha of T204 peach blocks were treated with the attract and kill system in the Goulburn Valley, northern Victoria. The attract and kill system worked more effectively when a larger area in an orchard was covered and the *Carpophilus* spp population was reduced by more than 100,000 beetles/ha within a year in orchards with high level of populations. To prevent invasion by beetles into target blocks from neighbouring blocks we studied the effects of treating the blocks, surrounding target blocks of T204 peaches with high beetle populations, with either two or three A&K stations/ha. Six target blocks (each with 3 A&K stations/ha) were selected. Three had neighbouring blocks treated with 3 A&K stations/ha and 3 had neighbouring blocks treated with 2 A&K stations/ha. Six control blocks, not treated with A&K stations, were selected for comparison. Fruit damage assessment was done in nine locations in each target and control block. The average fruit damage levels were 0.39%, 0.35% and 4.20% in blocks treated with 3 A&K/ha or 2 A&K/ha and control. Experiments were also conducted with two or three A&K stations/ha in T204 blocks in properties with medium and low beetle population levels. There was no difference in fruit damage between blocks with either two or three A&K stations/ha. This suggests that cost of control may be reduced without sacrificing efficacy.

Ticks and tsetse control in sub-Saharan Africa: particular reference to a 100 years of acaricides use in South Africa

Abdalla A Latif

Onderstepoort Veterinary Institute, Pretoria, South Africa

Ticks and tick-borne diseases TBDs and tsetse and trypanosomosis coexist in many situations in Africa and affect the same population of cattle. Different effective control methods can be planned for TBDs including treatment of cattle with chemical acaricides, presence of natural acquired immunity to most of TBD after initial infection in endemic areas, immunization against TBDs, vaccination against ticks, treatment of clinical cases, and using tick-resistant cattle. However, there are only few control options for tsetse and trypanosomosis in absence of naturally acquired immunity with the exception of the few trypano-tolerant breeds, absence of effective vaccines, and the wide-spread of drug-resistant strains of trypanosomes. Sterile insect technique is deemed to be expensive and aerial spraying is not appealing to environmentalists and conservation authorities. However, both techniques have been implemented and made successes. Many countries which have limited resources relied largely on its control operations on the application of pyrethroid insecticide on cattle and use of traps to control tsetse flies. Pyrethroid-treated cattle are introduced to graze fly-infested areas and tsetse flies are killed after feeding. The reports from different control projects have shown successful reduction in tsetse populations and incidentally, reductions in tick burdens on cattle. However, the regular use of pyrethroid-bait cattle to control tsetse fly populations, with the opportunistic and unplanned killing of ticks has many disadvantages. These arguments and the way forward will be discussed with particular reference to South Africa

Biological control of the *Sirex noctilio* wood wasp in pine plantations in South Africa

Geoff Tribe

ARC-PPRI, Stellenbosch, South Africa

Introduction: The Eurasian wood wasp *Sirex noctilio* was found in South Africa in April 1994 infesting pine plantations within a 90 km radius around Cape Town. A 3.2% mortality of trees was recorded. *Sirex* spread at an annual rate of 48 km within the Western Cape and reached George by 2001. *Sirex* appeared in parts of the Eastern Cape and KwaZulu-Natal in 2002 apparently by human assistance.

Methods: Three biological control agents have been utilized. Inoculations with the Kamona strain of the parasitic nematode *Beddingia (Deladenus) siricidicola* were carried out in 1995 and 1996. The larval parasitoid *Ibalia leucospoides* was imported in 1998 and 456 parasitoids were released from 1998 until 2001. In 1999, 38 mated females of the late-larval parasitoid *Megarhyssa nortoni* were released.

Results: The parasitism rate of *B. siricidicola* increased to 96.1% by 1998 and has since remained effective between 61% (2006) and 90.9% (2007). *Ibalia leucospoides* achieved a parasitism rate of between 33% (2006) and 25.7% (2007). *Megarhyssa nortoni* failed to become established.

Conclusions: Biological control has been highly effective in the Western Cape where *Sirex* is no longer an economic problem. This can be contrasted with KwaZulu-Natal where a reported 2 million trees were killed by *Sirex* in 2006. This appears to be due to: the biological control agents not being moved to the front as *Sirex* dispersed; a reported inoculation success rate of only 2% indicates non-viable nematodes; and the *Sirex* flight period beginning and ending earlier than in winter rainfall areas.

Isolation and toxicity evaluation of bacterial entomopathogens against phytophagous white grubs (Coleoptera: Scarabaeidae) in Indian Himalayan hills

Shahid Sami Siddique, Zubair Ahmad, Mohd Shamim, Parvez Qamar Rizvi

Aligarh Muslim University, Aligarh,uttarpradesh, India

White grubs (Coleoptera: Scarabaeidae) are the cosmopolitan insect pests of agriculture, forest and pasture lands. The western Indian Himalayan hill region has a vast biodiversity of nearly 40 species of phytophagous white grubs. Among them, *Anomala dimidiata* and *Holotrichia seticollis* are the most abundant species and cause serious damage on many crops. Under natural condition, bacterial epizootics on white grubs were observed to the extent of 20.6%. Hence an attempt was made to isolate and characterize a bacterium, which is most potent for the management of white grubs. Out of 27 bacterial isolates tested against 2^{nd} instar grubs of *A. dimidiata*, the isolate WGPSB-2 was found highly toxic. Based on various morphological, physiological and biochemical tests the isolate WGPSB-2 was identified as *Bacillus cereus*. The dose determination bioassay indicated that the 1^{st} instar grubs of *A. dimidiata* and *H. seticollis* were more susceptible than the 2^{nd} instars. Although the LT_{90} values for 2^{nd} instar grubs were more than eight weeks, the grubs stopped feeding after ingestion of spores, mostly after third week. Under micro plot condition, a dose of $1.7x10^{11}$ spores/m^2 in the form of root zone application was found satisfactory to manage both the species of white grubs. In the absence of any other viable and environmentally competitive biological control agents, the *Bacillus cereus* strain WGPSB-2 appears to be a potential bacterial pathogen for the management of white grubs.

Discussion: international themes and challenges in coffee pest management

Nilsa Bosque-Perez, Sanford Eigenbrode

Department of Plant, Soil and Entomological Sciences, University of Idaho, Moscow, Idaho, United Sates

The themes and challenges on integrated management of coffee pests and beneficial insects emerging from the Symposium will be discussed. Special emphasis will be placed on identifying subjects for future research and potential areas of collaboration between diverse institutions.

Effects of insect-resistant transgenic crops on nontarget organisms

Maureen O'Callaghan[1], Louise Malone[2]

[1]AgResearch, Christchurch, New Zealand, [2]Horticulture and Food Research Institute of New Zealand Ltd, Auckland, New Zealand

Introduction: Measuring nontarget impacts is an essential part of the risk assessment process for insect-resistant transgenic crops. While *Bacillus thuringensis* (Bt)-plants currently dominate the market for insect-resistant transgenic crops, plants expressing alternative insecticidal compounds such as lectins, protease inhibitors and biotin-binding proteins, are currently under development.

Testing nontarget impacts: Testing has focussed on measuring impacts on "ecosystem service providers" (e.g. natural enemies and pollinators), and insects of cultural or aesthetic value. The extensive testing on non-target plant-feeding insects and beneficial species that has accompanied the wide-scale and long-term use of Bt-crops has not detected significant adverse effects. There is also growing recognition of the need to determine nontarget impacts on soil ecosystem function; tests to date have shown that Bt-crops have little impact on soil biota such as earthworms, collembolans and general soil microflora. While extensive testing has been carried out with Bt-crops, plants expressing other insect resistant proteins with a broader spectrum of activity and differing modes of action have been tested on a very limited range of nontarget species to date. In addition, with the exception of Bt endotoxins, little is known about the persistence of other transgene-derived proteins in soil.

Conclusions: Major knowledge gaps remain in the nontarget testing of transgenic plants; for example, test species are often not representative of the environment in which the transgenic plants will be grown and detection of nontarget impacts resulting from novel combinations of insecticidal proteins may require a different set of testing methodologies than those used to date.

Biological control of water hyacinth – the Lake Victoria case

James Ogwang

National Crops Resources Research Institute, Kampala, Uganda

Introduction: Biological control of water hyacinth in Lake Victoria using two weevil species *Neochetina bruchi* and *Neochetina eichhorniae* reduced the weed biomass by 90% five years post release in 1995. Cases of resurgence of the weed have been reported in several points of the lake since 2000.

Methods: Samples were taken using a wooden quadrant tossed randomly in weed mats have been taken since 2000. Data taken included weed weight, petiole and root length in addition to weevil numbers, sex and species per plant were recorded

Results: Results showed that the resurgent mats initially had few (0.5 -2 weevils/plant) in the early 2002 but this has gradually built up to14 weevils/plant by December 2007. Additionally evidence of weed wilting due to pressure from weevil population was widespread in the lake

Conclusion: The collapse of water hyacinth mats in late 1990s resulted in a corresponding weevil population collapse. Sinking mats similarly significantly increased water nutrients which became favourable for the rapid germination of water hyacinth seeds deposited below the water surface. A combination of these factors was probably responsible for the weed resurgence. However, with the weevil build up, it is unlikely that water hyacinth biomass will revert to pre-control level

Species diversity and plant resources of stingless bees along a disturbance gradient in western Kenya

Mary Gikungu[1] and Manfred Kraemer[2]

[1]National Museums of Kenya. Zoology Department. P.O. Box 40658-00100 Nairobi, Kenya, [2]Faculty of Biology, Biological Collection, University of Bielefeld, P.O. Box, 100 131, 33501 Bielefeld, Germany

Introduction: Establishing the composition structure of stingless bee community is necessary for understanding the cumulative impact by anthropogenic factors and their resilience in natural habitats. The study aimed at examining the species diversity and food sources of stingless bees along a disturbance gradient in the study area.

Methods: The abundance of bees was sampled monthly using the belt transect method. Bees were sampled with a sweep net at each site three times per month from May 2002 to April 2004.

Results: The results of this study provide the first documentation of the stingless bees and their food sources of Kakamega forest. The recorded stingless bee species included Meliponula *bocandei, Meliponula lendliana, Meliponula ogouensis, Meliponula ferruginea, Pleibena hildebrandti, Hypotrigona gribodoi and Liotrigona bottegoi.* The highest diversity of stingless bees based on Shannon-Wiener index (H') was recorded in the farmland followed by moderate secondary forest and advanced secondary forest, while no significant difference was found along the gradient in terms of bee species richness. The most important plant families were Asteraceae, Acanthaceae, Labiatae, and Malvaceae while the most important plant species were *Maesa lanceolata*, *Tithonia diversifolia* and *Zea mays*. The stingless bee community was found to be highly influenced by the availability of food sources.

Conclusion: The research suggests that at least in some systems, conservation of native bees and the pollination service they provide depends on management of both natural forests and secondary forests together with the surrounding agro-ecosystems. Further, disturbed habitats in low-intensity farming systems may provide suitable resources for many bee species when there are less flowering plants in forested systems.

Baseline surveys of malaria vector mosquitoes from Guinea Conakry, West Africa

Samuel B Vezenegho[1], Samuel B Vezenegho[2], Basil D Brooke[1], , Basil D Brooke[3], Richard H Hunt[1], Richard H Hunt[4], Lizette L Koekemoer[1], Lizette L Koekemoer[3], Maureen Coetzee[1], Maureen Coetzee[3]

[1]Vector Control Reference Unit (VCRU),National Institude for Communicable Diseases, Johannesburg, South Africa, [2]School of Molecular Cell Biology, University of the Witwatersrand, Johannesburg, South Africa, [3]Division of Virology and Communicable Disease Surveillance, School of Pathology of the NHLS and the University of the Witwatersrand, Johannesburg, South Africa, [4]School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, Johannesburg, South Africa

Introduction: Malaria vector resistance to pyrethroid and DDT insecticides has been reported in West Africa. There is only limited information about vector composition and susceptibility status in Guinea Conakry. This study was designed to provide more information from three localities with very different environment.

Methods: *Anopheles* mosquitoes were collected in Mount Nimba, Siguiri and Boffa. Field bioassays using deltamethrin, DDT, dieldrin, malathion and bendiocarb were performed on *An. gambiae* s.l according to the standard WHO protocol. Further species identification by PCR, WHO standard insecticide susceptibility assays, sporozoite ELISA and the two-step PCR method for *kdr* detection were used.

Results: Field bioassays showed high susceptibility to all insecticides in Boffa. Full susceptibility to deltamethrin and malathion was demonstrated in Siguiri and Mount Nimba. Resistance to DDT, dieldrin and bendiocarb was shown in Siguiri and Mount Nimba. PCR assays identified 494 (82.3%) as *An. gambiae* and 2 (0.33%) *An. arabiensis* in a sample of 600 specimens. No amplification was achieved in the remaining 104 (17.33%) specimens. Plasmodium infection rate of 5%, 6% and 21% was obtained for Siguiri, Mount Nimba and Boffa respectively. *Kdr* PCR and sequencing revealed the presence of the leucine to phenyalanine mutation in the S form. Biochemical enzyme analysis in the F_1 progeny of wild *An. gambiae* s.s exposed to pirimiphos methyl indicated esterase and monooxygenase elevation.

Conclusions: The S molecular form of *An. gambiae* is the main malaria vector at these localities in Guinea Conakry and occurs in sympatry with the M form. The involvement of *Kdr* in phenotypic resistance to DDT is unclear but need to be considered when planning control strategies. Metabolic involvement in resistance is likely. *Kdr* detection by Pyrosequencing is being investigated. The use of long-lived pyrethroids and short-lived organophosphates throughout the year is recommended for vector control in Guinea Conakry.

Ethical Issues in the use of forensic entomology evidence

Robert Hall

University of Missouri, Columbia, Missouri, United States

The most frequent medicocriminal use of forensic entomology evidence is the inference of human postmortem interval (PMI) based on the thermal developmental profile of well-studied blow fly species. As criminal cases are litigated, there may exist extreme pressure on the entomologist expert witness to supply an analysis favorable to the retaining party. Aspects of entomological evidence vulnerable to such pressure include 1) use of remote temperatures obtained from a weather recording station where such temperatures produce an insect-estimated PMI most favorable to the desired outcome, 2) speculative explanations on when ovipositing females may have accessed a corpse when any form of “barrier” is present, 3) misuse of accumulated-degree-hour calculations when such are not warranted, 4) speculation regarding unmeasured maggot mass effects, 5) assertion of unique, “one of a kind” circumstances to achieve the desired result, and 6) selective use of blow fly developmental data sets to achieve a result favorable to the retaining party. The duty of the expert witness in U.S. courts is to provide the trier-of-fact with sound science, regardless of the ultimate legal outcome of the case at bar.

Evolution of wingless reproductives in ants: diversity in morphology and social structure

Christian Peeters

UPMC Paris Universitas, Paris, France

Introduction: A majority of ants produce winged queens that disperse by flight and found colonies independently. However many species belonging to all the major subfamilies shifted to obligate colony fission, and there is no longer a solitary founding stage. Hence selective pressures on reproductives are relaxed, and they become completely dependent on workers. Since fission in ants is synonymous with short-range dispersal on foot, because the workers are wingless, the production of flying queens is selected against. Except for about 200 species where workers can mate and reproduce (= 'gamergates'), in other taxa 'ergatoid queens' have evolved.

Methods: Species having either winged queens or wingless reproductives were studied in various genera, both poneroid and formicoid. Their alternative reproductive systems were compared using a variety of data: colonial demographies and caste ratios, behavioural observations, morphology and morphometry, dissection of ovaries.

Results: In *Cerapachys, Odontomachus, Proceratium* and others, a single ergatoid queen reproduces in each colony. The thorax is highly reduced but they are allometrically different from workers.This contrasts with other genera (*Mystrium, Eutetramorium,* ..) in which many ergatoid queens are present throughout the year. A few of these mate and reproduce, while the others remain in the nest to function as labourers. Colonial investment in ergatoid queens is always much reduced compared to congeneric species producing many winged queens annually.

Conclusions: Different solutions evolved to replace winged queens. Changes in the phenotype of reproductives are associated with modifications in colony-level investment, and both these adaptations contribute to the success of fission in ants.

Combining the mirid *Eccritotarsus catarinensis* and the weevils *Neochetina* spp. as biological control agents of water hyacinth *Eichhornia crassipes*.

Obinna Ajuonu[1], Marcus Byrne[2], Martin Hill[3], Peter Neuenschwander[1], Sam Korie [1]

[1]International Institute of Tropical Agriculture, Benin, Abomey, Calavi, Benin [2]University of the Witwatersrand, Johannesburg, South Africa, [3]Rhodes University, Grahamstown, South Africa

Introduction: The mirid *Eccritotarsus catarinensis* was released to complement biological control of water hyacinth *Eichhornia crassipes* by the weevil species *Neochetina eichhorniae* and *N. bruchi*. In two separate experiments, a) the influence of feeding scars by adult weevils on the survival of the mirid and b), the impact of biological control agents as single species and together on growth parameters of the host plant, were studied.

Methods: In the first study, water hyacinth plants with varying amounts of weevil feeding scars were exposed to adult mirids under laboratory conditions for three days, after which adults were counted to determine adult survival. After fifteen days, immatures were counted to determine reproduction and their survival. In the second study, water hyacinth plants grown in the screen house in competition with water lettuce (*Pistia stratiotes*) were inoculated with agents. Impact of agents was assessed by measuring water hyacinth plant growth parameters.

Results: The mirid survived well on plants with recent feeding scars from adult weevils and on leaves with more than 200 old scars. Combining both agents at half the population densities produced the same growth reduction in *E. crassipes* as the weevil *N. eichhorniae* at full density.

Conclusions: The weevil is not likely to prevent the establishment of the mirid and therefore it would be a good complement to the already established biological control agents of water hyacinth particularly on stranded plants where the weevil is prevented from pupation.

Application of *Sycanus collaris* as biocontrol agent for insect pests in plantation forestry

Budi Tjahjono, Abdul Gafur, Aswardi Nasution, G.D. Golani

APRIL Forestry R&D, PT RAPP, Pangkalan Kerinci 28300 Indonesia,

Introduction: The assassin bug *Sycanus collaris* (Hemiptera: Reduviidae) is well recognized as an important predator of numerous insect pests. In Indonesia, this insect has long been used as a predator to reduce the levels of caterpillar populations in oil palm plantations. Here we report on the application of *S. collaris* to manage *Helopeltis* spp. and leaf roller caterpillar populations in acacia, eucalypt, and *Melaleuca* plantations in south Sumatera. This has the advantage of limiting the application of chemical insecticides and it also promotes the economical and ecologically sound forestry.

Methods: For field introduction, *S. collaris* was produced in the laboratory. It was fed on *Corcyra cephalonica* (Lepidoptera: Pyralidae) and *Tenebrio molitor* (Coleoptera: Tenebrionidae). Up to 2007, it was possible to release as many as 4,571 individual insects into plantations in Sumatera, Indonesia.

Life cycle: The eggs of *S. collaris* are laid in clusters and cemented to each other and to the surface of the plastic boxes in which the insects are reared. The nymphs moult five times before they reach imago stage. The duration required from the first to the fifth instar of the nymph is about 12 weeks. Males and females can be distinguished by their body and abdominal sizes with the males being smaller.

Results: Reduction in pest population, plant recovery, and development of the predator after field release were used as indicators of the efficacy of *S. collaris*. Up to the present, *Helopeltis* incidence has dropped from 30 % to 10 % in *A. mangium* plantations and leaf roller incidence has dropped from 60 % to 10 % in *Melaleuca* plantations.

Inter-country collaborative efforts in vector control in Africa

Rajendra Maharaj

Malaria Research Programme, Medical Research Council, Durban, South Africa

Malaria is not a country specific disease but should be seen as a disease of regional importance. Most countries lack the infrastructure and/or the technical expertise to effectively control the disease in their countries. Therefore through close collaboration countries can share resources and technical expertise to implement more co-ordinated intervention strategies in a more sustainable manner

The Lubombo Spatial Development Initiative (LSDI) is one such initiative that aims to implement effective malaria control within a sub-region. Through proper scientific investigation, intervention strategies were designed to have maximum impact. Insecticide resistance studies and household surveys guided the selection of appropriate strategies. Coupled with a malaria health information system, the success of the vector control strategy could be evaluated. This facilitated continuous monitoring and evaluation. The outcome of these interventions was that prevalence at 28 sentinel sites showed an average decrease of 70% in children aged 2 to 15 years.

The success of the LSDI was acknowledged in the recognition that it presented a model upon which further initiatives could be built. This model was implemented on the Island of Bioko in West Africa and similar successes were achieved. In recognition of this success, this initiative was expanded to mainland Equatorial Guinea and Conakry Guinea. The recently established Trans-Zambezi malaria control initiative is to adopt a similar model that will be implemented in 15 contiguous districts in 5 southern African countries.

The face of vector control is changing to ensure that similar multi-country strategies are implemented across national borders to slow the development of resistance and encourage sustained malaria control. This in turn facilitates the implementation of malaria elimination strategies.

VectorBase: a bioinformatics resource for the analysis and display of vector genomes

Frank Collins

University of Notre Dame, Notre Dame, United States

VectorBase is a centralized relational database based on publicly available and supported database management tools that displays through an internet interface all data relating to the genomes of arthropod vectors of human pathogens. The basic 'engine' of VectorBase is the Ensembl genome browser and analysis system developed by the European Bioinformatics Institute. Genomes in VectorBase are displayed through the Ensembl genome browser, which is modified and 'branded' for VectorBase; genome annotations are updated by the EBI subcontract team using the Ensembl tools. VectorBase also displays data that are not managed and displayed by the Ensembl system. This has been done by creating a hybrid system based on two data schemas. All data in the non-normalized Ensembl schema are also mapped into a VectorBase instance of the GMOD Chado schema designed to be consistent with FlyBase Chado. This schema is also used to capture additional types of data, such as physical mapping data, expression data, controlled vocabulary, and other genome metadata that are not part of the core Ensembl data set. Additional data are brought into the Chado schema and then displayed in the Ensembl core of VectorBase through distributed annotation system (DAS) display tracks that are designed into the Ensembl display. This presentation will give an overview of the general structure of VectorBase as well as a summary of the genomes currently in VectorBase and data likely to be managed by VectorBase in the upcoming year.

Exploitation of wild relatives of crops as source of novel genes for resistance to insect pests

Hari Sharma, Venkateswaran Kamala, Stevenson Clement, James Ridsdill-Smith, G Sujana

[1]International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh, India, [2]National Bureau of Plant Genetic Resources Regional Station, Patancheru, Andhra Pradesh, India, [3]USDA-ARS, Washington State, Pulman, United States, [4]CSIRO Entomology, Wembley, WA, Australia, [5]International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra pradesh, India

Cultivated germplasm of many crops has only low to moderate levels of resistance to several insect pests such as bollworms, stem/shoot borers, pod borers, aphids, shoot flies, jassids, and white flies. As a result, progress in developing insect-resistant cultivars in several crops against several insect species has been quite slow. However, closely related wild relatives of several crops have high very levels of resistance o insect pests. Wild relatives with different genes and diverse mechanisms of resistance of resistance have been identified against *Heliothis/Helicoverpa* in cotton, pigeonpea, chickpea, and tomato; *Atherigona*, *Chilo*, and *Stenodiplosis* in sorghum; *Maruca* in cowpea; *Orseolia* and *Scirpophaga* in rice; *Amrasca*, *Aproaerema* and *Spodoptera* in groundnut; and *Maytiola* and *Diuraphis* in wheat. Considerable progress has also been made in understanding the physico-chemical mechanisms of resistance, and introgression of resistance genes from the wild relatives into the high yielding cultivars in several crops. Genes for insect resistance from the wild relatives can be utilized through wide hybridization, marker assisted selection, and sequencing and cloning to increase the levels and diversify the bases of resistance to insect pests for sustainable crop production.

Exploitation of wild relatives of crops as source of novel genes for resistance to insect pests

Hari Sharma, Venkateswaran Kamala, Stevenson Clement, James Ridsdill-Smith, G Sujana

[1]International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh, India, [2]National Bureau of Plant Genetic Resources Regional Station, Patancheru, Andhra Pradesh, India, [3]USDA-ARS, Washington State, Pulman, United States, [4]CSIRO Entomology, Wembley, WA, Australia, [5]nternational Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra pradesh, India

Cultivated germplasm of many crops has only low to moderate levels of resistance to several insect pests such as bollworms, stem/shoot borers, pod borers, aphids, shoot flies, jassids, and white flies. As a result, progress in developing insect-resistant cultivars in several crops against several insect species has been quite slow. However, closely related wild relatives of several crops have high very levels of resistance o insect pests. Wild relatives with different genes and diverse mechanisms of resistance of resistance have been identified against *Heliothis/Helicoverpa* in cotton, pigeonpea, chickpea, and tomato; *Atherigona*, *Chilo*, and *Stenodiplosis* in sorghum; *Maruca* in cowpea; *Orseolia* and *Scirpophaga* in rice; *Amrasca*, *Aproaerema* and *Spodoptera* in groundnut; and *Maytiola* and *Diuraphis* in wheat. Considerable progress has also been made in understanding the physico-chemical mechanisms of resistance, and introgression of resistance genes from the wild relatives into the high yielding cultivars in several crops. Genes for insect resistance from the wild relatives can be utilized through wide hybridization, marker assisted selection, and sequencing and cloning to increase the levels and diversify the bases of resistance to insect pests for sustainable crop production.

Sociality in nocturnal environments

Simon Tierney, Adam Smith, William Wcislo

Smithsonian Tropical Research Institute, Balboa, Panama

Introduction: Like most biologists, the majority of bees are active during the day. However a number of lineages have temporally shifted their foraging activity to low light or nocturnal environments. Dim-light foraging has repeatedly evolved among bees,, and some of these are social. The entry into this temporal niche requires some degree of physiological and morphological specialization, but how do dim-light environments affect social behaviour?

Methods: The origins of dim-light foraging in bees are examined within a phylogenetic context. Phenotypic adaptations postulated to be associated with such lifestyles are also briefly discussed. The social dim-light light taxa are then reviewed, with regard to the influence of low light environments on the ecology and social behaviour of these bees.

Results: Obligate dim-light foraging has independently evolved 18 times, in four of the nine bee families. Facultative dim-light foraging is more widespread, but does not require the same degree of phenotypic specialization. Evolution of dim-light foraging appears to be associated with an escape from competitors, predators and parasites. The Neotropical sweat bee genus *Megalopta* (Halictidae: Augochlorini) is the most intensively studied nocturnal social bee. Sociality is facultative and highly labile, reproductive dominance within social colonies is mediated by body size and recent studies suggest brood parasites significantly influence adult body size. Behaviour in *Megalopta* is contrasted with other social halictids and facultatively social bees generally.

Conclusion: Social dim-light foraging bees inhabit an uncommon niche, which presents excellent opportunities to investigate the role of extrinsic factors on social evolution.

An integrated approach to biosecurity threat identification and prioritization

Darren Kriticos, David Cook, Dean Paini, Shuang Liu, Jo Luck, Paul De Barro

CRC National Plant Biosecurity, Canberra, Australia

Biosecurity prediction is notoriously uncertain, and in planning biosecurity investments agricultural industries need confidence in the process. Most pest risk prediction rely upon some form of regression-based analysis of the habitat preferences of the target species, and application of the inferred relationships to novel environments where the invasion risk is being assessed. Regression-based methods tend to give results that include spurious modelling artifacts. Process-oriented models overcome some of these problems, but require skilled modellers to produce reliable results, take time to develop and currently lack a means of generating meaningful goodness of fit metrics. The outputs generated by habitat modelling software vary in their meaning, and are not provided in terms that are directly usable by pest risk assessors. Our research aims to relate CLIMEX outputs to damage functions that can be applied in economic impact assessments.

To a large extent systems of pest prioritisation depend on expert opinion regarding a number of uncertainties. While valuable, these subjective opinions have a profound impact on threat perception. Objective economic analyses are rarely used to inform prioritisation decisions, and where they are used their scope is generally limited to market impacts ignoring the effects on non-market goods. Our research aims to improve biosecurity planning and pest prioritisation by blending quantitative and qualitative expert-based impact assessment techniques in a structured, deliberative multi-criteria evaluation framework. A combination of neural network analyses estimating entry potential, bioeconomic impact simulation models and deliberative decision-facilitation tools are used to aid the design of appropriate risk mitigation and management strategies.

Tortricid morphology, phylogeny and systematics from a southern perspective

Marianne Horak

CSIRO Entomology, Canberra, ACT, Australia

The lucky constellation of early contact with the southern hemisphere fauna, exposure to Hennig's ideas and several generous and inspiring mentors provided an ideal foundation for my systematic career. A seminar on Hennig's phylogenetic systematics during my Ph. D. studies led to the rash decision to establish a hypothesis for the tortricid groundplan which has remained a crucial reference for all my future work. Trying to make sense of the conspicuously congruent genitalia morphology of many 'unusual' Gondwanan tortricids that defied tribal assignment, I realised that character states rare in the Holarctic fauna were often implicitly regarded as derived. Correction of this blinkered Holarctic viewpoint led to my reversing several tacitly accepted character polarities. Study of the large Australian Lepidoptera fauna, with only 50% of the species named, called for innovative methods, and Ebbe Nielsen initiated a monograph series based at the generic level to provide a stable framework, in a manner accessible to non-specialists. My olethreutine volume follows this model with one important change: two rather than one species are figured for each genus to provide generic rather than specific concepts. Even though the 90 olethreutine genera present in Australia are shared with or derived from the Oriental fauna, my study has provided comprehensive morphological evidence on which to build robust tribal concepts and furthered understanding of olethreutine phylogeny in a world-wide context. I am greatly indebted to Furumi Komai as without his contribution as first author for the very diverse Australian Grapholitini the olethreutine monograph could never have been completed.

Non-taxonomic biochemical tools for enhancing decision making at the border

Ilia Iline[1], Craig Phillips[1], Max Novoselov[1], Alan Flynn[2], Dave Voice[3], Sherly George[2]

[1]AgResearch & Better Border Biosecurity, Christchurch, New Zealand, [2]MAF Biosecurity New Zealand, Auckland, New Zealand, [3]MAF Biosecurity New Zealand, Lincoln, New Zealand

In addition to the daunting task of making taxonomic identifications of organisms that are intercepted at the border, regulatory authorities must also evaluate other characteristics of intercepted organisms such as their viability. When the intercepted organisms are sessile (e.g. eggs, pupae, scale insects) the challenge of rapidly and objectively assessing viability is significant, and the costs of incorrectly interpreting viability can be high. For example, if regulated scale insects associated with a consignment of imported produce were incorrectly assessed as being alive, the consignment may be unnecessarily rejected and either destroyed, fumigated or returned to the exporter. Alternatively, if the scale insects were incorrectly assessed as being dead, they could be allowed to cross the border into a new region or country, thus risking the establishment of a new pest. Viability assessments of sessile organisms are generally made using morphological criteria that demand high levels of user-experience to obtain reliable results. Moreover, morphological observations are often difficult to quantify or otherwise record in an objective manner, and this can cause problems when border authorities need to defend their viability assessments. This presentation describes a series of rapid, sensitive, inexpensive, simple-to-use biochemical tests that have been developed primarily for use by border authorities to make viability assessments of sessile organisms. The tests are also proving useful in other applications such as validating the efficacy of treatments that have been applied to consignments prior to export. The tests perform well across a diverse range of arthropods, and give easily interpreted, contrasting colour reactions depending on the viability of the organism; these can readily be quantified using a spectrophotometer or by measuring pixel values. The biochemical data have also shown that the physical appearance of sessile organisms can sometimes be misleading with respect to their viability. This work illustrates how relatively small research projects can help to increase the speed, reliability, objectivity, transparency, defensibility and overall efficiency of border biosecurity processes.

Bio-safety of insect-resistant genetically modified crops to non-target natural enemies of crop pests

Hari Sharma, Jorg Romeis, Mukesh Dhillon

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Andhra Pradesh, India, [2]Agroscope Reckenholz-Tänikon Research Station ART, Reckenholzstr. 191, 8046 Zurich, Switzerland, [3]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT),), Patancheru 502 324, Andhra Pradesh, India

Genes conferring resistance to insect pests have been inserted into several crops, and transgenic cotton and maize expressing *cry* genes from *Bacillus thuringiensis* (*Bt*) have shown considerable potential for pest management. Adoption of *Bt*-transgenic crops has resulted in increased yields and a decreased the pesticide use. However, there is a need for in-depth studies on the effects of genetically modified crops on nontarget natural enemies of crop pests. The effects of transgenic plants on the activity and abundance of natural enemies varies across crops, and the insect species involved. In general, there are no major adverse effects of genetically modified insect-resistant crops on the generalist predators, while some adverse effects have been observed on the host specific parasitoids, which are largely due to early mortality of the host larvae or poor nutritional quality of the inset host, rather than direct toxicity of the insecticidal proteins. Such effects are common for all pest control interventions, and in general, are not regarded as a risk. Highly specific, insect-resistant transgenic crops could play a significant role in integrated pest management in the future, and lead to a major reduction in the number of insecticide sprays, increase the activity of natural enemies. There is a need to harmonize the regulatory requirements to assess the bio-safety of transgenic crops to the non-target organisms for sustainable crop production.

A journal for pollination ecology.

Carolin Mayer

University of Hamburg, Hamburg, Germany

Despite pollination offering a huge, amazingly diverse and fundamental field of research, no ad hoc platform exists to exchange findings and knowledge in this field. Publications on pollination are scattered in various journals. This is due to the subject crossing multiple biological disciplines. This fact creates a few weak points, one being literature on pollination sometimes difficult and laborious to find. Journals find work on pollination inappropriate for publication on the grounds that it is neither botanical nor zoological. Publication, however, remains the mechanism for scientists to communicate their results, to earn a reputation and, finally, to receive funding for further research.

To promote the concept of pollination as an ecosystem service, researchers have to make themselves heard by stakeholders and the public. Bound publications and a forum for lively discussions will help to achieve this aim.

Therefore, a journal for pollination ecology to support the exchange of original knowledge and research in all area of pollination is proposed. Specifically, the journal should focus on evolutionary, ecological or conservational aspects of pollination, abiotic as well as biotic pollination, reproductive strategies of plants, community and population dynamics of plants and their pollinators as well as biodiversity and conservation issues.

The journal should be online and, most important, have open access to guarantee wide distribution. To keep a high standard of publications, all manuscripts and reviews should be based on original descriptive or experimental research worldwide, and should be peer-reviewed.

Molecular characterization of eggplant fruit and shoot borer, *Leucinodes orbonalis*, populations from India based on ISSR analysis

Leela Alamalakala, Girish Kamble, Bharat Char, Srinivas Parimi, Usha Zehr

Maharashtra Hybrid Seeds Co. Ltd., Jalna, Maharashtra. India

Introduction: Eggplant fruit and shoot borer (EFSB), an economically important pest of brinjal, is a species native to India. Understanding the genetic diversity of geographically distinct populations at molecular level prior to the commercialization of transgenic eggplant, helps in determining whether the differential susceptibility of populations to insecticidal proteins translates to significant differences at the molecular level. No reports were found in literature regarding the genetic diversity of EFSB populations. The goal of this study was to assess molecular genetic relationships among and within populations of EFSB from India using ISSR-PCR technique.

Methods: Larval DNA from 18 locations were genotyped individually using ISSR primers. ISSR- PCR products were resolved on 2.5% Tris-Boric Acid- EDTA agarose gels and stained with ethidium bromide. Primers that generated distinct, reproducible bands across three different amplifications were scored as binary data matrix and analysed with the software NTSYS-pc.

Results: ISSR-PCR technique revealed considerable levels of genetic differentiation both within and between EFSB populations. The ISSR fingerprints of individuals belonging to the same geogrpahical location exhibited a number of bands that varied between individuals, thus reflecting individual differences and high genetic diversity within a population. However, there was no correlation between the geographical distances between the population and genetic similarity or distance.

Conclusions: The results reported in this study demonstrate the utlity of ISSRs for assessing the genetic diversity in EFSB populations and for providing quantitative estimates of genetic similarities.

Comparative analysis of natural predation on colorado potato beetle eggmasses in cry-expressing experimental fields

Salvatore Arpaia[1], Grazia M. Di Leo[1], Joerg E.U. Schmidt[2]

[1]ENEA, National Agency for New Technologies, Energy and Environment, Rotondella, MT, Italy, [2]ETH, Federal Institute of Technology, Zurich, Switserland

Generalist predators, mainly egg feeders, are the most relevant natural enemies of the Colorado potato beetle (CPB) in Italy. In genetically modified (GM) fields expressing Cry toxins, some of these species could be exposed to the toxins either directly (e.g. via pollen or plant sap), ore indirectly through their preys. This guild may then be important to study potential environmental impacts of GM plants. CPB shows a “bet hedging” strategy for oviposition which enables the species to minimize the risks of progeny loss due to adverse environmental conditions (Voss & Ferro, 1990, Environ. Entomol. 19: 123-129). CPB is known to be sensitive to Cry3b toxins expressed in plants (Arpaia et al., 1997, Theor. Appl. Genet. 95(3): 329-334) while in the Cry1 class, only the Cry01IA1 is reported to be toxic to the larvae upon ingestion (van Frankenhuyzen and Nystrom "The *Bacillus thuringiensis* toxin specificity database" (2002) http://www.glfc.cfs.nrcan.gc.ca/bacillus). Potato and eggplant fields were setup in Southern Italy using GM plants expressing Cry1Ab and Cry3Bb toxins respectively, for two cropping seasons. Natural infestation was recorded. Eight newly laid eggmasses per plot were marked at the beginning of four following weeks. In daily visual samplings, the number of intact or preyed eggs and neonate larvae were counted. Moreover, on twelve randomly chosen plants, the number of eggmasses laid was recorded weekly. The egg predators observed were Nabidae, Miridae, Chrysopidae, Coccinellidae and Anthocoridae. In potato fields (where CPB represented a non-target herbivore), egg laying was similar between transgenic and control plots both in terms of number of eggmasses and number of eggs per mass. Likewise, predation rate was comparable between treatments. In eggplant fields, which expressed CPB resistance, the same results were obtained in the year of higher infestation. In the second cropping season, when CPB population was less abundant, egg predation in Bt-expressing plots was significantly more relevant. According to these results, the ecological function of natural predation on CPB eggs does not seem to be impaired by GM plants.

A short history of the commercialisaition and the benefits of MON810 Bt maize in South Africa

Hendrik Kruger

Monsanto, Johannesburg, South Africa

Over the past decade Monsanto has developed its YieldGard® technology protecting maize against insects, especially Lepidopterians. MON810 was initially intended to control *Busseola fusca* and *Chilo partellus*. However, it was observed that the technology also suppressed *Helicoverpa armigera*. Later, *Sesamia calamistis* was added to the list of target organisms. Testing on MON810 commenced in 1994, application for commercial release was done in 1996 and it was first sold commercially in 1998. Initial growth of MON810 sales was slow due to limited inclusion in the best maize hybrids and low seed availability. In recent years, sales have grown exponentially as these factors were overcome. In spite of financial and other benefits for small scale farmers, market acceptance for them has been low due to factors that will be explained in the presentation. Monsanto intends to introduce better events in the next years to further improve the performance of MON810. The technology still holds significant financial and other value for South African farmers in 2008.

Field tests of neem oil and neem seed water extract for the management of sucking and chewing pests attacking cotton.

Masood Khattak[2], Mohammad Rashid[2], Khalid Abdullah[1]

[1]Agriculture Research Institute, Dera Ismail Khan, Pakistan, [2]Gomal University, Dera Ismail Khan, Pakistan

Field trials were carried out to evaluate the effect of neem (*Azadirachta indica* A.Juss) oil and neem seed water extract on some economically important insect pests attacking cotton.

Neem oil at 1, 1.5 and 2% and neem seed water extract was applied at 1, 2 and 3% were compared with that of synthetic insecticide (Polytrin C® 440 EC) [profenophos + cypermethrin]. The treatments were administered four times during the cotton season and observation were recorded before and after 1, 3, 7 and fifteen days of treatment application. Data were recorded on incidence of whitefly (*Bemisia tabaci* [Hemiptera: Aleyrodidae]), jassids (*Amrasca devastans* [Hemiptera: Cicadellidae], thrips (*Thrips tabaci* [Thysanoptera: Thripidae]) spotted bollworm (*Earias insulana* [Noctuidae: Lepidoptera]) pink bollworm (*Pectinophora gossypiella* (Gelechiidae|: Lepidoptera)) and American bollworm (*Helicoverpa armigera* [Noctuidae: Lepidoptera]

Results indicated Neem oil at 2% and neem seed water extract at 3%significantly reduced the Whitefly, Jassids and Thrips infestation up to 12 days after spray as compared to that in the control. Similar trend in population reduction of sucking pests of cotton was observed after rest of the three treatment applications. Synthetic insecticide proved to be a better than neem based treatments at any interval.

Neem derivatives at higher concentrations badly affected the attack of pink bollworms and at all concentrations the attack of Spotted bollworm 12 days after spray. Plots treated with 1.5 % and 2 % neem oil and 3 % neem seed water extract resulted in to significantly higher yield as compared to that in the control. Polytrin C® 440 EC [profenophos+cypermethrin] in all cases was highly toxic to the test insects as compared to any other treatment.

Integrated management of fruit flies *Bactrocera* sp. (Diptera: Tephritidae) infesting mango (*Mangifera indica*) in Pakistan

Khalid Abdullah[1], Said Khan[2], Masood Khattak[1]

[1]Agriculture Research Institute, Dera Ismail Khan, NWFP, Pakistan, [2]Gomal University, Dera Ismail Khan, NWFP, Pakistan

In a series of experiments, food and sex lure, and neem oil was tested in comparison with untreated check to devise the IPM model for fruit fly management in mango orchards. The assessment was based on percent infestation in dropped and harvested fruits. All treatments were significantly effective than untreated check in controlling fruit fly. Neem oil at 50 ml and 30 ml/l of water were equally effective. Pheromone traps lured with methyl euginol integrated with intermittent food bait of protein hydrolysate application reduced the fruit fly population by 86.48 and 94.18% in dropped and harvested fruits in year-1 and 87.5 and 89.2 in dropped and harvested fruits in year-2, respectively. On the basis of experiments the IPM models were tested on a sizeable mango orchard. The model comprised of 1) installation of sex lure traps (4/acres), 2) Crop Hygiene (CH) [removal of weed flora and fruit fly resting and sheltering places], 3) twice hoeing under the trees; 4) twice intermittent food bait application during the fruiting season. Data revealed that IPM practices reduced the % infestation dropped to 0.4 and 0.8% in dropped and harvested fruits respectively in comparison with that of farmer's practice where it was 7% in dropped fruits and 10.5% in harvested fruits.

Neural circuits in the insect brain

I.A Meinertzhagen

Life Sciences Centre, Dalhousie University, Halifax, NS, Canada,

A well-entrenched theme in insect neurobiology is to uncover neural circuits that underlie clear behaviours such as locomotion, flight, olfaction, vision, and learning and memory. This theme is re-emerging from studies especially on *Drosophila*, in which genetic and molecular tools can, with new imaging technologies, be brought to bear on these old questions. The list of speakers will represent both the established and emerging aspects of our theme, from the perspectives of both wiring and neuromodulation, drawing evidence from different systems and insect species, and from different stages of their development.

Saline tolerance in mosquito larvae

Timothy J Bradley

Dept. of Ecology and Evolutionary Biology, University of California, Irvine, California, United States

The osmoregulatory strategies of the larvae from various species of mosquitoes can be divided into three categories. The most common strategy is that the larvae are restricted to fresh water and always regulate the osmotic concentration of the hemolymph at values around 250-300 mOsm (stenohaline hyper-regulators). These larvae produce an isosmotic urine in the Malpighian tubules, and remove ions in the rectum to produce a dilute urine. The anal papillae are used to absorb ions, particularly sodium, potassium and chloride. A second strategy is that of osmotic regulation in dilute media and osmotic conformation in media more concentrated than 300mOsm (euryhaline osmoconformers). This strategy has been shown to occur in some larvae in the genera *Culex* and *Culiseta*. In highly concentrated media trehalose is used as an extracellular compatible osmolyte while proline is used as both an extra- and intracellular compatible osmolyte. The third strategy is that of osmoregulation in both hyper and hyposomotic media (euryhaline osmoregulators). This strategy has been well studied in larvae from the genera *Aedes*, *Opifex*. *Ochlerotatus*. In these larvae, there is an additional segment in the hindgut that is not found in freshwater forms. This segment serves as salt gland, secreting a concentrated salt solution. The taxonomic distribution of these three strategies and the evolutionary patterns by which they arose will be discussed.

The impact of *Wasmannia auropunctata* on local ant species in its invasive range

Merav Vonshak, Tamar Dayan, Abraham Hefetz

Department of Zoology, Life Science Faculty, Tel Aviv University, Tel Aviv, Israel

Invasive ant species are a worldwide threat to biodiversity. 15 ant species are listed in the IUCN's list "100 of the World's Worst Invasive Alien Species", among them is the little fire ant, *Wasmannia auropunctata* (LFA). Native to South and Central America, it is now spreading around the world. It arrived to Israel about 10 years ago, and to date it is found at least in 15 localities.

Microsatellite analyses revealed that the Israeli population reproduces clonally, and are descendants of a single introduction of one queen and one male; laboratory aggression tests confirmed that the ants form one supercolony. Using pitfall traps and baits we found that at high densities the LFA displaces almost all the local ant species, and it represents 99.05% of the ants' diversity. They also had a significant impact on spiders' abundance, and to a lower level on beetles.

We compared the LFA foraging behavior in the laboratory with that of two other species that are generally displaced by it in the field. Surprisingly in short term studies the LFA proved to be an inferior forager as well as competitor, whether it was present first at the resource, or arrived to it simultaneously with the other species. However, preliminary, long duration, nest-merging experiments revealed that the LFA invaded the opponent nest within a few days and killed the whole nest. We propose that the LFA high reproduction rate and lack of intraspecific aggression as well as its powerful sting, enable the species to reach high densities and thus to displace other ant species.

Overcoming the taxonomic impediment: automating the generation of taxonomic information

John La Salle

CSIRO Entomology, Canberra, ACT, Australia

Global initiatives are now addressing many aspects of managing and delivering biodiversity information using modern technology. However, they are not addressing the heart of the taxonomic impediment: that we have been naming species for over 200 years, and have named less than 20% of species. We do not have centuries to finish the job; we need to create an “orders of magnitude” paradigm shift in taxonomy by automating the process of species discovery and description.

Role of commercial bee-attractants in the pollination and yield parameters of Niger

V Sivaram, .V. Jayaramappa

Laboratory of Biodiversity and Apiculture, Dept. of Botany, Bangalore University, Bangalore, India

Introduction: Honeybees and flowering plants are interdependent and a good example for mutualism and co evolution. Bees are considered as most efficient pollinators in the ecosystem and utilization bees as pollinators for various entomophilous crops is the cheapest method for increasing crop yield. Niger is the principal oil seed and cross pollinated crop.

Methods: The commercial bee attractants like Bee-Q, Fruit Boost and Tuberose floral scent and sugar solution of different concentrations were sprayed on Niger flowers during the booming period in the experimental plot. The number of honeybees visiting the Niger flowers was recorded from 0600 to 1800 hrs by following standard techniques. Data on number of flowers, flower head, seed weight, seed yield, oil content, seed germination were obtained.

Results: Spraying of Bee-Q @ 12.5 gm /l attracted 7.13 honey bees/10 flowers/ 5min and Fruit boost at 0.75ml/l attracted 8.26 honey bees/10 flowers/5 min up to 5^{th} day after spray in blooming stage. Spraying of Bee-Q @ 12.5gm/l produced 30.33seeds/ flower head and Fruit boost @ 0.75 ml/l produced 30.66seeds/flower head against 23.66seeds/flower head in open pollinated plot. Spraying of Bee-Q @ 12.5gm/l produced higher 1000 seed weight of 3.55gms and Fruit boost @ 0.75 ml/l produced 3.63gms against 3.03gms in open pollinated plot. Spraying of Bee-Q @ 12.5gm/l produced higher seed yield of 4.76q/ha and Fruit boost @ 0.75 ml/l produced 4.95q/ha against 2.70q/ha in open pollinated plots. The spray of honeybee attractants did not increase oil content of Niger. However, spraying of Bee-Q @ 12.5gm/l and Fruit boost @ 0.75ml/l has enhanced the germination percentage to 89.33 and 90.33% against 74.66% in open pollinated crop. Spraying of Bee-Q @ 12.5gm/l has enhanced root length to 8.66%, Tuberose floral scented water to 8.75% and Fruit boost 0.75ml/ to 8.81% against 8.25 % in open pollinated plot. Spraying of Bee-Q @ 12.5gm/l has increased shoot length to 8.63%, Tuberose floral scented water to 8.51% and Fruit boost 0.75ml/ to 8.41% against 6.66 % in open controlled plots.

Conclusion: In all the 10 different concentrations of bee attractants, Bee-Q @ 12.5g/l and Fruit Boost @ 0.75 ml/l found to be very effective in increasing seed productivity in Niger.

Species conservation – a time of crisis and opportunity

Sacha Spector

Center for Biodiversity and Conservation, American Museum of Natural History, New York, United States

By most measures insect conservation has yet to fully join the mainstream of global conservation efforts. In addition, new signals both from the field and in the literature suggest that large numbers of insect species are on a downward trajectory toward extinction raising the urgency for increased conservation action on behalf of insects. Species level conservation can provide an important fine-filter safety net for insect biodiversity, particularly given the small ranges and specific habitat needs that characterize many endemic insect species. Efforts to assess and recognize threatened insect species have recently received boosts across a number of sectors of the global conservation arena. Advances in bioinformatics and cybertaxonomy are increasing access to nomenclatural, natural history and distribution data on hundreds of thousands of insect species. Restructuring of invertebrate conservation efforts at the IUCN-World Conservation Union's Species Survival Commission has led to the creation of the Terrestrial Invertebrate Red List Authority, which now provides a very flexible mechanism for accepting and processing conservation assessments of insect species' status. These and other new developments are providing opportunities to take a broad, synthetic view of the tools needed to deal with the threats to insect species.

The Crop Diagnostic Training and Research Center – the place for in-field "hands-on" training for field crop insect pests

Corey K Gerber

Department of Agronomy, Purdue University, West Lafayette, Indiana, United States,

Introduction: The Purdue University Crop Diagnostic Training and Research Center (DTC) is known across the Midwestern US for its unique "hands-on" approach to teaching the art and science of accurately diagnosing agricultural crop and pest problems. Entomology is one of the six key areas the Center emphasizes during educational programs.

Methods: The DTC employs multiple methodologies to enhance the educational learning experience of its clientele. The Center conducts in-field, "hands-on" diagnostic training workshops. During these workshops, DTC clientele learn how to accurately identify insects associated with field crops, diagnose insect injury, evaluate sampling methods and techniques, and are exposed to threshold levels for managing insect pests. Along with the workshops, the Center also developed two widely utilized training publications; the *Corn and Soybean Field Guide* and the *Forage Field Guide*.**Results:** Since the Center's inception, approximately 15,000 individuals have been trained at nearly 450 workshops, which have included over 2,500 presentations by almost 200 university faculty and staff. From 1988 to 2008, over 383,000 *Corn and Soybean Field Guides* have been sold, and since 2004, 9,000 *Forage Field Guides* have also been sold, with an additional 10,000 guides pre-sold for 2008.

Conclusions: Due to the ever changing dynamics of production agriculture in the US, specifically with more and more individuals moving away from the agriculture industry, it is evident based on the trend of DTC activities that this Center is a valuable resource for diagnostic training and education.

Phenology models from day-degrees to complex simulations: how to increase their benefit for integrated production?

Jörg Samietz

Swiss Federal Research Station Agroscope Changins-Wädenswil ACW, Wädenswil, Switzerland

Especially in perennial cultures, forecasting tools to predict insect phenology assure precise timing of pest monitoring and management particularly under integrated production regimes. The aim of such tools should be to establish reliable and readily available information for growers and consultants. Consequently they have to consist of a technical side to establish phenologies or population dynamics and of an end-user side to communicate the according decision support.

On the technical side, since decades temperature sums above theoretical developmental thresholds are used to predicts certain events in the pest life cycle or decisions to be made on base of phenology. Such simple day-degree models rely on linear relationships between temperature and stage specific development rates. Improvements of the precision can be achieved by calculation of temperature sums by following the diurnal cycle with sinus integration or by using temperature data on hourly basis *a priori*. Also temperature sums can be calculated for different stages of the life cycle which allows for a more complex prediction. More sophisticated mathematical tools like time-varying distributed delays allow to include and manipulate variability in development time and assure overlapping generations. Approximation of habitat- or body temperatures and the use of high temperature cut-offs or non-linear rate functions further help to improve the precision of the modelling basis. Multispecies models even allow to predict predator-prey dynamics, pest outbreaks and complex management decisions.

Several examples of different approaches are presented in the symposium on phenology modelling. The recent discussion as final part of the symposium is intended to discuss which developments – especially on the end-user side – are needed in future and where we should invest to increase the positive influence of phenology models and according decision support systems on integrated production in perennial cultures.

Phenology models from day-degrees to complex simulations: how to increase their benefit for integrated production?

Jörg Samietz

Swiss Federal Research Station Agroscope Changins-Wädenswil ACW, Wädenswil, Switzerland

Especially in perennial cultures, forecasting tools to predict insect phenology assure precise timing of pest monitoring and management particularly under integrated production regimes. The aim of such tools should be to establish reliable and readily available information for growers and consultants. Consequently they have to consist of a technical side to establish phenologies or population dynamics and of an end-user side to communicate the according decision support.

On the technical side, since decades temperature sums above theoretical developmental thresholds are used to predicts certain events in the pest life cycle or decisions to be made on base of phenology. Such simple day-degree models rely on linear relationships between temperature and stage specific development rates. Improvements of the precision can be achieved by calculation of temperature sums by following the diurnal cycle with sinus integration or by using temperature data on hourly basis *a priori*. Also temperature sums can be calculated for different stages of the life cycle which allows for a more complex prediction. More sophisticated mathematical tools like time-varying distributed delays allow to include and manipulate variability in development time and assure overlapping generations. Approximation of habitat- or body temperatures and the use of high temperature cut-offs or non-linear rate functions further help to improve the precision of the modelling basis. Multispecies models even allow to predict predator-prey dynamics, pest outbreaks and complex management decisions.

Several examples of different approaches are presented in the symposium on phenology modelling. The recent discussion as final part of the symposium is intended to discuss which developments – especially on the end-user side – are needed in future and where we should invest to increase the positive influence of phenology models and according decision support systems on integrated production in perennial cultures.

The role of Cadherin protein in the mode of action of Cry1A toxins from *Bacillus thuringiensis* is to induce oligomeric structures responsible of pore formation in insect membranes

Mario Soberon[1], Liliana Pardo-Lopez[1], Nuria Jimenez-Juarez[1], Isabel Gomez[1], Sarjeet S. Gill[3], Bruce E. Tabashnik[2], Alejandro Bravo[1]

[1]Instituto de Biotecnología, Universidad Nacional Autónoma de México., Cuernavaca, Morelos, Mexico, [2]Department of Entomology. University of Arizona, Tucson, Arizona, [3]United States, Department of Cell Biology and Neurosciences, University of California, Riverside, California, United States

Bacillus thuringiensis Cry1Ab and Cry1Ac toxins are produced in transgenic maize and cotton to protect crops from insect attack. Cry1A toxins kill lepidopteran targets by a mechanism that involves the sequential binding to multiple receptors in the larvae midgut. First, the Cry1A toxins bind to a cadherin receptor which facilitates removal of N-terminal helix-1 and induce oligomer formation. The Cry1A oligomers then bind to GPI-anchored receptors as aminopeptidase N or alkaline phosphatase, inserting into membranes of midgut epithelium cells creating pores and causing cell burst and larval death. However, it has been proposed that binding to cadherin triggers a signal transduction pathway that leads to oncotic–like cell death. The binding interaction of Cry with cadherin is complex involving three different binding sites. Cry1Ab and Cry1Ac protoxins lacking the N-terminal helix-1were constructed (Cry1AbMod and Cry1AcMod) and their toxicity and mode of action analyzed. *In vitro* oligomer formation assays showed that Cry1Ab and Cry1Ac protoxins produce a 250 kDa oligomer when activated with trypsin in the presence of cadherin repeats CR7, CR11 or CR12 that contain the Cry1A binding sites, in contrast with the production of the 60 kDa monomer when no cadherin fragments were present in the assay. The Cry1AbMod and Cry1AcMod protoxins produced the 250 kDa oligomer when activated with trypsin without any cadherin fragments. Moreover, Cry1AMod toxins killed cadherin-silenced *M. sexta* and Bt-resistant *Pectinophora gossypiella* that had cadherin deletion mutations. In addition mutant Cry toxins affected in oligomerization are non-toxic to *M.sexta* larvae despite the fact that they retain high affinity to cadherin receptor. Our findings show that cadherin promotes Bt toxicity by facilitating toxin oligomerization and not by triggering a signal transduction pathway. The modified Bt toxins may be useful against pests resistant to standard Bt toxins.

A GPI-anchored alkaline phosphatase is a functional receptor of *Bacillus thuringiensis* Cry11Aa toxin in *Aedes aegypti*

Luisa E. Fernandez[1], Jianwu Chen[2], Erandi Lira[1], Salvador Hernandez-Martinez[1], Humberto Lanz-Mendoza[3], Alejandro Bravo[1], Sarjeet S. Gill[2], Mario Soberon[1]

[1]Instituto de Biotecnología, Universidad Nacional Autónoma de México, Cuernavaca, Morelos, Mexico, [2]Department of Cell Biology and Neurosciences, University of California, Riverside, California, United States, [3]Centro de Investigación sobre enfermedades infecciosas, Instituto Nacional de Salud Publica, Cuernavaca, Morelos, Mexico

Bacillus thuringiensis subs *israelensis* (Bti) produces Cry and Cyt toxins active against mosquitoes that are vectors of human diseases. Previous work identified a GPI-anchored alkaline phosphatase of *Aedes aegypti* as a functional receptor of Cry11Aa toxin produced by Bti. Three ALP cDNA sequences were cloned from *A. aegypti* midgut tissue and expressed in *E. coli*. Among these, ALPAR93 protein bound Cry11Aa and Cry4Ba and also a peptide phage (P1.BBMV) that was previously shown to bind the ALP protein identified in *A. aegypti* BBMV and to lower the toxicity of Cry11Aa in bioassays. Binding analysis of ten overlapping ALPAR93 protein fragments with Cry11Aa identified two Cry11Aa binding sites, one of which interacts with Cry11Aa domain II loop alpha-8. Binding competition of Cry11Aa binding to BBMV's showed that recombinant ALPAR93, the two ALPAR93 fragments comprising the binding sites and an anti-ALPAR93 antibody competed binding, Using *in vitro* cultured living midguts, we showed that Cry11Aa toxin specifically killed caeca and posterior midgut cells. The toxicity of Cry11Aa to cultured midguts was competed by P1.BBMV and the anti-ALPAR93 antibody but not by an anti-V-ATPAse antibody. These results show that the ALPAR93 protein is the functional receptor of Cry11Aa involved in toxicity to *A. aegypti* larvae.

Evaluation of Transgenic Bt cotton under Integrated Pest Management

N.V.V.S.D Prasad, N.H.P Rao

[1]Regional Agricultural Research Station, A. N.G. R Agricultural University, Andhra Pradesh, India, [2]AICRP on Biological Control of crop pests, College of Agriculture, A.N.G. R Agricultural University, Andhra Pradesh, India

Introduction: Bt cotton introduction from 2002 in India has resulted in phenomenal increase in cotton production and more economic returns to the farmers. Bt cotton enabled to tackle major bollworms complex but at the same time experienced surge in sucking insect pests activity. Transgenic Bt cotton has been evaluated under integrated pest management regime with emphasis on sucking insect pests.

Methods: Transgenic Bt cotton hybrid and correspondingly non Bt hybrid were grown with IPM components for managing pest complex of cotton in a holistic approach during 2004-2005 and 2005-06 crop seasons. The impact of IPM regime on pest complex, natural enemies and economics of cotton production were evaluated.

Results: Sucking pests were kept under control in both Bt cotton and non Bt cotton by seed treatment of insecticide, stem application of insecticides - a noval approach for suppressing early season sucking pests and growing of intercrops besides need based chemical interventions. Natural enemies in the cotton ecosystem were conserved during the vegetative stage of the crop. Transgenic Bt cotton as a component of IPM strategies proved effective against *Helicoverpa armigera* and *Pectinophora gossypiella* resulting in negligible fruiting body damage and minimum insecticidal interventions and also observed safe to beneficial insects. IPM strategies to Transgenic Bt cotton involved four eco friendly interventions with higher cost benefit ratio, due to reduction in plant protection cost and high seed cotton yield compared to non Bt cotton which required as many as eight insecticidal interventions.

Conclusions: Transgenic Bt cotton cultivation with eco friendly IPM practices plays a vital role in managing sucking and bollworm pest complex of cotton for sustainable cotton cultivation.

Frequency and characteristics of alleles conferring resistance to the Bt toxin Cry2Ab in populations of the non-profile Australian target pest *Helicoverpa punctigera*

Sharon Downes[1], Tracy Parker[1], Rod Mahon[2]

[1]CSIRO Entomology, Australian Cotton Research Institute, NSW, Australia [2]CSIRO Entomology, Black Mountain Laboratories, Australian Capital Territory, Australia

H. punctigera and *H. armigera* are important pests of numerous field and horticultural crops in Australia. While *H. armigera* has developed resistance to virtually every insecticide employed against it, there has been only one report of resistance to any insecticide in *H. punctigera*. In 1996 the Australian cotton industry adopted Ingard® which expresses the Bt toxin gene *cry1Ac* that is specific to Lepidopterans including *Helicoverpa* species. To date, no field resistance to Cry1Ac has been detected for *H. armigera* or *H. punctigera* in Australia. In 2004/05 Bollgard II® (which expresses Cry1Ac and Cry2Ab) replaced Ingard® in Australia, and now comprises 80% of the area planted to cotton. In 2002, we began F_2 screens of field populations of *H. armigera* and *H. punctigera* to investigate the frequency of alleles that confer resistance to Cry2Ab. In both species, these alleles are more common than expected. The characteristics of the first allele detected in *H. punctigera* (denoted HP4-13) will be described. Our current estimate of the frequency of alleles in field populations is 0.0022 (n = 3064 alleles) with a 95% credibility interval between 0.0009 and 0.0042. We have not yet tested whether the 6 isolated cases are allelic. We will discuss the genetics, resistance levels, cross resistance to Cry1Ac, and dominance associated with Cry2Ab resistance in HP4-13, and the relevance of these findings to managing Bollgard II®.

Light brown apple moth in California: ecology, impact and management of a new invader

Nick Mills

Department of Environmental Science, Policy and Management, University of California, Berkeley, United States

The confirmation of light brown apple moth (*Epiphyas postvittana*) in California in March 2007 posed a new threat to the agricultural and horticultural industries of the state, with the potential to cause millions of dollars in damage. It has subsequently been found in 8 San Francisco Bay Area counties and in Monterey, Santa Cruz and Los Angeles counties, and climate matching models suggest that it may have the potential to spread more widely throughout the North American continent. Light brown apple moth originates from southeastern Australia, where it has been recorded from more than 250 plant species including crops, weeds, and ornamentals and thus California provides ample opportunity for establishment of this new pest. Here I review the ecology and phenology of light brown apple moth, its potential ecological impacts in California, and the management options available for this new invader.

Insect community ecology: the challenge of hyperdiversity

Charles Godfray

Department of Zoology, University of Oxford, Oxford, United Kingdom,

Insects that feed on plants, the predacious and parasitic insects that attack them, and the micro-organisms with which they are associated, are some of the most numerous and diverse groups of organisms on the planet. I will explore current ideas about the biological processes that might structure these insect-based communities, giving examples from work on assemblages based on aphids and leaf-mining insects. I will also discuss the particular challenges faced by community ecologists studying hyper-diverse groups such as phytophagous insects.

Biological control of emerging weeds in South Africa: an effective strategy to counter invasive alien plants at an early stage

Andrew McConnachie

PPRI Weeds Lab, Hilton, South Africa

Biological control of emerging weeds (plants in the early stage of invasion) is internationally an uncommon practice due to restricted research funds being allocated to weeds which have already reached detrimental levels. Previously in South Africa, because of limited funds and, as a result, few opportunities to conduct overseas exploration work, researchers have capitalised on their survey trips by collecting potentially useful biological control agents from as many target plants as possible. Earlier exploration for agents against high-priority weeds thus allowed simultaneous collection of natural enemies of low-priority weeds in the same region. Such opportunistic programmes have been beneficial for South Africa in the management of several emerging weeds. Formal classification systems, however, have since been developed in South Africa for the prioritisation of invasive alien plants. In light of this, the 'Working for Water' Programme, the main funding agency for weed biological control research in South Africa since 1996, officially recognised and awarded funds for five emerging weed projects in 2003. Several new weed projects have since been added to this list. This paper reviews the cases where emerging weeds were opportunistically targeted for biological control in South Africa and where successes were achieved; the use of classification systems to prioritise the management of invasive plants; and the progress achieved with the emerging weed projects currently underway in South Africa.

Biological control of emerging weeds in South Africa: an effective strategy to counter invasive alien plants at an early stage

Andrew McConnachie

Islamic Republic of, PPRI Weeds Lab, Hilton, South Africa

Biological control of emerging weeds (plants in the early stage of invasion) is internationally an uncommon practice due to restricted research funds being allocated to weeds which have already reached detrimental levels. Previously in South Africa, because of limited funds and, as a result, few opportunities to conduct overseas exploration work, researchers have capitalised on their survey trips by collecting potentially useful biological control agents from as many target plants as possible. Earlier exploration for agents against high-priority weeds thus allowed simultaneous collection of natural enemies of low-priority weeds in the same region. Such opportunistic programmes have been beneficial for South Africa in the management of several emerging weeds. Formal classification systems, however, have since been developed in South Africa for the prioritisation of invasive alien plants. In light of this, the 'Working for Water' Programme, the main funding agency for weed biological control research in South Africa since 1996, officially recognised and awarded funds for five emerging weed projects in 2003. Several new weed projects have since been added to this list. This paper reviews the cases where emerging weeds were opportunistically targeted for biological control in South Africa and where successes were achieved; the use of classification systems to prioritise the management of invasive plants; and the progress achieved with the emerging weed projects currently underway in South Africa.

Beware of bats, beware of birds: the auditory responses of eared moths to bat and bird predation.

David S Jacobs[1], John Ratcliffe[2], James Fullard[3]

[1]Department of Zoology, University of Cape Town, Rondebosch, South Africa, [2]Department of Neurobiology and Behavior, Cornell University, Ithaca, United States, [3]Department of Biology, University of Toronto at Mississauga, Mississauga, Canada

Introduction: The Allotonic Frequency Hypothesis (AFH) proposes that the preponderance of moths in the diets of some bats (e.g. Rhinolophidae) is the result of these bats echolocating at frequencies outside of the typical hearing range of most moths (approx. 20 – 60 kHz). The broader hearing range of African moths (5 – 110 kHz) suggests that their ears may function at frequencies usually considered allotonic. We investigated 1) whether moth ears were functionally audible to the Cape horseshoe bat, *Rhinolophus capensis* (Rhinolophidae) which echolocates at 84 kHz, and 2) whether moth auditory sensitivity below 10 kHz allows them to detect the rustling noises made by bird predators as they pursued moths through vegetation.

Methods: We used standard neurological preparations of the auditory nerves of moths to measure the auditory sensitivity of moths to rhinolophid calls and the rustling sounds that bird predators made. We also observed whether birds preyed upon moths.

Results: Moths responded both neurologically and behaviourally to the calls of *R. capensis* and the rustling sounds made by birds as they pursued moths.

Conclusion: The AFH cannot explain the preponderance of moths in the diets of rhinolophids and we suggest that the constrained spaces in the cluttered habitat in which rhinolophids forage give moths both less time and less space within which to react to an attacking bat. Furthermore, the high sensitivity of moths to frequencies from 5 – 10 kHz allows them to avoid avian attacks by using responses that have traditionally been considered solely anti-bat behaviour.

Insecticide resistance – can we prevent it?

T Perry, P Daborn, C Robin, P Batterham

Department of Genetics, University of Melbourne, Victoria, Australia

While insecticides remain the primary agent used for the control of most insect pests, the evolution of resistance to any given insecticide seems inevitable. Our capacity to stall or prevent the spread of resistance is minimal because our understanding of insecticide targets and metabolism in pests is rudimentary. Taking the example of the nicotinic acetylcholine receptors, targeted by the neonicotinoids and spinosyns, the potential for resistance prediction and rational insecticide design will be discussed. Taking the example of the Cytochrome P450s, the capacity to use the model insect, *Drosophila melanogaster*, to predict metabolic resistance will be considered.

Chromosomal evolution, molecular phylogeny and trophic affiliation in *Chrysolina* (Coleoptera: Chrysomelidae).

E. Petitpierre[1], Y.E Mikhailov[2], J.A Jurado-Rivera[1]

[1]Dept. of Biology, Univ. of Balearic Islands, Palma de Mallorca, Spain, [2]Dept. of Botany and Forest Protection, Urals State Forestry-Engineering Univ., Yekaterinburg, Russian Federation

The diploid numbers and male sex-chromosome systems have been analysed in seven species of *Chrysolina* mostly from the Urals and Siberia. *Ch. (Arctolina) poretzkyi* and *Ch. (Arctolina) tundralis* have 2n = 26 (Xy_p), *Ch. (Timarchoptera) haemochlora* 2n = 27 (XO), *Ch. (Ovosoma) susterai* 2n = 40 (Xy_p), *Ch. (Heliostola) schewyrevi* 2n = 44 (Xy_p), *Ch. (Crositops) pedestris* 2n = 47 (XO), and *Ch. (Sulcicollis) rufoaenea* 2n = 50 (Xy_p). These findings increase up to 70 cytogenetically known taxa, belonging to 35 subgenera, more than a half of the 65 presently described. Their range of chromosome numbers is very wide, from 2n = 22 to 2n = 50, and four types of sex-chromosome systems have been encountered, Xy_p, XY_p, XY and XO, although the first one is clearly prevalent. The modal haploid numbers are n = 12 found in 39% and n = 20 in 21% of the so far studied species. We assumed previously a chromosomal evolution from the most widespread and common number of n = 12, by frequent increases in different adaptive radiations. To substantiate this hypothesis, a combined molecular phylogeny by Bayesian methods was inferred from the sequences of a 550 bp fragment of 16S, another of 760 bp of cox1 mitochondrial DNA, and one of 362 bp of histone-3 nuclear DNA, in 50 species of 33 subgenera. Many current subgenera are well-supported in the cladogram, but a few might be synonymized on these molecular grounds, namely *Chrysolinopsis* and *Taeniochrysea, Arctolina* and *Pleurosticha, Crositops* and *Paraheliostola,* and *Chalcoidea* and *Pezocrosita* (gr. *convexicollis*). Furthermore, five species of the genus *Oreina* are included with three of *Chrysolina* in a supported clade. Most species with 12 haploid chromosomes and having a trophic affiliation on Lamiaceae plants, appear in the plesiomorphous clades, while those of higher chromosome numbers and living on Scrophulariaceae, Apiaceae, Hypericaceae, Plantaginaceae and Asteraceae, are in apomorphous clades. However, the recruitment of a new plant family for the trophic affiliation in *Chrysolina* was not achieved as an unique event but by several independent events of colonisations, except for Hypericaceae, which were presumably selected in a single lineage. Besides this, the cladograms also suggest, that at least some species with low chromosome numbers, arose from others of higher by centric fusions, contrary to the prevalent trend of increases.

Intrinsic and extrinsic factors in social evolution and the geographical distribution of spider sociality

Leticia Aviles[1], Eric C. Yip[2], Kimberly S. Powers[2], J Guevera[1]

[1]Department of Zoology, University of British Columbia, Vancouver, Canada, [2]Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, United States

Why organisms live in groups and cooperate is one of the central problems in behavioral ecology. Using social spiders as a model system, we illustrate how intrinsic organismal characteristics interact with specific environmental factors to yield social systems in some geographical areas and not in others. We show that social spiders in the genus *Anelosimus* are concentrated in areas where an abundant supply of large insects is available, namely the lowland tropical rain forest up to mid-elevation cloud forests. Field observations further show that as social spider colonies grow in size, prey capture area per spider and thus number of insects caught per capita decline. Where large insects are abundant, the spiders make up for this decline by cooperatively capturing increasingly large insects as colony size increases. The resulting per capita prey biomass intake function is maximal at intermediate colony sizes. Paucity of large insects at high latitudes and elevations, on the other hand, results on biomass per capita being a monotonically declining function of colony size. The varying shapes of the per capita intake functions would explain why *Anelosimus* spiders in the lowland tropical rainforest form large social groups while those at high elevations or latitudes live in small single-family groups that disintegrate prior to reproductive maturity. These findings illustrate the interplay between intrinsic and extrinsic factors---the scaling properties of tri-dimensional spider webs and local insect size distributions, in this case---in shaping social systems and their geographical distribution.

How did the Netherlands handle the risk evaluation of 150 natural enemies in a few months time?

Antoon J.M. Loomans

Senior Scientist, Department of Entomology, National Reference Laboratory, Plant Protection Service, Wageningen, Netherlands,

When designing a general framework for regulation of the import and release of for biological control agents in The Netherlands, we used a so-called quick scan as an initial screening method, based on the available information for known non-target impacts. Except a proper characterization of the agent, evaluation of risks posed to human and animal health this quick scan included an environmental risk assessment as well. Environmental risks posed by introduced species were determined by several ecological factors, such as the potential of the agent to establish, its abilities to disperse, its host range and its direct and indirect effects. We applied the quick scan method, based on the available information of these ecological determinants, to 150 natural enemies currently commercially available in The Netherlands. About 5% of the species were considered too risky for (continuation of) release and 80% were considered safe. For the remaining 15% of the species, information was either still inadequate, inappropriate or lacking to complete the quick scan. However, when no evidence was available on any significant non-target effects, or was not foreseen, it was advised for most species to continue release. As a result, 134 species were placed on a "white list", which will be exempted from further regulatory measures. All other species, BCAs and other beneficial organisms, not exempted or new, need authorization by derogation. For these BCAs a comprehensive full scan method is used as a tool for risk assessment, including all information available or when relevant newly generated information.

Characterization of *Clostridim bifermentans malaysia* that is active to *Anopheline* species.

Supaporn Likitvivatanavong[1], Amy Evans[1], Han Lim Lee[2], Sarjeet S. Gill[1]

[1]Department of Cell Biology and Neuroscience, University of California, Riverside, California, United States, [2]Department of Entomology, Institute for Medical Research, Kuala Lumpur, Malaysia

Formulations of bacterial strains with insecticidal activity have been used for the control of insect pests in public health and agriculture. For example, the dipteran active *Bacillus thuringiensis* subsp. *israelensis* has been used with remarkable success against both *Aedes* and *Culex*, thereby attenuating viral diseases vectored by these mosquito species. Similarly, *B. sphaericus* has been used with remarkable success against *Culex* mosquito vectors. However, the activity of these two bacterial strains against *Anopheles* is not sufficiently high, necessitating the use of recombination technology to develop strains that could be used in the field against anopheline mosquitoes. In contrast, *Clostridium bifermentans* subsp *malaysia* strain has the highest toxicity to *Anopheles* spp. but has no non-target toxicity. We have recently begun characterization of this bacterial strain. Using a variety of approaches we have show the genome of this bacterium is AT rich with a genome of about 4 Mb. No plasmids were identified, indicating the mosquitocidal genes are chromosomally encoded. A number of potentially toxic genes that could be mosquitocidal are present in the genome. The presentation will include a discussion of the genome of this mosquitocidal strain.

Characterization of *Clostridim bifermentans malaysia* that is active to *Anopheline* species.

Supaporn Likitvivatanavong[1], Amy Evans[1], Han Lim Lee[2], Sarjeet S. Gill[1]

[1]Department of Cell Biology and Neuroscience, University of California, Riverside, California, United States, [2]Department of Entomology, Institute for Medical Research, Kuala Lumpur, Malaysia

Formulations of bacterial strains with insecticidal activity have been used for the control of insect pests in public health and agriculture. For example, the dipteran active *Bacillus thuringiensis* subsp. *israelensis* has been used with remarkable success against both *Aedes* and *Culex*, thereby attenuating viral diseases vectored by these mosquito species. Similarly, *B. sphaericus* has been used with remarkable success against *Culex* mosquito vectors. However, the activity of these two bacterial strains against *Anopheles* is not sufficiently high, necessitating the use of recombination technology to develop strains that could be used in the field against anopheline mosquitoes. In contrast, *Clostridium bifermentans* subsp *malaysia* strain has the highest toxicity to *Anopheles* spp. but has no non-target toxicity. We have recently begun characterization of this bacterial strain. Using a variety of approaches we have show the genome of this bacterium is AT rich with a genome of about 4 Mb. No plasmids were identified, indicating the mosquitocidal genes are chromosomally encoded. A number of potentially toxic genes that could be mosquitocidal are present in the genome. The presentation will include a discussion of the genome of this mosquitocidal strain.

Biological study of mealybug, *Nipaecoccus viridis* (Newstead), and possibility of its biological control by *Cryptolaemous montrouzieri* Mulsant in citrus orchards of north Khuzestan

Mohammad Saeed Mossadegh[1], Rahim Eslamizadeh[2], Mehdi Esfandiari[1]

[1]Plant Protection Department, College of Agriculture, Shahid Chamran University, Ahwaz, Islamic Republic of Iran, [2]Safi Abad Agricultural Research Centre, Dezful, Islamic Republic of Iran

Introduction: The mealybug *Nipaecoccus viridis* (Newstead) is one of the major pests of citrus orchards of north Khuzestan province, southwest Iran. Although the pest has many indigenous natural enemies in the region, but it damages the fruits at the early spring due to the low population densities of its natural enemies at this season.

Methods: From November 2005 to March 2007, altogether 1100 ha of citrus orchards were inspected for *N. viridis* infestation. A total of 12000 *Crytolaemous montrouzieri* Mulsant were librated in 5 citrus orchards with 6.7 ha area with heavy infestation from March to July during a period of 2 consecutive years. The developmental period of mealybug and its natural enemies as well as biology and survival of librated Crypt beetles on citrus trees were recorded biweekly in 2 out of 5 citrus orchards. Five citrus trees in each orchard were chosen at random at 5 different locations and sampled at 70, 140 and 210cm above the ground on four different sides of a tree by cutting 15cm branches for further study.

Results: The results indicated that *C. montrouzieri* was able to control *N. viridis* population and produced one spring generation at north of Khuzestan conditions. But, as the temperature increases, its reproduction and activities were suppressed in July.

Conclusion: Apart from the hot summer, the honeydew secreted by *N. viridis* attracts ants and creates a symbiotic behavior between ants and the pest. This symbiotic behavior has a negative influence on biological control by *C. montrouzieri* in citrus orchards of north Khuzestan.

Biological control of *Icerya purchasi* Maskell by *Rodolia cardinalis* Mulsant in citrus orchards of north Khuzestan, southwest Iran

Mohammad Saeed Mossadegh[1], Rahim Eslamizadeh[2], Mehdi Esfandiari[1]

[1]Plant Protection Department, College of Agriculture, Shahid Chamran University, Ahwaz, Islamic Republic of Iran, [2]Safi Abad Agricultural Research Centre, Dezful, Islamic Republic of Iran

Introduction: The cottony cushion scale *Icerya purchasi* Maskell, was observed and identified in June 2003 at severe infestation of citrus trees at Sharaf-Abad in Dezful, north of Khuzestan province and later on a biological control project using *Rodolia cardinalis* Mulsant was worked out from October 2003 to May 2007.

Methods: The Vedalia beetles were reared on mealybug at 27±1°C, 65±5% R.H. and 14:10, L:D. From March to November 2004, beetles were released as adult in groups of 5 or 2-4 larval instars in groups of 10 per tree which was heavily infested with scale. Altogether 1874 adults and larval beetles were librated at 32 times in 21 citrus orchards on area 38 ha. The development and survival of librated Vedalia beetles and larvae on citrus trees as well as adjacent orchards and weeds were recorded weekly. Samples were taken at 70,140 and 210 cm above the ground on four different sides of a tree by cutting 15cm branches for further study.

Results: *R. cardinalis* tolerated the hot summer conditions of Dezful, established at the region, reproduced through all the seasons with its high potential searching capacity (2.5 Km per month) and was able to cleaned 156 ha of very heavily infested of citrus orchards during a period of 9 months. The established Vedalia beetles were appeared in other infested orchards and cleaned up another 1042 ha during 3 years and prevented further infestation by scale to the rest of 4500ha of other citrus orchards.

Conclusion: As *R. cardinalis* has been established in the region, the sever outbreaks of scale in citrus orchards of north Khuzestan is not possible.

Trees or bins? Determining the natal sites of *Rhyzopertha dominica* (F.) using chemical and physical techniques

Rizana M. Mahroof, Thomas W. Phillips

[1]Department of Biological Sciences, South Carolina State University, Orangeburg, S.C, United States [2]Department of Entomology, Kansas State University, Manhattan, K.S, United States,

The relationship between the abundance and occurrence of *Rhyzopertha dominica* (F.), a primary pest of stored grain, in distinctly different habitats is poorly known, and previous work suggests that a primitive wood-boring habit of this bostrchid beetle may persist in natural populations. Movement of insects can be studied using methods of tissue elemental analyses or mark-release-recapture. We used natural stable isotopes and trace elements to track the dietary history of *R. dominica*, as adult insects may retain elemental markers from their larval host plants. Insects collected from the periphery of granaries or inside woodlands in Stillwater, Oklahoma, USA and insects reread on standard diets in the laboratory were used to compare and contrast isotope signatures and trace elements. Insects reared on the C_3 plant-based seeds of wheat or oak showed much depleted $\delta^{13}C$ values (– 23.7 or – 26.2‰, respectively) as opposed to insects reared on seeds of the C_4 corn (– 11.3‰). A majority of the field-collected *R. dominica* showed $\delta^{13}C$ values similar to a C_3 host, however a few insects had $\delta^{13}C$ signatures similar to the C_4 plant-reared insects. Stored grain of C_4 crops were lacking at many of the sample field sites. These results suggest that *R. dominica* occurs on either C_3 or C_4 based hosts in the field, and point to utilization of non-grain C_4 plants as hosts. Trace elemental analyses showed that discriminating trace elements for field collected *R. dominica* were P, Ca, Fe, Zn, and Cu related to different hosts. In this paper we also summarize results on mark-release-recapture studies that suggest variation in dispersal patterns by related to ecologically different field sites.

Breeding systems in social insects: causes and consequences of within colony genetic diversity

Claudia Husseneder[1], Edward L. Vargo[2]

[1]Department of Entomology, Louisiana State University, Agricultural Center, Baton Rouge, L.A, United States, [2]Department of Entomology, North Carolina State University, Raleigh, N.C, United States,

Social insects are one of the most ecologically diverse and successful groups on this planet. The variety and complexity of their colony breeding structures and the causes and consequences of genetic diversity within colonies has been a hot topic in research for many decades. This symposium focuses on the reproductive strategies that determine genetic diversity in colonies and populations as well as on the costs and benefits of genetic diversity. Breeding systems of a wide variety of social insects will be introduced ranging from the social Hymenoptera (bees, ants and wasps) to termites and social spiders.

Insecticidal toxins from *Photorhabdus*: comparative genomics and Rapid Virulence Annotation (RVA).

Richard Ffrench-Constant[1], Andrea Dowling[1], Isabella Vlisidou[2], Maria Sanchez Contreras[2], Nicholas Waterfield[2]

[1]*School of Biological Sciences, University of Exeter in Cornwall, Falmouth, United Kingdom,*
[2]*Department of Biology and Biochemistry, University of Bath, Bath, United Kingdom,*

The genomes of bacteria in the genus *Photorhabdus* encode numerous novel toxins including members of the Toxin complex (Tc) family, Makes Caterpillars Floppy (Mcf) toxins, PirAB toxins and many others. Following the recent completion of two complete genome sequences, one from *P. luminescens* and one from *P. asymbiotica*, we will describe the comparative genomics of toxin encoding genes in these two very different pathogens. We will also discuss what we know about the mode of action of these different toxin classes. Finally, we will describe novel massively parallel screens to perform functional annotation of novel toxin genes in bacteria. We have termed this approach Rapid Virulence Annotation or RVA and its applications to bacteria other than *Photorhabdus* will be discussed.

Invertebrate conservation in British Columbia, Canada

Jennifer Heron

BC Ministry of Environment, Wildlife Science Section, University of British Columbia Campus, Vancouver, B.C, Canada

British Columbia (B.C.) is one of the most biologically diverse provinces in Canada. The province's vast landscapes host approximately 50,000 invertebrate taxa, 40,000 of which are estimated to be insects. Little is known about the life history, distribution and habitat requirements of these invertebrates, thus posing a challenge to conservation planning.

Legislation to protect species at risk has its origins as applied to vertebrates, with conservation assessments made on a species by species basis. Within this current structure, approximately twenty invertebrates from B.C. are federally listed as "at risk", with dozens more to be assessed on the growing list of potentially threatened species. While this approach works for some invertebrate groups, there are other taxa for which this approach is not ideal.

Determining the conservation status of B.C.'s invertebrates and the approaches taken are tasks addressed through multiple levels of government policy and legislation, multi-species and ecosystem approaches through stewardship initiatives, as well as the single species approaches. For example, wildlife habitat features of unique importance to invertebrates at risk (e.g. water springs and rock outcrops) are targeted for protection where the identification of invertebrate taxa is difficult. These features often elude traditional definitions of required habitat, yet may be a key component for a life stage of a species at risk. Ecosystem approaches to conserving invertebrates are addressed through coordinated efforts in the Garry oak and Okanagan desert ecosystems, both areas among the four most endangered ecosystems in Canada. These and other approaches to invertebrate conservation in B.C. are given.

Defining critical habitat for the endangered butterfly Taylor's checkerspot (*Euphydryas editha taylori*), in British Columbia, Canada

Jennifer Heron

BC Ministry of Environment, Wildlife Science Section, University of British Columbia Campus, Vancouver, B.C, Canada

Taylor's Checkerspot is a federally endangered butterfly in Canada, thought to be extirpated until the discovery of a population on Denman Island, British Columbia in 2005. The butterfly is historically known from fifteen locations throughout Garry oak ecosystems in southern British Columbia, and recovery efforts for the Taylor's Checkerspot have focussed on these habitats.

Policy and legislation that protect invertebrate species at risk in British Columbia is relatively new and quickly emerging as a significant challenge to conservation practitioners. A major part of the recovery process involves identifying critical habitat (*habitat necessary for the survival or recovery of a species*) and protection of the species residence (*a dwelling-place occupied or habitually by individuals during all or part of their life cycles*).

There are multiple challenges to defining critical habitat and residence for Taylor's Checkerspot. Legislation for species at risk was designed for the listing of birds and mammals, but each of the four life stages of an insect may have different habitat requirements and habitat may be ephemeral or spatially and temporally difficult to define. Compounding the challenges is a shift in the understanding of what habitat(s) Taylor's Checkerspot requires. Historically, the butterfly was observed within Garry oak and associated ecosystems, including open natural maritime meadows. Yet recent surveys show the adult and larval stages of the butterfly inhabiting young clearcuts, where recent logging activities have created disturbed habitats.

Endocrine and genetic network regulation of social life histories

Gro V. Amdam

Arizona State University, School of Life Sciences, Tempe, Arizona, United States

A mechanistic explanation for the emergence of insect sociality is that regulatory systems present in solitary ancestors are co-opted during social evolution to serve as building blocks for social phenotypes. This hypothesis predicts considerable pleiotropy between physiological and behavioral traits in social species that would mirror trait associations expressed during the life cycle of solitary ancestors. We will review recent results on pleiotropic hormonal- and gene regulatory systems that affect insect life histories, and ask how these systems can contribute to a better understanding of the evolutionary origins and current control of social living.

Return to the little-known planet: species exploration at warp speed

Quentin Wheeler, Virginia M. Ullman

[1]College of Liberal Arts and Sciences, Founding Director of the International Institute for Species Exploration, Arizona, [2]United States, Professor of Natural History and the Environment, Arizona State University, Tempe Arizona, United States

Wake up calls by entomologists Howard Ensign Evans and Edward O. Wilson have not been heeded by the insect taxonomy community. As threats from the biodiversity crisis and an expanding need for reliable taxonomic information for a changing world become clear, so too does the need to take action. A revolution in cyberinfrastructure is taking place that will transform science and engineering. Will insect taxonomy take advantage of this revolution to reinvent and reassert itself as an independent science? Or will it compromise its core theories, missions, and questions under peer pressure to appear modern and compliant with the perspectives of other disciplines? An emerging new field of cybertaxonomy represents a fusion o f the best of taxonomy with cyberinfrastructure and an unprecedented opportunity to reconceive taxonomy for the 21st century. Insect taxonomists need not accept either the constraints of the past nor the compromises of the present in order to advance their science. Decades of compromise by taxonomists, museums and herbaria have failed to advance taxonomy. It is time to set an ambitious insect taxonomy agenda and work together as an international community to design and demand the infrastructure and instrumentation necessary for its success. Outlines of such an agenda are proposed as “Project 2020” with a call to arms.

Identification and population dynamics of mango white scale (*Aulacaspis tubercularis* N. (Hemiptera: Diaspididae) in Tapachula, Chiapas, México

Ricardo Magallanes-Cedeño, Alberto Pérez-Mendoza, Alfonso Pérez-Romero, Javier Paxtián-Hernández, Mario Ernesto Cabrera-Alvarado

Universidad Autonoma de Chiapas, Huehuetan, Chiapas, Mexico

Introduction: To prevent yield losses, many mango growers in Chiapas spray chemicals on the foliage of trees to kill ants, aphids and white scales. Such practice might affect the guild of natural enemies, increasing opportunities of phytophagous insects outbreaks. This study was conducted to acquire fundamental knowledge on taxonomy and population dynamics of mango white scale.

Methods: Weekly samplings were taken during 2005 in a mango orchard without insecticide sprays 9 km NW of Tapachula, Chiapas; the sampling unit was a branch including pre-flowering buds; four of these branches were sampled in each of ten trees to complete a sample size of 40. Alive and dead white scale colonies observed on leaves, stems or fruits were registered; also a record was kept on numbers of predators observed during each inspection.

Results: White scale specimens observed in the field corresponded to description of *Aulacaspis tubercularis* N., (Hemiptera: Diaspididae). Population of white scale increases sharply at beginning of year taking advantage of the dry season, however a guild of predators including syrphids, coccinelids and mostly chrysopids synchronizes well with white scale colonies, preventing outbreaks. Numbers of both white scales and predators drop drastically during the rainy season.

Conclusions: The community of natural enemies in mango plays a major role in the regulation of mango white scale abundance: Considering the biotic potential of white scale, an inadequate use of pesticides might initiate a serious ecological disturbance if numbers of predators are diminished.

Acknowledgments: This research was partially supported by CONACYT and SAGARPA, Mexico.

Digestive enzymes of insects and the insecticidal effect of plant ureases

Celia R. Carlini

Dept. of Biphysics & Center of Biotechnology, Univ. Federal do Rio Grande do Sul, Porto Alegre, RS, Brazil

Ureases (EC 3.5.1.5) are enzymes that hydrolyze urea to ammonia and CO_2, widespread in plants, fungi and bacteria. Little is known about the physiological role of ureases in plants. We have shown that ureases display antifungal and insecticidal properties independent of their ureolytic effect. The kissing bug *R. prolixus,* and crop pests such as the cowpea weevil *C. maculatus,* the green stinkbug *N. viridula* and the cotton stainer bug *D. peruvianus* died after feeding on diets containing jackbean or soybean urease at 0.1 % w/w level. These insects have cathepsins as digestive enzymes, which hydrolyze urease to release an internal entomotoxic peptide of 10 kDa. Changes in the profile of digestive enzymes during life cycle of hemipterans correlate with their susceptibility to ureases. No effect was seen in insects relaying on trypsin-like digestive enzymes, which apparently destroy the proteins. A recombinant urease-derived entomotoxic peptide was produced in *E. coli*. Besides showing toxicity to hemipterans, the recombinant peptide was also lethal to the fall armyworm *S. frugiperda*, which is not affected by intact ureases as it has trypsin as digestive enzyme. Bioassay using leaf discs of transgenic tobacco expressing this peptide were also toxic to *S. frugiperda*. The recombinant peptide showed no toxicity after intraperitoneal injection in mice or given intragastrically to neonate rats. We conclude that ureases probably participate in plant defense against insect predation. The potential use of these proteins and derived peptides as bioinsecticides or a putative transgene to engineering insect resistance into plant is presently under consideration.

Individual reproduction in stingless bees (Meliponini)

Vera Lucia Imperatriz Fonseca, Dirk Koedam

University of S. Paulo, Sao Paulo, Brazil

Stingless bees are eusocial, monandric and feed their brood cells with a liquid larval food before the queen oviposits in them. Since Sakagami & Zucchi (1963), the worker oviposition at the presence of the queen showed that the comb was the main place where interactions and conflicts occur. The provisioning and oviposition processes (POP) were studied for several species, and a special attention was given to the trophic eggs laid by the workers, always in a standard sequence for each species concerned. In these studies sealing of the cells received a few attentions, and reproduction by the workers was confused several times in literature with their ability to lay trophic eggs. To improve our knowledge of maternity of males, molecular studies of the males produced in the colonies and behavioral studies considering individual marked bees working in the combs were developed. Here we will summarize what we know from molecular studies and from studies of individual participation of workers in POP, focusing provisioning and sealing of the cells, as well as individual reproductive behavior by workers of *Melipona bicolor bicolor*, including the dynamics of laying trophic or reproductive eggs.

Collaborating in pollination science

Connal Eardley[1], Lucie Rogo[2], Michael Ruggiero[3], David Schindel[2], Scott Miller[2], Laurence Packer[4], Barbara Herren[5]

[1]Agricultural Research Council, Pretoria, South Africa, [2]The Consortium of the Barcode of Life, Washington, United States, [3]Integrated Taxonomic Information System, Washington, United States, [4]York University, Toronto, Canada, [5]Food and Agricultural Organization of the United Nations, Rome, Italy

A pre-congress workshop was held on July 1-4, 2008 in South Africa to assemble 40 scientists, research managers and postdoctoral graduate students mostly from the United States and Africa. A variety of bee research initiatives were represented. A special emphasis of the workshop was exploring collaborative opportunities with institutions in the USA, with partial support from the US National Science Foundation. Major programs represented were the African Pollinator Initiative, Consortium of the Barcode of Life, GBIF Global Pollinator Species Campaign, Integrated Taxonomic Information System, and the Global Pollination Project of the Food and Agricultural Organization of the United Nations. These initiatives, and others represented, have different but complementary and overlapping goals, stemming from the central role that taxonomy plays in each of them, and their concern for declining bee populations.

The workshop brought together basic and applied scientists, taxonomists and ecologists, bioinformatics specialists, and scientists involved in DNA-based methods and database management. Participants discussed shared goals, challenges and opportunities in bee science. They also developed specific actions and recommendations for a global campaign to create and make available taxonomic data on the world's bees and other pollinator species. One important component of the campaign would be the improvement of bee collections in Africa. Mechanisms to foster interaction and improve pollinator biodiversity conservation were proposed, collaborative research concept papers developed, and training needs identified.

The challenges of commercializing microbial pest control agents in the U.S.

Stefan Jaronski

Northern Plains Agricultural Research Laboratory, Agricultural Research Service of the U.S. Department of Agriculture, Sidney, M.T, United States.

Despite considerable research effort in both public and private sectors in the United States, only a small number of microbial pest control agents, aside from *Bacillus thuringiensis*, have been successfully commercialized. None has had a major impact on American agriculture (I am ignoring Bt-transformed crops because these are not microbial agents). This lack of salient success, despite the ostensibly obvious need for alternatives to chemical pesticides, can be ascribed to numerous causes. A dearth of candidate microbials has not been the problem, nor have insurmountable technical challenges. Rather the main obstacles have been socio economic. The momentum of commercialization has been in the hands of small, venture-capital biotech companies, many of whom have had precarious, often fatal, financial footing, and not with the larger, more stable agricultural companies. My premise for discussion is that two factors – the U.S. regulatory environment and a U.S. economic system heavily dependent on private venture capital and expectations of short-term profitability -- structure the size of commercial microbial enterprises, and, fundamentally force them to a size large enough that high efficiency, low labor input production is necessary. Low-tech, labor intensive systems are not feasible for the size of business needed for long term survival in the U.S. Are there other models for implementation? More fundamentally, microbials have not reached full potential, because historically they have been developed in a chemical rather than an holistic, biological paradigm. This chemical paradigm, the mainstream American agricultural orientation, is often commercially fatal for microbials given their inherent, biological characteristics.

A tool to assist with invasive pest recognition

Glynn Maynard, Ken Walker

Australian Government, Department of Agriculture, Fisheries and Forestry & CRC National Plant Biosecurity, Canberra, Australia

The best biosecurity measures are aimed at keeping invasive species offshore or away from the borders. To do so, invasive species need to be able to accurately and efficiently recognised, both outside and inside a country. Most of this task falls to diagnosticians working within a localised fauna. Also, diagnosticians support surveillance and monitoring programmes, hence need information and images to facilitate reporting on submitted specimens. Added to the complexity of this task are two factors: first, the majority of invasive pests encountered are not local, hence diagnosticians often require a world-wide knowledge of the invasive pests; and second, there is a worldwide decline in the availability of diagnosticians and taxonomists for invasive pests.

To address these issues a virtual Pest and Disease Image Library (PaDIL) has been developed. PADIL (http://www.padil.gov.au/) is a website that provides high quality, colour, diagnostic images and information on invasive pests (ie. taxonomy, distribution, hosts). No software downloads are required to make full use of the site. The software allows the user multiple query points and the ability to build user-defined image tables which combine characters chosen by the user. PaDIL is freely accessibly and the images are available for non commercial use. Currently, it includes 1200 pests. Australia has developed PaDIL to enhance its biosecurity capability with the recognition of invasive species domestically and internationally.. Although the primary user audience is phytosanitary diagnosticians, the image-based website can be easily used by specialists and non-technical persons in all areas of prevention of invasive species.

Identification and population dynamics of mango white scale (*Aulacaspis tubercularis* N. (Hemiptera: Diaspididae) in Tapachula, Chiapas, México

R. Magallanes-Cedeno, A. Perez-Mendoza, A. Perez-Romero, J. Paxtian-Hernandez, M.E. Cabrera-Alvarado

Cuerpo Academico Consolidado de Proteccion Vegetal, Facultad de Ciencias Agricolas Campus IV, Universidad Autonoma de Chiapas, Huehuetan, Chiapas, Mexico,

Introduction: To prevent yield losses, many mango growers in Chiapas spray chemicals on the foliage of trees to kill ants, aphids and white scales. Such practice might affect the guild of natural enemies, increasing opportunities of phytophagous insects outbreaks. This study was conducted to acquire fundamental knowledge on taxonomy and population dynamics of mango white scale.

Methods: Weekly samplings were taken during 2005 in a mango orchard without insecticide sprays 9 km NW of Tapachula, Chiapas; the sampling unit was a branch including pre-flowering buds; four of these branches were sampled in each of ten trees to complete a sample size of 40. Alive and dead white scale colonies observed on leaves, stems or fruits were registered; also a record was kept on numbers of predators observed during each inspection.

Results: White scale specimens observed in the field corresponded to description of *Aulacaspis tubercularis* N., (Hemiptera: Diaspididae). Population of white scale increases sharply at beginning of year taking advantage of the dry season, however a guild of predators including syrphids, coccinelids and mostly chrysopids synchronizes well with white scale colonies, preventing outbreaks. Numbers of both white scales and predators drop drastically during the rainy season.

Conclusions: The community of natural enemies in mango plays a major role in the regulation of mango white scale abundance: Considering the biotic potential of white scale, an inadequate use of pesticides might initiate a serious ecological disturbance if numbers of predators are diminished.

Molecular analysis of predation and parasitism: problems and future directions

William O.C. Symondson

Reader in Invertebrate Molecular Ecology, Cardiff School of Biosciences, Cardiff University, Cardiff, United Kingdom

This Discussion session is designed to give everyone the opportunity to exchange ideas, to highlight problem areas, to cement collaborative links and to discuss future directions and opportunities within this field. Issues raised in the preceding talks can be discussed at greater length, clarifying technical issues of interest to those new to the field. New approaches, particularly those involving quantitative and multiplex PCR, can be evaluated. We can discuss the need for databases of primers of known specificity. The complexity of ecological studies that can be attempted will increase with sequence and primer databases, allowing us to study not just rates of predation on single prey species but also how whole food webs interact. Finally we should identify opportunities for collaborative research projects, exchanges of personnel and training.

The commercialisation of microbial biocontrol agents

Peter Lüth

Prophyta Biologischer Pflanzenschutz GmbH, Malchow/Poel, Germany

Introduction: Many good scientific results do not reach the market. The reason for this unsatisfying situation is that the scientists often completely neglect the economics of a new biocontrol system. For this reason, we find it necessary to release some economic data to the scientific community regarding the development of new microbial biocontrol agents.

Methods: The production, registration and marketing process has been analysed concerning the costs required to bring a microbial biocontrol agent onto the market.

Results: The cost structure of a company is well known. Only one part of the total costs originates from the production process. But all the other costs, such as development costs (including registration costs and licence fees), overhead costs and marketing and distribution costs also need to be considered. Finally, a profit must be added. So, considering all of these positions, the manufacturing of the final product, containing a particular amount of microbial cfu (e.g. fungal spores), may cost EUR 5000 per batch (one fermenter run). The distribution of the product through 2 to 3 distribution levels may cost another EUR 7500 per batch (150 %). Now, the size of the acreage which could be treated with one production batch is very important to calculate the economic feasibility of the product. At a price for the competitive product of EUR 50 per hectare, an area of at least 250 hectares would be necessary to make the product cost efficient. In other words, it makes a big difference whether you can produce 10^{13}, 10^{14} or 10^{15} cfu per batch, and whether you need 10^{11}, 10^{12} or 10^{13} cfu per hectare to ensure reliable pest control. In addition, the market must be large enough. If it is too small, a company will never be able to recoup the development costs. These costs, including the licensing costs for the microbial strain, the costs for the development of an appropriate fermentation and formulation technique, the registration costs, including all efforts needed to prove the efficacy of the new product in different countries, on different crops and under different conditions, may easily amount to EUR 1,000,000. Consequently, it makes no sense to develop a biocontrol agent for only one country, to be used on a minor crop.

Conclusions: When starting a comprehensive and cost-intensive project to develop a new biocontrol agent, 4 important parameters should be ascertained first: The size of the market, the price of the competitive chemical products, the amount of cfu which can be produced per fermenter, and the amount of cfu needed to ensure reliable control. Knowing these parameters, one can easily assess whether a potential new product would be marketable or not.

The entmofauna of Greenland and its zoogeographical status

Jens Bøcher

Natural History Museum of Denmark (Zoology), University of Copenhagen, København, Denmark

Greenland is an arctic area with a comparatively depauperate biota, the origins of which have been a subject of much interest and debate for more than a century. The expectation that the distribution and abundance of insects and arachnids at high latitudes will prove particularly susceptible to global climate change has recently added extra momentum to studies of the Greenland entomofauna, giving an updated stock-taking and continuous inventory of this fauna high priority. As a basis for such work the compilation of an identification manual of this fauna has been undertaken by the Entomology staff of the Natural History Museum of Denmark in collaboration with a large international specialist team. The revision of available museum holdings and new field work carried out in preparation for this publication have provided massive new information about the composition and distribution patterns of the Greenland entomofauna, now known to consist of about 1100 species.

Geological evidence points to a ”tabula rasa” at the height of the last glaciation, so that all Greenland taxa had to immigrate during the only 10.00 years of the Holocene. In spite of the position of the island, close to the North American continent, the Greenland faunas of particularly soil-bound taxa like Coleoptera, Collembola, Oribatida and Mesostigmata have sizable components of species of Palaearctic origin. A number of explanations of this strong Palaearctic element in the Greenland biota have been suggested, and these will be discussed in the light of the extensive new data and evidence from recent palaeo-entomological work.

Globins in *Drosophila*: oxygen carrier, ROS detoxifier or else, contd.

Thomas Hankeln[1], Eva Gleixner[1], Stefan Zimmerling[1], Thorsten Burmester[2]

[1]University of Mainz, Mainz, Germany, [2]University of Hamburg, Hamburg, Germany

Introduction: Respiratory proteins have been considered unnecessary in most insects, which do not dwell in hypoxic habitats. However, our survey has revealed that globins are a natural constituent of the insect gene repertoire. In Drosophila, three globin genes of unknown function have been identified. This presentation continues abstract no. 3243. Methods: see above

Results: see above

Conclusions: see above

Status of the market, commercialization and opportunities for biological insecticides

Pam Marrone

Marrone Organic Innovations, Inc. (MOI), Davis, CA, United States

More than 50% of human pharmaceuticals are derived from natural products from microorganisms and plants, while only 11% of pesticides are derived from natural products. Biopesticides are reduced risk products based on biological or naturally derived chemistry. They are either microbial pesticides or biochemical pesticides (plant extracts, pheromones, etc.). The global chemical pesticide market is approximately $30 billion and is flat to declining, while the market for biological pesticides and organic food is growing at 20% per year. By combining performance and safety, biopesticides offer value through a variety of benefits, some generally not realized by conventional pesticides:

- Better yields and quality when incorporated into the pest management system
- Provide customers the flexibility of minimum application restrictions (spray in the morning and be back in the field in the afternoon)
- Novel and complex modes of action that reduce the risk of pest resistance
- Provide human and environmental safety benefits
- Provide unique solutions for organic crops
- Environmentally friendly and sustainable production processes (use of renewable raw materials vs. fossil-fuel dependent synthetic processes)
- Accelerated time-to-market. (3 years versus ten years for synthetic chemicals)

What new bioinsecticides have come to market since Bt? What market opportunities are there for new insecticides? What new products are on the horizon?

At Marrone Organic Innovations, we are developing two new insecticides, one from plants and one from a new species of bacteria. For our microbial natural product screening, we isolate and screen naturally occurring microorganisms to identify those that may have novel, effective and safe pest management characteristics. We then employ natural product chemistry to analyze and characterize the compound structures of selected microorganisms to identify product candidates for further development and commercialization. We optimize the pesticidal natural product compounds during fermentation of the microorganism, and develop analytical methods to these compounds. We are isolating and testing bacteria (not Bt), fungi and actinomycetes against insects.

Opportunities for biological and biologically-derived insect control products in the global marketplace

Prem Warrior

Bill & Melinda Gates Foundation, Global Development Program, Seattle, WA, United States

The recent spike in food prices is driving millions of poor people around the world deeper into hunger and poverty. The crisis is threatening political and financial security globally. Commercial and non-commercial organizations around the world are attempting to address this crisis using a variety of tools – both short and long term. The need to enhance food production as well as to protect and preserve the produce is urgent. Commercial products of biological origin continue to play a critical role in the management of insect pests and plant diseases. While product formulations based on *Bacillus thuringiensis* dominate the field of biological insect control, efforts at development and commercialization of plant or microbial products continue at various laboratories around the world. The key to development and successful commercial products lies in (a) defining specific niche markets (b) identification of specific agents/organisms capable of affecting critical stages in the life cycle of the insect pest (c) development of commercially viable and sustainable production processes in fermentation and formulation delivery systems and (d) sound understanding and downstream communication all the way to the grower level about the specific mechanisms of action and use methods. This discussion on key attributes of bioinsecticide development will also address some of the critical issues in global agriculture.

Stingless bees and the reproductive ground plan hypothesis

Klaus Hartfelder

Depto. Biologia Celular e Molecular e Bioagentes Patogenicos, Universidade de Sao Paulo, Ribeirao Preto, Brazil

Recent results on the physiology of honey bees have contributed to firmly establish the reproductive ground plan hypothesis as a major explanatory framework for reproduction and division of labor in the castes of eusocial Hymenoptera. Stingless bees, the largest group of eusocial bees, are an excellent resource for comparative studies due to their variability in natural histories and life history strategies. I will provide an overview on what is known about physiological parameters related to reproduction and division of labor in this group. The comparison of vitellogenin expression in three meliponine species suggests divergence in regulatory mechanisms that directly relate to the mode of worker reproduction. Furthermore, juvenile hormone and ecdysteroid titer analyses in adult queens and workers of *Melipona quadrifasciata* indicate a lack of function for these hormones in division of labor. Comparing these data with honey bees and bumble bees may shed light on how evolutionary trajectories in caste physiologies can be viewed under a reproductive ground plan perspective.

Control of the African stalk borer (*Eldana saccharina*) by expression of a truncated *Bacillus thuringiensis cry1Ac* gene in the sugarcane endophyte *Gluconacetobacter diazotrophicus*

Gustav Bouwer

University of the Witwatersrand, School of Molecular and Cell Biology, Wits, South Africa

Introduction: The potential of controlling the sugarcane pest *Eldana saccharina* with a *Gluconacetobacter diazotrophicus* strain expressing a *Bacillus thuringiensis* insecticidal crystal gene (*cry1Ac*) was evaluated.

Methods: A novel truncated *cry1Ac* gene construct was created. The *cry1Ac* construct consisted of a synthetic ribosome recognition site, a truncated *cry1Ac* gene, and a synthetic stop codon. To confirm the functionality of the *cry1Ac* construct, the construct was cloned under control of the T7 promoter of the expression vector pDEST14 and *Escherichia coli* BL21-SI cells were transformed with the resultant plasmid. After evaluating the functionality of the construct in *E. coli* BL21-SI using SDS-PAGE and Western blotting, the *cry1Ac* construct was cloned downstream of the kanamycin resistance promoter of the broad host-range plasmid pKT230 and *G. diazotrophicus* PAl 5 cells were transformed with the resultant plasmid.

Results: SDS-PAGE and Western blot analysis confirmed the functionality of the *cry1Ac* construct in *E. coli* BL21-SI. In contrast to untransformed *G. diazotrophicus* PAl 5 cells, *G. diazotrophicus* PAl 5 cells transformed with pKT230 carrying the *cry1Ac* construct were toxic to *E. saccharina* larvae.

Conclusions: On the basis of the mortality and cessation of feeding observed during bioassays, *G. diazotrophicus* PAl 5 cells expressing a truncated *cry1Ac* gene were toxic to *E. saccharina.* The study suggests that it may be possible to control *E. saccharina* by expression of a truncated *B. thuringiensis cry1Ac* gene in *G. diazotrophicus*.

Recent increase of water hyacinth in Lake Victoria and reduction of lake water level increased breeding habitats for *Anopheles funestus*

Noboru Minakawa[1], Gorge Sonye[2], Gabriel O. Dida[3], Kyoko Futami[1], Satoshi Kaneko[1]

[1]Institute of Tropical Medicine, Nagasaki University, Nagasaki, Japan, [2]International Centre for Insect Physiology and Ecology, Mbita, Kenya, [3]School of Public Health, Maseno University, Maseno, Kenya

Introduction: The water level of Lake Victoria has fallen more than 1.5 m since 1998, and a narrow strip of land emerged along the lakeshore. Water hyacinth increased considerably in the lake after the heavy rainfall in 2006. This study examined whether these environmental changes increased habitats for malaria vectors in the lake basin.

Methods: Stagnant water habitats were examined for presence of malaria vectors (the *Anopheles gambiae* complex and *A. funestus*) in the north-eastern part of Suba district in western Kenya in 2008. Masses of water hyacinth along the lakeshore were also examined. House resting malaria mosquitoes were sampled in the villages along the shore. Locations and numbers of breeding habitats were compared with those of 1999. The density of house resting mosquitoes was also compared with that of 1999. Spatial relationships between breeding sites and mosquito densities were examined.

Results: Several breeding habitats for malaria vectors were found in the newly emerged land. It was confirmed that *A. funestus* also inhabits in the lake water with water hyacinth. There were more aquatic habitats in 2008 compared with 1999. The proportion of *A. funestus* to the *A. gambiae* complex in 2008 was significantly higher than that of 1999. The abundance of *A. funestus* in houses was negatively correlated with the distance to the habitats in the newly emerged land and water hyacinth.

Conclusion: The recent increase of water hyacinth in Lake Victoria and reduction in the water level created more breeding habitats for *A. funestus*.

Plant biosecurity capacity to protect national and internal borders against invasive insects

David C. Nowell

IPPC Secretariat, Agriculture and Consumer Protection Department, Food and Agriculture, Organization of the United Nations, Rome, Italy

Invasive insects have had, and still have, a very significant negative economic, social and / or environmental impact. Such impacts in agriculture are usually quantifiable as loss of production or financial losses (incursions can have a major economic impact on market access and trade), many other impacts such as environmental and social impacts are less easily quantified. It is economically and ecologically far more cost effective to prevent pest entry into a country, than trying to manage or eradicate the pest after it has established.

Although national legislative and institutional frameworks, based on the International Plant Protection Convention (IPPC), are necessary for a *Biosecurity* system to function, science provides the foundation for this process. However, the biology, ecology or impacts of many invasive insects are often not completely understood making the accurate assessment of risk and the development of mitigation options difficult. Management tools to support this process are often limited or poorly developed. Anticipated climate changes will ensure that we have to revise all current risk assessments and mitigation measures as the environment changes. Pivotal to managing increasing challenges by invasive insects are international cooperative approaches. The IPPC is developing standards for countries to use in trade, as well as building the capacity to implement these on a worldwide basis.

We need to find new ways of working more efficiently (e.g. risk assessment and emergency response), greater integration and coordination (e.g. public, academic and private research), improved communication and transparency, increased cooperation (e.g. surveillance, diagnostics and reporting), and develop new tools (e.g. diagnostics and treatments).

Diversity patterns of African Galerucinae (Chrysomelidae)

Thomas Wagner

Universität Koblenz-Landau, Institut für Integrierte Naturwissenschaften, Koblenz, Germany

Afrotropical species of the most diverse group of the Galerucinae (Chrysomelidae), that includes taxa which have been traditionally assigned to the “Monoleptites”, were recently revised. Many taxonomic changes became necessary since the generic allocation of many taxa was mainly typological and also the original species descriptions, which were mainly published between 1870 and 1950, based on a typological species concept. After the taxonomic revision, the phylogeny of these leaf-beetles could be studied on base of external and genital characters, as well as molecular data for a better characterization of species and monophyletic groups.

After revision of about 65000 specimens, mainly of species-rich groups such as *Monolepta*, *Candezea, Bonesioides, Galerudophia, Afrocrania, Afromaculepta* and *Afrocandezea* detailed data on distribution patterns are now available for the first time. Centers of diversity are the montane regions along the Albertine and the East African Rift System as well as isolated montane areas in Cameroon, the Eastern Arc Forest in Tanzania and montane regions in southeast South Africa. Speciation processes of the mainly forest dwelling species have been probably strongly influenced by habitat isolation in forest refugees during the quaternary period.

A gene for social parasitism in honeybees

Michael Lattorff

Institut für Zoologie, Martin-Luther-University Halle-Wittenberg, Halle, Germany

Social parasites exploit the social ressources of their hosts. Often, social parasites are close relatives of their hosts, also known as Emery's rule. Hence, social parasites do not differ substantially from their hosts with respect to their genes and genomes.

The Cape honeybee, *Apis mellifera capensis*, is a particularly suitable system to investigate the genetic basis of social parasitism. In contrast to all other subspecies of the honeybee, workers of *A. m. capensis* are able to produce female offspring by thelytokous parthenogenesis. Furthermore, they are able to mimic queens with respect to behaviour and physiology. They show a high potential for fast ovary development and usually are able to produce queen-like pheromone bouquets in large quantities.

We used backcrosses between *A. m. capensis* and *A. m. carnica* to investigate the genetic basis of the type of parthenogenesis as well as the ovary development and the pheromone biosynthesis.

Using more than 500 microsatellite markers we were able to identify a single genomic region, that is highly associated with the type of parthenogenesis. Moreover, the queen-like pheromone production and the speed of ovary activation are linked to the type of parthenogenesis suggesting that the very same gene influences these three different phenotypes. Within the candidate region we could identify 16 genes, of which the transcription factor *gemini* is a very likely candidate for pleiotropically influencing these three phenotypes.

To our knowledge, this is the first report on a single gene that has a high impact on the development of a social parasitic lifestyle.

Dedication to Dr Andrew Spielman

Glen R. Needham

Department of Entomology, Ohio State University, United States

Comments on the contributions of the late Dr Andrew Spielman to research on the biology and control of insect vectors.

How plants use empty flowers to manipulate pollinators

Steven Johnson

School of Biological and Conservation Sciences, University of KwaZulu-Natal, Private Bag X01, Scottsville, Pietermartizburg 3209, South Africa

It has been estimated that one-third of all species in the orchid family have empty (non-rewarding) flowers. Non-rewarding orchids tend to produce fewer fruits per flower than rewarding orchids, thus making it difficult to understand how they gain a fitness advantage from deception of pollinators. In experiments in which we supplemented empty orchid flowers with nectar, bee and fly pollinators visited more flowers per plant. This resulted in increased levels of pollen deposition and removal, and, importantly, an increase in levels of self-pollination. The costs of pollinator-mediated self-pollination for both male and female pollination success can result in selection against rewarding flowers. When pollinators are rare and plant reproductive success is pollen-limited, selection generally favours rewarding flowers despite the costs associated with self-pollination

POSTER PRESENTATIONS

To Search, preferably use the Adobe search facility (under the ‘binoculars’ icon), otherwise press “CTRL” and “F” on your keyboard, type in the keyword then press “ENTER”

POSTER PRESENTATION

An experience of using ecological method for Sunn pests' control in Iran

Mehdi Zarabi

University of Tehran, Tehran, Islamic Republic of Iran

Introduction: Sunn pest, *Eurygaster integriceps* (Hemiptera: Pentatomidae) is an endemic serious pest of wheat in Middle East countries. It has been under insecticides pressure since three past decades in Iran. This situation will lead to appearance of resistant populations.

Methods: In this study, some new ecological approaches conducted as control method instead of using insecticides. For, this purpose, a wheat pilot field near 20 ha, selected in Zanjan province (west of Iran). Middle of this field (near one hectare) designed with 12 strips and the rest of it planted as whole-wheat areas, which surrounded the strip plots. Twelve strips were included six wheat rows (each with 6m wide) and six unplanted band (each with 2m wide, which covered with spring weeds). Sunn population density evaluated two times: in early spring when the adults fly from hibernate localities in mountains to wheat fields and then in mid of summer when the new generation appearance in the fields.

Results: Collected data analyzed and the results showed that there was a significant difference between population densities of adults in strip plots in comparison with the whole-wheat areas. In addition, the nymph's population density decreased in the strip plots.

Conclusions: It seems that the strip cultural design can disrupt the migratory adult's vision while they land successfully in whole-wheat area. This method will help growers to decrease insecticides usage in their fields in early season and certainly will prevent the appearance of pest's resistant populations.

POSTER PRESENTATION

Insect fauna (Psocoptera) in the forests of Croatia

Irma Kalinovic, Vlatka Rozman, Anita Liska

Faculty of Agriculture, University of Josip Juraj Strossmayer in Osijek, Osijek, Croatia

Introduction: Insects of order Psocoptera (psocids) with about 4400 species are worldwide known. In the forests they have a good ecological living area. This note is a reviev of Psocoptera fauna fauna in the forests from the eastern part in Republic of Croatia.

Methods: From different forest trees (leaves and barks) psocids have been collected by beating tray methods and by aspirator or fine brush. All specimens (adults, larvae, nymphs) were preserved in 70% alcohol with glycerol and identified using the key, given by Günther, 1974, Smithers, 1990. Representatives of genera Liposcelididae after maceration method and slides making, were identified by the same key.

Results: During 1975-2005 year on forest trees (Salix alba, Populus alba, P. nigra, Quercus robur, Castanea sativa, Ulmus campestris, Morus sp., Robinia pseudoacaccia, Fraxinus americana, F. excelsior, Tillia sp., Fagus sylvatica, Cathalpa cathalpa, Pinus nigra, Abies sp., Picea sp., Cupressus sempervirens) 3766 psocids individuum, from 8 genera and 25 species were identified. The most numerous was genera Ectopsocidae, with 2 species Ectopsocopsis cryptomeriae, E. meridionalis (72%), than generas Lachesillidae 3 species - 14%, Liposcelididae - 4 species with 4%, Peripsocidae with 3 species - 4%, Psocidae 6 species - 3%, Caecillidae 4 species - 1%. Stenopsocidae 2 species - 1% and Trogiidae 1 species with 1% spreading.

Conclusions: All mentioned investigated Psocoptera taxons are new in the forestes of eastern part of Croatia.

POSTER PRESENTATION

Plants' tolerance to insect pest attack, an effectiveness method for decreasing pesticides application

Mehdi Zarabi

University of Tehran, Tehran, Islamic Republic of Iran

Introduction: Colorado beetle, *Leptinotarsa decemlineata* is a serious pest of potato in cold regions of Iran. Resistant pest's populations released because of using of different insecticides throughout of country. Ecological methods are the best way for control of insect's resistant populations. Among these methods, increasing of tolerance rate in host plants is a practical one.

Methods: In this study, some microelements sprayed against Colorado beetle instead of insecticides usage. For this purpose, a potato field pilot (near one ha) was selected in Zanjan province (west of Iran). Three potato varieties planted in a split plot design as main plots and three kinds of microelements; BMX, Sollopotas and Fosamco sprayed one time based on their commercial introduced amounts (three treatments of fertilizers and one treatment as control plot, which sprayed with water) as sub plots. Then population density of adults and larvae evaluated in different treatments after one week.

Results: Results showed that the plots, which sprayed with Sollopotas and BMX, were free of larvae in comparison of Fosamco plots and control ones. In addition, there was not a significant difference between yields of varieties. Only total yields of two varieties Marfona and Agria were increased up to 14 and 8 ton/ha respectively in plots which were treated by BMX.

Conclusions: It seems that some compounds, which included potassium, can increase the rate of potato tolerance to this pest or the stand plants, which sprayed with these microelements, are not desirable for larvae. In any way, this is a success method for controlling of resistant population.

POSTER PRESENTATION

Temporal patterns of some greenhouse pests in the Netherlands

Jan Kaas

Biopre biological pest control, Langeraar, Netherlands

Introduction: Commercial greenhouses in the Netherlands are subject to a limited number of serious pest species. One of the most destructive key pests is the Western Flower Thrips *Frankliniella occidentalis*. Thrips populations in greenhouses are mainly monitored using yellow or blue sticky traps. Several lepidopteran pests in greenhouses are monitored using low frequency light traps. Pest management decisions are based on the result of these generally weekly measurements.

Methods: For a period of eight years, weekly thrips catches on colored sticky traps were recorded. Also weekly light trap counts of *Sufetula* and *Duponchelia* were made.
Results: A graphical representation of statistics is presented. Periodicity and trends in population numbers are indicated.

Discussion: Thrips numbers follow a clear annual cycle with lower numbers near December and a unimodal or bimodal distribution during the rest of the year. The results of weekly light trap collections of two species of Lepidoptera over several years are presented and discussed. Implications for use in pest prediction models are discussed.

POSTER PRESENATION

Predation potency of the predator *Clitostethus arcuatus* (Rossi) on jasmine whitefly *Aleuroclava jasmini*

Mohammed Z. Khalaf*, Ahmed K.Abed*, Huthaifa M.Al-Rubaie* and Hala T. Omran*

**Integrated pest control research center, Ministry of science & technology, P.O.Box; 765, Baghdad, Iraq*

Introduction: Laboratory studies were conducted to evaluated the predation potency of the predator *Clitostethus arcuatus* (Rossi) (Coccinellidae: Coleoptera) on jasmine white fly *Aleuroclava jasmini* on Citrus.

Methods: Establishment of laboratory culture of *C. arcuatus* was achieved by using eggs, movable nymphs and stationary nymphs of *A. jasmini* as food which is considered the main step of mass rearing, the average number of eggs and nymphs consumptive by the larva and adult of predator were recorded.

Results: Results indicated that larvae of *C. arcuatus* consumed an average of 966.2, 1050 and 460 of eggs, movable nymphs and stationary nymphs respectively during one week period.

In addition, Adult predator consumed an average of 1451 eggs, 980 movable nymphs, 367 stationary nymphs and 115 adults during one week period.

Conclusion: Predator potential as apart of pest management was discussed and results of this study can be used in the practical application of biological control to *A. Jasmini* on citrus.

POSTER PRESENTATION

The effects of sex allele homozygote phenomenon on the performance and honey bee production

Abolfazl Asadi Dizaji, Naser Maheri Sis, Hamideh Moeni Alishah, Eynollah Valizadeh

University, Shabestar, Islamic Republic of Iran

Since the homozygote of sex alleles or inbreeding has a great role in the different characteristics of honey bees colony's like the production of honey, this phenomena has been considered in Mianeh. In order to do this %5 of modern hives were chosen and considered in this area. According to the given method by Rotner. The cells which were free of brood were recorded and considered as index of inbreeding. Also the honey production was measured by weighting the hives. Inbreeding studies showed no significant differences between several of Mianeh so that the percent inbreeding was 9.22, 10.93 and 23.48 for Kandowan, Torkmanchai and Kaghazkonan, respectively. The total mean value in Mianeh was estimated as 15.05%. Mean honey production per hive was 11.9 kg. According to this study there were significant negative relationship between inbreeding and honey production (r=-0.57).

POSTER PRESENTATION

Action threshold for controlling pistachio psylla nymphs (Hemiptera: Psyllidae) on *Pistacia vera* cv. Ohadi

Mohammad Reza Hassani, Gadir Nouri Ganbalani, Hamzeh Izadi, Mahmoud Shojai

Islamic Azad University, Rafsanjan, Iran, Rafsanjan, Iran

Introduction: The pistachio psylla, *Agonoscena pistaciae* Burckhardt & Lauterer is a major pest of pistachio in Iran. The economic injury level is an important practical tool for decision-making in IPM programs. Our objective was to determine economic injury level for *A. pistaciae* on pistachio cultivar Ohadi.

Methods: Different density levels of *A. pistaciae* nymphs were maintained on pistachio trees by application different dosages of insecticides. Psyllid nymph densities were monitored weekly by counting psyllid nymphs per terminal leaflet. At harvesting time, yield of every tree was individually harvested and samples of weight of 1000 nuts measured. Regression analysis was used to determine the relationship between psyllid nymph densities and weight of 1000 nuts. The economic injury level was estimated by using pedigo *et al*., (1986) equation.

Results: The infestation levels of psyllid nymphs were different between treatments at different control levels. The weight of 1000 nuts was significantly affected by number of psyllid nymph. Regression equation obtained to describe the relationship between psyllid nymph densities and yield loss is: $Y= -2.89X+841.21$, $R^2=0.96$. The economic injury level estimated for various combinations of management cost and market value. The economic injury level is a function of market value, management costs and efficiency of insecticide. The economic injury level of pistachio psylla nymph on cultivar Ohadi was ranged from 7.7 to 30.7 psyllid nymphal-days per terminal leaflet.

Conclusion: This information may be considered by pistachio plantation for decision-making and help to reduce costs and insecticides application based on economic injury level.

POSTER PRESENTATION

Mating competitiveness value of the blow fly (OWS), *Chrysomya bezziana,* exposed to gamma rays

Ayad Ahmed Al-Taweel, Layla Jabbar Al-Bahadyli, Udo Feldmann

MoST/Directorate of Agricultural Research & Food Technology, Baghdad, Iraq

Introduction: The OWS, *Chrysomya bezziana* is an obligatory parasite of warm blooded animals and human beings. The total cases reported by Iraqi Veterinarian Service from Sept.1996 till Dec.\2004 was 118497 in addition to 23 cases in human beings, while, 414 and 1998 cases were reported during 2005 and 2006, respectively. Chemical insecticides are usually used to control this pest but unfortunately no success has been obtained. Therefore, SIT was suggested as an effective strategy. One of the aspects of this technique which is supposed to be excellent is mating competitiveness value (CV), therefore, this investigation concentrated on studying the effect of gamma rays on CV of OWS irradiated as 4-5 old pupa with either 30 Gy or 60 Gy.

Method and Results: CV of OWS males and females were measured according to the Fried method (1971). Results showed that irradiated males with 30 Gy and released with unirradiated males and females at different ratios had excellent CV in comparison with those irradiated with 60 Gy, while irradiated females with either 30 Gy or 60 Gy and released unirradiated females and males had poor CV. Finally the CV for irradiated males and females irradiated with 30 Gy and released together with unirradiated males & females had excellent CV in comparison with those irradiated with 60 Gy.

Conclusion: These results were encouraging and useful for suggested programs to use SIT for controlling this invasive pest in the near future.

POSTER PRESENTATION

The relationship between the vine mealybug, their parasitoids and ants in South Africa vineyards

Kwaku Akoming Achiano

ARC, Stellenbosch, Western Province, South Africa

Introduction: The mealybug *Planoccocus ficus* infestation is one of the most serious problems for vine growers in South Africa. It is the major vector of grapevine leafroll and causes direct damage by its feeding and honeydew secretions. The presence of mealybug on exported table grapes may lead to rejection of consignments. The study was to establish the relationship that exists between the vine mealybug, their parasitoids and ants.

Methods: Four wine grape vineyards (± 3 ha each) with a history of mealybug infestation were chosen for studies. Female mealybugs and ants were assessed physically every two weeks. For each vine, the presence/absence of vine mealybug on the stem, lateral branches and leaves were noted. Yellow sticky traps Agribiol® (200 mm X 100 mm) were used to sample parasitoids.

Results: There was a progressive upward movement of the female mealybug from the stem onto the lateral branches and finally on the leaves. Later as the season progressed there was a downward movement from the leaves to lateral branches and stem. The predominant parasitoid encountered was *Anagyrus pseudococci* whilst *Leptomastix dactylopii* and *Coccidoxenoides perminutus* were also observed. The low population of parasitoids lagged behind that of the female mealybugs, whilst the increase in ant numbers was in tandem with increase in the female mealybug numbers. Furthermore, low numbers in ant population coincided with high numbers of parasitoids.

Conclusion: Low numbers of ants must be maintained to ensure high numbers of parasitoids. Farmers should consider augmenting existing natural enemies with commercially available parasitoids.

POSTER PRESENTATION

The presence of a forest affects honey yields: One more reason to conserve forests

Susan Sande[1], Sue Nicolson[1], Robin Crewe[1], Ian Gordon[2]

[1]University of Pretoria, Pretoria, South Africa, [2]International Centre of Insect Physiology and Ecology, Nairobi, Kenya

Introduction: To conserve globally threatened tropical forest ecosystems, community-driven conservation projects including beekeeping have been undertaken. Bees, with their specific requirements for nutrition and nesting, are good indicators of landscape structure and overall biodiversity of a forest, provided the ecological and seasonal patterns are taken into consideration. Although some studies worldwide have been carried out on honey quality and pollination services of bees, with others in relation to forests, none has targeted this question; is honey quality and quantity enhanced by the presence of a forest?

Methods: Beehives situated, 0-1 km, 1-2 km, and 2-3 km away from the forest was selected. Bees are known to forage for up to 5km (Hepburn and Radloff, 1998) and only go further if there is acute shortage of pollen and/or nectar. At each distance a fixed number of hives facing North, South, West and East of the forest was selected.

Results: The yield of honey, especially from top bar hives, decreases at a distance of more than 3km from the forest. The moisture content, pH, free acidity, HMF and proline content did not differ significantly among honey collected from various distances away from the forest.

Conclusion: High species diversity and floral density provide a better food base for bees and naturally sustain a higher population per honeybee colony leading to higher honey yields. We suggest that a maintenance of a high Apiflora species diversity and floral density, which happens naturally inside the forest, can be emulated by farmers in order to ensure high yields away from the forest. A catalogue of such species has also been drawn as a result of this study.

POSTER PRESENTATION

Control of maize weevil *Sitophilus zeamais* (Motsch.) using indigenous plants for stored maize protection in Africa

Donald A. Ukeh[1], Michael A. Birkett[2], John A. Pickett[2], A. Jennifer Mordue (Luntz)[1]

[1]School of Biological Sciences, University of Aberdeen, Tillydrone Avenue, AB24 2TZ,, Scotland, United Kingdom, [2]Centre for Sustainable Pest and Disease Management, Biological Chemistry Department, Rothamsted Research, Harpenden, Herts., AL5 2QJ, England, United Kingdom

Introduction: The repellency potential of ginger, *Zingiber officinale*(Zingiberaceae), West African black pepper, *Piper guineense* (Piperaceae) and alligator pepper, *Aframomum melegueta* (Zingiberaceae) were tested against the maize weevil, *Sitophilus zeamais* (Coleoptera: Curculionidae), in laboratory behavioural assays and under field conditions.

Methods: Using a four-arm olfactometer, single choice bioassays were conducted using 2 g of yellow or white maize or winter wheat seeds, and 2 g *Z. officinale* rhizome, *P. guineense* and *A. melegueta* seeds against 3 d old *S. zeamais* adults. In field trials, 10% (w/w) crushed *Z. officinale* rhizomes, *P. guineense* seeds and a combination of *Z. officinale* and *A. melegueta* (5% each) were admixed with shelled and sun dried maize cobs in baskets and sampled weekly for natural infestation for 12 weeks in traditional granaries.

Results: In laboratory assays, both sexes of *S. zeamais* showed strong attraction to maize and wheat seed volatiles but were significantly ($p < 0.001$) repelled by odours emanating from *Z. officinale* rhizomes, *P. guineense* and *A. melegueta* seeds. In field experiments, crushed *Z. officinale* rhizomes, *A. melegueta* seeds and a combination of *Z. officinale* and *A. melegueta*, significantly repelled *S. zeamais* from traditional maize granaries ($p < 0.001$), with maize seeds giving higher germination from untreated cobs.

Conclusions: Thus, under small-scale farmer conditions, protecting grains with indigenous repellent plants could decrease the quantity of toxic insecticides required, and lead to the development of more sustainable crop protection strategies.

POSTER PRESENTATION

Identification and field evaluation of the sex pheromone of an invasive pest, fall webworm *Hyphantria cunea* in China

Zhongning Zhang, Mowen Su, Yuling Fang

Institute of Zoology, Beijing, China

The fall webworm, *Hyphantria cunea* (Lepidoptera: Arctiidae) as an invasive pest insect was found in china in 1979 and had been introduced into four provinces of north of Chins, such as Beijing, Tianjin, Hebei, Shandong and Shaanxi. Currently, pheromone gland extracts of the pest insect were analyzed by gas chromatography and gas chromatography-mass spectrometry. Based on comparison of retention times and mass spectra of synthetic standards, four compounds were identified as (9*Z*, 12*Z*)-octadecadienal, (9*Z*, 12*Z*, 15*Z*)-octadecatrienal, (3*Z*, 6*Z*, 9*S*, 10*R*)-9, 10-epoxy-3, 6-heneicosadiene and (3*Z*, 6*Z*, 9*S*, 10*R*)-9, 10-epoxy-1, 3, 6-henicosatriene with ratio as 2:33.6:58.4: 6 and the ratio was different as 0.6:6.6:27.9:0.1 in New Zealand. Trapping tests showed that quaternary blend of these compounds was highly attractive to male *H. cunea*. Unitraps baited with the quaternary blend loading of 200-300µg on a gray rubber septum were very effective for monitoring *H. cunea* populations.

POSTER PRESENTATION

Influence of rainfall on the occurrence of adult black maize beetles, *Heteronychus arator* (Coleoptera: Scarabaeidae) in the Eastern Cape of South Africa.

Graham Petty

Institute for Tropical and Subtropical Crops, Bathurst, Eastern Cape, South Africa

Introduction: Because pineapple farmers are no longer permitted to apply long residual chlorinated-hydrocarbon insecticides e.g. Aldrin and Dieldrin, as preventative control measures for Black Maize Beetle, *Heteronychus arator* (Fabricius), the species has assumed greater importance. Predicting the incidence of these pests before they cause serious damage to plantations would therefore be useful to the grower.

Methods: Annual field development of Black Maize Beetles was determined by monthly samplings in a pineapple field. Adult beetles were captured in a Robinson light trap, during their flight period, for 13 years and their numbers studied in relation to the rainfall occurring during the different development stadia of this species.

Results and Discussion: The total number of Black Maize Beetles collected in the light trap during January, February and March, was found to be related to the rainfall which occurred during the lifecycle of the parental (P1) generation of beetles and that of their immature offspring (F1). It is thus possible to predict an outbreak of adult Black Maize Beetles thereby permitting a timeous application of control measures. From a review of relevant literature, possible reasons are given for the effects of either wet or dry conditions, during different stages of development on beetle mortality.

POSTER PRESENTATION

Effect of host density (*Ephestia cautella*, larvae) and exposure period on the efficacy of *Bracon hebetor* under field conditions

Ayad Ahmed Al-Taweel[1], Emad Ahmed Mahmmod[2], Alla Abdul-Alhassan Muhsen[2]

[1]MoST/Directorate of Agric. Res. & Food Tech., Baghdad, Iraq, [2]College of Sci. for Woman, Baghdad, Iraq

Introduction: Iraq produces more than 500000, tons of dates annually during its development fill ripening and collecting it form trees it expected to be infested by date moth belong to Ephestia genus specifically *Ephestia cautella* . this infestation cause problem for marketing processes, therefore insecticides usually used to control this pest but unfortunately it is appeared impossible to control this pest biological control using the larval ecto parasite *Bracon hebetar* is suggested.

Materials and Methods: Experiments were carried out under field condition, *E. coutella* larvae at numbers 10 ,20,30,40 and 50 were exposed to five pairs of *B.hebetor* in an cage of 20×20×20 cm after period of exposure which were 24,48 and 72 hrs . the *B.hebeor* was removed from the cages and they kept in the field after the number of paralyzed *E. cautella* larva were counted these cages were examined daily to count the number of *B.hebetor* larvae, pupae and adults produced. Five replicates for each *E.cautella* larval number and for each period of exposure were made.

Results: It is appeared from the results that the B.hebetor females were very active in paralyzing *E.coutella* larvae at all numbers and period of exposure tested this was noticed from the number of eggs, larvae, pupae and adults of *B. hebtor* produced.

Conclusion: The results suggested the possibility of using *B.hebetor* as an biological agent to control E.coutella in the field or date store within an IPM programmed to control *E. cautella* .

POSTER PRESENTATION

Dragonfly (Odonata) phenology and assemblage response to elevation in a sub-tropical region (South Africa)

Augustine Niba, Michael Samways

[1]Walter Sisulu University for Technology & Science, Mthatha, Eastern Cape Province, South Africa, [2]University of Stellenbosch, Stellenbosch, Western Cape Province, South Africa

Little is known of African dragonfly response to elevational gradients. We studied dragonflies and environmental variables over two years (from September 2001 to October 2003) in a series of reservoirs in KwaZulu-Natal, South Africa, and over an elevational gradient of 100 - 1350 m a.s.l.

The aim was to determine how elevation and climate (as regional processes), as well as local factors, influenced species assemblages and phenology. Seven families and 47 species were recorded. Larvae showed positive correlation in species richness and abundance with increasing elevation, while adult did not.

Ordinations of two odonate sub-orders showed that certain measured site variables strongly explained the main variation in species assemblages. These included local factors e.g. pH, marginal grasses, percentage shade, exposed rock, marginal forest and to a lesser extent, marshes and water flow. These conditions varied from one season to another, being optimal in summer, and minimal in winter, and influenced dragonfly species phenologies accordingly.

However, elevation and climate as regional processes had very little influence on dragonfly assemblages over this 1250 m gradient during the study.

Although there were more widespread and elevation-tolerant species (S=44), these sub-tropical odonate species are similar to their tropical counterparts in that they have long flight periods with overlapping generations. Yet they also showed temperate characteristics by over-wintering principally as larvae.

The national endemics: Pseudagrion citricola and Africallagma sapphirinum only occurred at high elevations, while Agriocnemis falcifera was throughout all elevations, suggesting that regional endemism does not necessarily equate to elevational intolerance. This study also offered baseline information for comparing the effects of future global climate change.

POSTER PRESENTATION

Factors influencing population density of bees in Bwindi Impenetrable National Park, Uganda

Robert Kajobe

National Agricultural Research Organisation (NARO), National Livestock Resources Research Institute (NaLIRRI), Tororo, Uganda

Introduction: In the first study of native African honeybees and honey-making stingless bees in the same habitat, humans and chimpanzees are the primary bee nest predators. This study was carried out in Bwindi Impenetrable National Park, Uganda. The park is a UNESCO World heritage site and contains half the world's population of mountain gorillas. The study was undertaken because little is known about bee ecology in Uganda.

Methods: Fieldwork was guided by the local Batwa Pygmies, the indigenous honey-hunters residing near the park. Sometimes, the dwarf honey-guide *Indicator pumilio*, a tiny bird that is endemic to the Albertine Rift Mountains, helped direct the Pygmies to stingless bee nests. Eighty seven plots were established for the study and two parallel 500 m transects were made in each plot, separated by 100 m. Flying bees were searched for in the plots and at nest entrance tubes on tree trunks.

Results: A total of 5 stingless bees (*Meliponula* and subgenera *Axestotrigona* and *Meliplebeia*) and *A. mellifera adansonii* were found. Of the total stingless bee colonies, 15 percent were destroyed by man and 10 percent by chimpanzees. The other predators, civets, gorillas, and baboons destroyed 3 percent of the nests. Sticks used by chimpanzees to harvest brood, honey, and pollen were found on the ground near trees with stingless bee nests. Sticks were missing bark from one or both ends and were peeled or chewed.

Conclusions: The Pygmies were the most important predators. The other agricultural communities neighboring the park mostly kept *A. mellifera* instead of Meliponini.

POSTER PRESENTATION

Factors influencing population density of bees in Bwindi Impenetrable National Park, Uganda

Robert Kajobe

National Agricultural Research Organisation (NARO), National Livestock Resources Research Institute (NaLIRRI), Tororo, Uganda

Introduction: In the first study of native African honeybees and honey-making stingless bees in the same habitat, humans and chimpanzees are the primary bee nest predators. This study was carried out in Bwindi Impenetrable National Park, Uganda. The park is a UNESCO World heritage site and contains half the world's population of mountain gorillas. The study was undertaken because little is known about bee ecology in Uganda.

Methods: Fieldwork was guided by the local Batwa Pygmies, the indigenous honey-hunters residing near the park. Sometimes, the dwarf honey-guide *Indicator pumilio*, a tiny bird that is endemic to the Albertine Rift Mountains, helped direct the Pygmies to stingless bee nests. Eighty seven plots were established for the study and two parallel 500 m transects were made in each plot, separated by 100 m. Flying bees were searched for in the plots and at nest entrance tubes on tree trunks.

Results: A total of 5 stingless bees (*Meliponula* and subgenera *Axestotrigona* and *Meliplebeia*) and *A. mellifera adansonii* were found. Of the total stingless bee colonies, 15 percent were destroyed by man and 10 percent by chimpanzees. The other predators, civets, gorillas, and baboons destroyed 3 percent of the nests. Sticks used by chimpanzees to harvest brood, honey, and pollen were found on the ground near trees with stingless bee nests. Sticks were missing bark from one or both ends and were peeled or chewed.

Conclusions: The Pygmies were the most important predators. The other agricultural communities neighboring the park mostly kept *A. mellifera* instead of Meliponini.

POSTER PRESENTATION

Relative abundance of *Bactrocera zonata* and *Ceratitis capitata* on fruit hosts in Egypt

S. Elnagar[1], M.A.K. El-Sheikh[1], A.G. Hashem[2], Y.E. Afia[2]

*[1]Department of Economic Entomology and Pesticides, Faculty of Agriculture, Cairo University, Cairo, Egypt, [2]*Horticultural Pests Department, Agricultural Research Centre, Cairo, Egypt*

Ceratitis capitata (Weid) is a highly polyphagous tephritid that was reported in Egypt early last century. In (1990), another harmful tephritid species, *Bactrocera. zonata* (Saunders), was recognized in Egypt causing most of fruit damage. Recently, *B. zonata* has become so widespread that dominating *C. capitata.* The relative abundance of the two fruit flies (Family: Tephritidae): Mediterranean fruit fly, *C. capitata* and the peach fruit fly, *B. zonata* has been compared for three successive seasons on eight different fruit hosts (peach, apricot, mango, guava, navel, balady, mandarin and Valencia) cultivated in three different localities in Egypt . The obtained results revealed that the total captured males of *B. zonata* were, in general higher than that of *C. capitata*. *B. zonata* represented the high majority of fuit flies population in general. The rate of replacement by *B. zonata* over *C. capitata* was evident in all areas under investigation. It is confirmed, that *B. zonata* was abundant throughout the season, except in winter months. On the other hand, *C. capitata* was less abundant during the summer months.

POSTER PRESENTATION

New polar constituents in the pupae of the silkworm *Bombyx mori* L.

Ryuichiro Tanaka

Setsunan University, Hirakata, Osaka, Japan

In addition to serine (L:D = 68:32), a methanol extract of *Bombyx mori* L. pupae contained methionine sulfoxide (MSO), L-methionine sulfone (L-MSO_2), trehalose, and disodium γ-cyclic di-L-glutamate. MSO was isolated as a diastereomeric mixture of L(+)- and D-(+)-MSO in a ratio of 99:1. The presence of these compounds at other developmental stages, including eggs, larvae (1^{st}, 4^{th}, 5^{th}, and mature 5^{th} instar), adults, and excrement (feces and urine) was investigated. The L(+)-isomer of MSO was present in extracts of the 1^{st} and 5^{th} instar larvae, adults, and eggs, but was not detected in feces or urine. The D(+)-isomer was found only in pupal stage extracts, and was excreted into the meconium with the L(+)-isomer. L-MSO_2 and γ-cyclic di-L-glutamate were not detected at other insect life stages or in the insect excrement. γ-Cyclic di-L-glutamate is thought to be produced on blockage of the glutamate synthetic pathway (glutamine synthetase) by L-MSO_2 and Mg^{2+}. During the pupal stage, the quantities of L-MSO_2 and L-MSO increased initially, decreased, and then subsequently increased again, and became maximal the day before emergence; the L-MSO_2 disappeared immediately after emergence. With advancing emergence time, the sugar content (*i.e.*, trehalose) also changed. The biochemical role of L-MSO_2 during the pupal life stage remains unknown, but its stage-specific expression suggests that it is a candidate molecule that induces diapause.

POSTER PRESENTATION

Facilitating learning towards sustainable integrated pest management in organic cocoa production in Ghana

Godwin Ayenor, Daniel Obeng-Ofori, Beatrice Padi, Arnold van Huis, Neils Roling

University of Ghana, Legon, Accra, Greater-Accra, Ghana

Introduction: Cocoa is an important foreign exchange earner for Ghana. However, until recently, production had plummeted due to low producer price and high incidence of pests and diseases. Paradoxically, only 3.5% of cocoa farmers adopt pest management technologies developed by the Cocoa Research Institute of Ghana.

Methods: To improve research uptake and adoption, technographic and diagnostic studies followed by participatory technology development tools were used to address pest and disease constraints of cocoa in the Eastern region of Ghana. Three innovative pest control methods were selected for for field participatory experimentation with key stakeholders including 10 volunteer farmers referred to as Local Agricultural Research Committee (LARC), research scientists, and agricultural extension agents. The pest control methods evaluated were: the use of pheromone traps, crude aqueous neem (*Azadirachta indica* A. Juss) seed extract (ANSE), and the use of the red ants *Oecophylla longinoda* as biological control agents. The temporal distribution of capsids and other insects in the cocoa ecosystem was also investigated to determine the correct timing of the control methods.

Results: Capsid population peak occurred in March contrary to previous findings. Results from the field experiments indicated that where *O. longinoda* occurred in high numbers, the reverse was true for capsids, especially under shady conditions. As a monitoring and control measure, the use of sex pheromone traps did not only confirm March as the peak population period for capsids but it also controlled the capsids by trapping the males. These results contradict previous findings that capsid population increases to a peak in November-January and drops in February-June. The efficacy of ANSE against capsid bugs in both cage and field experiments was encouraging (100% & 80% mortality, respectively), and was even more effective against *Helopeltis* spp (cocoa mosquito) with 100% mortality in the field. Its effect on other insect pests such as cocoa mealy bugs, shield bugs and aphids was also promising.

Conclusion: The three methods investigated might prove to be effective and compatible within the context of an Integrated Pest Management (IPM) strategy for sustainable production of organic cocoa in Ghana.

POSTER PRESENTATION

Action of a biopesticide, Spinosad, and a nonsteroidal ecdisteroid, methoxyfenozide, on *Spodoptera exigua*

Samuel Pineda[1], Aniceto Osorio[1], Ana Mabel Martinez[1], Marcela Ines Schneider[2], Ovidio Diaz[3], Jose Luis Corrales[4], Mayra Crimilda Aviles[5], Guy Samagghe[6]

[1]Instituto de Investigaciones Agropecuarias y Forestales, Universidad Michoacana de San Nicolás de Hidalgo. Km. 9.5 Carr. Morelia-Zinapécuaro., 58880 Tarímbaro, Michoacán, Mexico, [2]Centro de Estudios Parasitológicos y de Vectores CEPAVE., La Plata, Buenos Aires, Mexico, [3]Facultad de Agronomía, Universidad Autónoma de San Luis Potosí., San Luis Potosí, Mexico, [4]Facultad de Agronomía, Universidad Autónoma de Sinaloa., Culiacán, Sinaloa, Mexico, [5]Instituto Nacional de Investigaciones Forestales y Agropecuarias, Campo Experimental del Valle de Culiacán., Culiacán, Sinaloa, Mexico, [6]Laboratory of Agrozoology, Faculty of Bioscience Engineering, Ghent University., Ghent, Belgium

Introduction: Spinosad –a nerve poison biopesticide derived from the soil actinomycete *Saccharopolyspora spinosa* Mertz & Yao- and methoxyfenozide –a nonsteroidal ecdisteroid compound- are considered to be environmentally safer alternatives to broad-spectrum pesticides. Therefore, both biorational insecticides can play an important role in the future as part of beet armyworm, *Spodoptera exigua* (Hübner) (Lepidoptera: Noctuidae), management programs.

Methods: The selection experiments were carried out with a field population (Se-La Floriza) by exposing for 24 h third-instar to corresponding LC_{50} of Spinosad and methoxyfenozide for over six generations (G_2-G_7). Sublethal effects caused by methoxyfenozide were evaluated on insects of the G_7, the final generation subjected to selection procedures. In another experiment, five populations of *S. exigua* were collected from fields of vegetable crops in three states of Mexico (Sinaloa, Guanajuato, and San Luis Potosi) in 2005 and 2006 for susceptibility tests.

Results: Experiments to select insects artificially from a field population revealed no significant loss in susceptibility to both compounds for up to five generations. In G_7, LC_{50} values for insects exposed to Spinosad and methoxyfenozide were 2.75-fold and 1.25-fold greater than G_1 larvae, respectively. Oral treatment with methoxyfenozide also reduced the fecundity and fertility in the adults of G_7, confirming reproductive effects. In susceptibility tests of the five *S. exigua* populations collected from fields, LC_{50} values on third-instar ranged from 0.17 to 2.98, and 0.09 to 0.67 mg per kg diet for spinosad and methoxyfenozide, respectively.

Conclusions: We conclude that resistance management programs should be established, particularly in areas where *S. exigua* has developed resistance to Spinosad.

POSTER PRESENTATION

Goryphus or *Skeatia*?: Genus confirmation using molecular technique

Nur Azura Adam[1], Idris Abd. Ghani[3], Adura Mohd Adnan[2]

[1]Department of Plant Protection, Faculty of Agriculture, Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia, [2]School of Environmental and Natural Resource Sciences, Faculty of Science & Technology, Universiti Kebangsaan Malaysia, 43600 UKM Bangi, Selangor, Malaysia, [3]School of Bioscience & Biotechnology, Faculty of Science & Technology, Universiti Kebangsaan Malaysia, 43600 UKM Bangi, Selangor, Malaysia

Introduction: *Gorpyhus* and *Skeatia* are two ichneumonids (Hymenoptera) genera with a very high morphological resemblance. Previous authors separate this two genus only base on the length of the first tergite and the ratio of the postpetiole. Despite these two characters, other morphological characteristics are heterogenous. Therefore, application of molecular technique was conducted to confirm the identity of both genera.

Methods: Samples from both genera were extracted using phenol-chloroform method. The 18s rDNA gene were amplified and purified before sending for sequencing. Sequences obtained were edited and aligned in ClustalX program, Phylogenetic analyses of the sequences were conducted in PAUP program using Maximum Parsimony(MP) and Neighbour-Joining(NJ) methods.

Results: A 550 segment of the 18S gene was successfully sequenced from both genera. The phylogenetic trees constructed from both methods (MP and NJ) showed that *Goryphus* and *Skeatia* are in different clades. The genetic distance (Tamura-Nei Algorithm) between both species of *Skeatia* is very low (0.02), indicating that both species have a very close phylogenetic relationship. The average distance of *S. fuscinervis* and *S. versatilis* with the *Goryphus* species are 0.045 and 0.047 respectively. These values are higher comparing with the average genetic distance within the *Goryphus* species (0.039).

Conclusion: Results from molecular phylogenetic analyses confirmed that *Goryphus* and *Skeatia* are two completely different genera despite their very close morphological resemblance.

POSTER PRESENTATION

Identification and Investigation some of species of Trifinae of Noctuidae in Iran Forests and rangelands.

Nasser Farrar[1], Mahmood Yarmand[2], Helen Alipanah[3], Reza Golestaneh[1], Reza Zahiri[3]

[1]Agricultural & Natural Resources Research Center, Bushehr, Bushehr; [2]Forests & rangelands Research Institute, Tehran; [3]Plant Protection Research Institute, Tehran, Tehran, Islamic Republic of Iran

Introduction: Noctuidae is the largest family in the order, with more than 25000 species. The subfamilies fall broadly into tow groups; The Trifinae (including: Noctuinae, Heliothinae, Hadeninae, Cucullinae, Acronictinae and Amphipyrinae) and Quadrifinae. The design result of this project is identification and investigation fauna of forests and rangeland that were collected in national project. The taxonomic significance of male genitalia is constant. It is most important as a character with high weight.

Methods: The aedeagus or more precisely its tube usually provides good taxonomic character in moths because of sclerotization on the vesica (pars inflabilis) or structure of the outer wall. The structure of the tube is uniform. The abdomen was removed with a small dissecting needle and then cleared in KOH, and the genitalia and aedeagus were dissected out after clearing. They were washed in water with a little acetic acid added. Vesica was averted with small needle. After the study they were mounted with oil clave and xylem and canada balsam on microscope slide.

Results and Conclusions: According with international references the specimens were identified.

Subfamily: Heliothinae: *Heliothis peltigera* (Denis & Schiffermüller), *Heliothis viriplaca* (Hüfnagel, 1766), *Helioverpa armigera* (Hübner, 1808), *Periphanes delphinii* (Linnaeus, 1758). **Subfamily: Acronictinae**: *Acronicta aseris* (Linnaeus,1758), *Acronicta megacephala* (Denis & Schiffermüller). **Sub Family: Amphipyrinae;** *Trachea atriplicis* (Linnaeus, 1758), *Auchmis peterseni* (Chritoph, 1887), *Amphipyra pyramidea* (Linnaeus, 1758), *Amphipyra boursini* Hacker, 1998, *Phlogophora meticulosa* (Linnaeus, 1758), *Dicycla oo* (Linnaeus, 1758), *Spodoptera exigua* (Hübner, 1808). **Subfamily: Hadeninae:** *Mythimna l-album* (Linnaeus, 1767), *Mythimna vitellina* (Hübner,1808), *Acantholeucania loreyi* (Duponchel, 1827), *Polia nebulosa* (Hüfnagel), *Polia serratilinea* (Alpheraky, 1887), *Mamestra persicariae* (Linneus). **Subfamily: Cuculline:** *Cuculia argentina* (Fabricius, 1787), *Cuculia syetana iranica* (Brandt, 1941), *Lithophane furcifera* (Hüfnagel, 1767). **Subfamily: Noctuinae:** *Euxoa basigramma* (F. Wagner,1913), *Amathes triangulum diadochica* Hacker& Ebert, *Agrotis exclamatinis* (Linnaeus, 1758), *Xestia c-niarum (*Linnaeus, 1758*), Ochropleura plecta* (Linnaeus, 1761), (Hübner, 1808), *Euxoa temera* (Hübner, 1808), Hübner,1813*, Euxoa agricola* (Boisduval,1829), *Dichagyris forficula* (Eversmann, 1851).

POSTER PRESENTATION

Population dynamics and on-farm fruit fly integrated pest management in mango orchards in Senegal

Mbaye Ndiaye, Elhadji Omar Dieng, Gilles Delhove

[1]National Plant Protection Service, Dakar, Senegal, [2]PIP/COLEACP/EU, Brussells, Belgium

The trend of the population of fruit flies follows the dynamic of the rains. This tendency is more perceptible on Bactrocera invadens than on *Ceratitis cosyra*. From 350 individuals captured per trap, *B. invadens* seemed to disrupt the presence of C*. cosyra* and the other related Ceratitidae species. This behavior is probably due to an interspecific competition. Such behavior could be due by the fact that *C. cosyra* dominated the emergences from the incubated fruits of alternate host plants up to 87 % even though *B. invadens* was observed. The sex ratio was dominated by females especially at the end of the harvesting period of mangoes, corresponding to the end of the rainy season. Integrated pest management (IPM) package which including 1) male annihilation using wood blocks soaked in insecticide and lure (methyl eugenol and terpinyl acetate), 2) two (2) protein hydrolysate bait applications (Success Appat at 1 liter per ha) and 3) sanitation (mechanical weeding, destroying of the collected fallen fruits in using black plastic bags, digging holes and burning with a barrel transformed into incinerator), were used for the control of the fruit flies in mango orchards in the natural region of Niayes in Senegal. Results showed an inferred improvement in fruit fly (*B. invadens* and *C*. cosyra) infestations in the treated plot up to 83% compared to the untreated. When comparing lures, we found that methyl eugenol attracted significantly *B. invadens* than the home-made baits of grinded nutmeg and NET (beauty cream). Methyl eugenol's half life is also significantly longer (5 weeks) than the grinded nutmeg (less than 1 week) ($P = 0.0109$; $t = 9.4935$; $Df = 2$). There were no capture recorded in the NET based trap.

POSTER PRESENTATION

Long distance dispersal of the island sugarcane planthopper*:* is culture contributing?

Kylie Anderson[1], Mohamed Sallam[2], Bradley Congdon[1]

[1]James Cook University, Cairns, Queensland, Australia, [2]BSES Ltd, Gordonvale, Queensland, Australia

The island sugarcane planthopper, *Eumetopina flavipes*, is the only known vector for Ramu Stunt disease of sugarcane. Ramu Stunt disease appears confined to Papua New Guinea, but disease free populations of the vector are known to occur throughout the Torres Strait archipelago and on the northern tip of Cape York, Australia. The ability of *E. flavipes* to hitch-hike on sugarcane moved by people throughout the region is unknown, but is a process which may explain the initial and subsequent colonisations of the Torres Strait islands and mainland Australia.

We assessed the ability of mobile life stages of *E. flavipes* to survive over time on cut sugarcane stalks. Results indicated that whilst nymphs and adults leave the stalk at different rates over time, almost half of the initial population of nymphs and almost one third of the adults survived six days *in situ* on cut stalks. Therefore, *E. flavipes* is capable of surviving extended periods of time on deteriorating sugarcane. These results imply that human mediated movement may play an important role in the dispersal of *E. flavipes*.

POSTER PRESENTATION

Host location and behavioural response patterns of the parasitoid, *Tachinaephagus zealandicus (*Hymenotpera: Encyrtidae*)*, to host and host-habitat odours

Sasha Voss[1], Helen Spafford[2], Ian Dadour[1]

[1]Centre for Forensic Science, University of Western Australia, Perth, Western Australia, Australia, [2]School of Animal Biology, Perth, Western Australia, Australia

Introduction: To overcome the challenge of host location in patchy and complex environments, many parasitoids exploit host-habitat derived odour cues. This study investigated the role of odour cues used during host location by the generalist parasitoid, *Tachinaephagus zealandicus.*

Methods: A Y-tube olfactometer was used to test aspects of host searching behaviour of *T. zealandicus* females under different choice scenarios. A variety of odour cues were tested: host/liver complex, eaten liver, unwashed host larvae, washed host larvae and liver in six stages of decay. Results were compared to assess the suitability of residency time as opposed to 'first choice' as an indicator of parasitoid attraction to odour stimuli.

Results: *T. zealandicus* females demonstrated an innate response to, and preference for, odours arising from liver substrates following interaction with the host, dependant on the stage of meat decay. Females were not attracted to liver that had never been in contact with a host, regardless of the stage of decay. Analysis of residency time showed discernable differences in parasitoid movement and behaviour under different choice scenarios. The absence of any odour stimulus elicited limited movement about the olfactometer while females remain by an attractive odour source even when denied access to it. Both first choice and residency time were good indicators of parasitoid preference.

Conclusions: Our findings demonstrate that the tritrophic relationship commonly observed in plant-herbivore-parasitoid interactions can also evolve in the absence of selective pressure on the host-habitat.

POSTER PRESENTATION

Life table parameteres of *Hippodamia variegata* (Coleoptera: Coccinellidae) on *Aphis fabae* (Homoptera: Aphididae) under laboratory conditions

Reza Jafari

University Borojerd, Lorestan province- Borojerd, Islamic Republic of Iran

In this study life table parameters of *Hippodamia variegata* (Goeze) as an important predator of *Aphis fabae* Scopoli were studied under laboratory conditions. Ten pairs of male and female adults were released into a cage (6×11×23 cm) set on aphid separately. Experiments were carried out in a growth chamber at 25±1degrees C ,65±5 RH and 16:8(L:D) photoperiod. The most basic life table(survival subtable) parameters were age x,surviving from birth to exact ages x (lx),using these factors for calculation of life table parameters such as number of survival (lx), age specific mortality (qx), and life expectancy (ex), and the curves were prepared. The most basic life table (fecundity subtable) parameters such as number of female produced (mx), intrinsic rate of increase (rm), Net reproductive rate (Ro),mean generation time (T) and doubling time (DT) were calculated . The results of biological parameters studies revealed that proportion of a cohort surviving from birth to exact ages x(Lx) began at 31st day and fell to zero at the 70th day, also age specific mortality (qx) began at the 30th day and reached highest at 69 days. Also life expectancy (ex) was 51.02 at the initiation of development. Total fecundity was 910 eggs, sex ratio was .7, The number of females produced were more than males. Rm =.287, Ro=509, T=21.7 days and DT=2.4 were estimated.

POSTER PRESENTATION

Composition and food properties of red palm weevil *Rhynchophorus ferrugineus* (Curculionidae: Coleoptera)

Ahmed AlJabr

Plant Protection Department, Faculty of Agriculture and Food Sciences, King Faisal University., Hofuf, AlHassa, 31982, Saudi Arabia

Abstract: Red palm weevil *Rhynchophorus ferrugineus* female, male and last instar larva were analyzed for their Nutrient composition and amino acid composition. The data indicate that both sexes and larva are very rich in protein, fat and carbohydrates. Larva contains the highest contents of crud fat (41.8%), protein (25.91%) and ash (3.41%). Male adult contains the highest contents of carbohydrates (50.85%) and fiber (4.36%). Substantial amount of nitrogen, phosphor, potassium, iron, copper and zinc were found in all weevil stages. Traces of iron, copper and zinc were detected in all stages, while there was no detection of manganese in all stages. Larva contains the highest levels of macro and micro elements. It contains the highest contents of nitrogen (4.36%), phosphors (0.43%), potassium (0.85%), calcium (1.45%), sodium (0.22%) and zinc (130 ppm). Female has the highest contents of iron (170 ppm) , while both adult stages are high in copper levels (20 ppm). Hemolymph was rich of many amino acids, especially proline, aspartic and lysine. Adult female contains the highest levels of 15 of the 18 amino acids detected. It is contains the highest levels of aspartic acid (29.91), serinine (13.45), glutamic acid (25.52), praline (45.38), gliycine (11.91), alanine (16.77), valine (10.99), isoleucine (9.80), leucine (16.28), tyrosine (7.88), pheynylalanine (9.18), histidine (9.87), lysine (20.87), NH4 (68.99) and arginine (8.49). These food properties evoke a serious thinking of including such source of food in animal food if not human being.

POSTER PRESENTATION

The impact of *Beauveria bassiana*, *Trichogramma*, *Bt* sprays and Spinosad on the lepidopteran (C*rambidae*) cereal stalk borer - the European corn borer

Rostern N. Tembo[1], Daniel M. Pavuk[2]

Biological Sciences Department, Bowling Green State University, Bowling Green, Ohio 43402. USA.

Introduction: The research examined the effects of microbial control strategies on the European corn borer (ECB). The European corn borer is one of the most devastating pests of field corn in corn-growing regions of the United States.

Method: Our research had 7 Microbial treatments and each treatment had five replications making a total of 35 plots. The treatments included Spinosad, an insect growth regulator from bacteria, the entomopathogenic fungus *Beauveria bassiana*, *Trichogramma pretiosum*, foliar applied *Bt spray,* plus two combinations *Beauveria bassiana* and *Bt* spray, and Spinosad and *Trichogramma pretiosum*.

Results: The infections by the European corn borer larvae on stalks of corn were severe in all the control treatments. The Microbial treatments applied to the corn imposed various degrees of restraints on the European corn borer larvae. In all the parameters there was a significant difference between the control and other treatments with a P value of <0.001. Spinosad emerged as the most effective biological agent in the control of the European corn borer.

Conclusion: The results of the research done on the abundance and composition of the arthropods in the treatment plots showed that different treatments applied to various plots had no effect on the abundance and composition of the arthropods. The P values obtained by one way ANOVA were greater than 0.005.

This research is relevant in boosting alternative control strategies, underutilized control strategies for *Ostrinia nubilalis* and increasing farmers' adoption of integrated pest management practices especially in organic farming thereby reducing the use of conventional insecticides.

POSTER PRESENTATION

Biology of *Hippodamia variegata* (Coleoptera: Coccinellidae) on *Aphis fabae* under laboratory conditions

Reza Jafari, Karim Kamali, Mahmod Shojai

University, Lorestan, Islamic Republic of Iran

The *Hippodamia variegata* is one of the most important predators of *Aphis fabae* In this survey biological characteristic of *H. variegata* including duration of different life stages,feeding capacity, tolerance to starvation , cannibalism and life table parameters were studied under laboratory conditions Experiments were carried out in a growth chamber under 25±1degrees C ,65±5 Rh and 16:8(L:D) photoperiod. Under laboratory condition at 20±1,25±1 and 30±1 degrees C developmental period from egg to adult lasted 27.75±.38,21.35±.39 and 15.40±.33 days respectively.Both adult and 4th. Larvae feed on each stage of growth. Minimum and Maximum of Starvation were 8.1+0.84 and 2.3+0.11 in larvae and female adult respectively. The mean total fecundity was 910 eggs, the number of females produced were more than males. Mean preoviposition, oviposition and postoviposition periods were 6.20,52.8 and 7.4 days respectively. The number of eggs produced by each female was between 0 to 103 in a day, females produced (mx)=7.40±1.01

POSTER PRESENTATION

The faunistic survey of ladybirds (Coleoptera: Coccinellidae) in Lorestan province (Iran)

Reza Jafari

University, Lorestan, Islamic Republic of Iran

In this study species diversity of coccinellids was studied in Lorestan province during 2001-2005. Altogether 28 species from 14 genera, 7 tribes and 4 subfamilies were collected and identified. External characters plus characteristics of the male and female genitalia were used in order to diagnose species. Among coccinellid species collected: two species were new records for Iran. Many species were predacious, preying on various species of aphids, mites and coccids. The scientific names of the species according to their subfamilies and tribes are as follows.Species marked with asterisk (*) are considered as new records from Iran.Some species were also sent to Dr.Helmut Fursch in Germany for identification or confirmation.

1-*Coccinella septempunctata* Linnaeus
2-*Hippodamia variegata* (Goeze)
3-*Oenopia conglobata* (Linnaeus)
4-*Oenopia oncina* (Olivier)
5-*Adalia bipunctata* (Linnaeus)
6-*Adalia decimpunctata* (Linnaeus)
7-*Aphidecta obliterata* (Linnaeus)
8-*Propylaea quatuordecimpunctata* *
9-*Psyllobora vigintiduopunctata* (Linnaeus)
10-*Chilocorus bipustulatus* Linnaeus
11-*Exochomus melanocephalus* Zoubkoff
12-*Exochomus nigromaculatus* (Goeze)
13-*Exochomus quadripustulatus* Linnaeus
14-*Exochomus pubescens* Kuster
15-*Brumus gebleri* (Weise)
16-*Brumus undulatus* (Weise)
17-*Platynaspis luteorubra* (Goeze)
18-*Scymnus apetzi* Mulsant
19-*Scymnus pallipes* Mulsant
20-*Scymnus pallipediformis* Gunther
21-*Scymnys frontalis* Fabricius
22-*Scymnus apetzoides* Capra&Fursh
23-*Scymnus subvillosus* (Goeze)
24-*Scymnus syriacus* (Marseul)
25-*Scymnus mediterraneus* Khnzorian
26-*Scymnus araraticus* Khnzorian*
27-*Stethorus gilvifrons* Mulsant
28-*Pharoscymnus ovoides* Sicard

POSTER PRESENTATION

Concentration and loading of pesticide residues in Gorganrud and Qaresu rivers (Iran)

Mansoreh Shayeghi, Fatemeh Bagheri, Hassan Nasirian, Seyed Mohammad Abtahi

Department of Medical Entomology and Vector Control, School of Public Health and Institute of Public Health Research, Medical Sciences/University of Tehran, P. O. Box 6446-14155, Tehran, Islamic Republic of Iran

Introduction: Pesticide contamination of fresh water, which has emerged as an important environmental problem in the last few decades, is causing concern with respect to the long-term and low dose effects of pesticides on public health. The Qaresu and Gorganrud rivers (Golestan province) are typical rivers flowing through an agricultural area in northern of Iran, which is the natural inlet of Caspian Sea.

Methods: The concentrations and residues rates of two insecticides (azinphous-methyl and diazinon) which are most used for pest control of the agricultural fields and fruit gardens were estimated over a period of 1 year in the Qaresu and Gorganrud rivers by TLC scanner method and CATS-4 software. Water samples were collected from six localities through the rivers flowing in order to near the Caspian Sea.

Results: Azinphous-methyl and diazinon were found at the higher frequencies with maximum concentrations of 14.6, 22.4 and 14.9, 26.8 ppm in the influent of Qaresu and Gorganrud rivers, respectively. These peak concentrations were observed during the application period of pesticides for agricultural pest control by farmers in summer. The concentrations of the total amount of pesticide residues through the different localities of the rivers to the basin in downstream were estimated to be 2.67, 14.6, 0.2, 0 and 3.1, 22.4, 0.5, 0 ppm in Qaresu and 1.8, 14.9, 0.04, 0 and 3.7, 26.8, 0.6, 0 ppm in Gorganrud for azinphous-methyl and diazinon in spring, summer, autumn and winter, respectively.

Conclusions: Pesticides, which may be a potential hazard to humans and the environment, show an effect even in low concentrations. This study provides information on the concentrations of azinphous-methyl and diazinon in Qaresu and Gorganrud rivers in northern of Iran and offers background data on pesticide residues in river water.

POSTER PRESENTATION

Temporal synergism controls highly resistant poultry red mite

Georgina Bingham, Peter Bates, Graham Moores

[1]Rothamsted Research, Harpenden, Hertfordshire, United Kingdom, [2]Veterinary Laboratory Agency, New Haw Surrey, United Kingdom

The poultry red mite (*Dermanyssus gallinae*) is one the most important ectoparasites affecting broiler and egg layers in all types of production system across the UK and Europe. Management regimes continue to rely heavily on the use of chemical control, such as the synthetic pyrethroids. These pesticides have become increasingly less effective at controlling red mites in recent years due to the development of resistance; in some cases no available pesticides confer effective control.

Pesticide resistance is often due to the enhancement of metabolic enzyme systems within the pest, particularly non-specific esterases and microsomal oxidases. If synergists are allowed sufficient time to fully inhibit these enzymes (temporal synergism) then the sensitivity of insect pests to pesticides can be increased by several orders of magnitude.

In this laboratory study a 42-fold increase in the level of susceptibility to α-cypermethrin was found when a 12 hour pre-treatment of 100ppm PBO was applied to a standard laboratory susceptible strain of *D. gallinae* and a 750-fold enhancement was found with resistant field strains under the same treatment.

This demonstrates the exciting potential temporal synergism could have in the area of ectoparasite control.

POSTER PRESENTATION

Repellent bioassay of anti-mosquito mattresses, treated with HealthguardTM PLB Technology, under laboratory conditions, against two Venezuelan strains of *Aedes aegypti* Linnaeus 1762 on the dengue mosquito vector

Matias Reyes-Lugo, Ivan Salvi, Wilmer Gelves, Ana Avilan, Daniel Llavaneras, Carlos Sanchez

[1]*Medical Entomology Section, Tropical Medicine Instituto, Universidad Central de Venezuela, Caracas, Venezuela,* [2]*Confort de Venezuela C.A, Los Teques, Miranda, Venezuela*

Introduction: The repellent efficacy of the mattress anti-mosquitoes® Confort of Venezuela C.A tried with Healthguard™ PLB technology is evaluated against two Venezuelan strains of *Aedes aegypti* dengue mosquito vector, with different susceptibilities to insecticides.

Methods: 50 fasted females of the *Aedes aegypti* with 5 days of age as adults, were placed with a sample of the mattress anti-mosquitoes® of Confort de Venezuela C.A in two experimental glass cages 42 lt. In other cages or controls, the same number of mosquitoes and a sample of another mattress that were not treated. The number of *Ae. aegypti* females on, or biting the arm of a volunteer, counted during the first 30 seconds per minute during 10min. This was repeated in the morning and the afternoon. For each strain of mosquitos i.e. West Africa susceptible international reference, La Candelaria low susceptibility to organophosphate and El Mojan organophosphate and pyrethroid- resistant and susceptible to carbamic (Reyes-Lugo & Neus 1998), were carried out in two replicates, for a total 100 individuals per strain and moment of the day. ANOVA, F and Student Test (α=0.95) applied to frequency distribution of mosquitoes posed or biting evaluated the differences in the repellent from anti-mosquitoes® mattress between the strains.

Results: In order, the West Africa La Candelaria, El Mojan, repellents go from 61.8% to 91%. The temperature and relative humidity registered: 26.5ºC +/- 1.04 and 80.45% +/- 11.67, respectively.

Conclusion: The mattress anti-mosquitoes® with Healthguard™ PLB protects from the bites of the *Aedes aegypti* and possible dengue control transmission.

POSTER PRESENTATION

The association of *Triatoma maculata* Ericsson 1848, with the gecko *Thecadactylus rapicauda* Houttuyn, 1782 (Reptilia: Squamata: Saurian: Gekkonidae): A strategy for the colonization of dwellings for the vector of Chagas diseases in Venezuela?

Matias Reyes-Lugo, Ma. Isabel Reyes-Contreras, Ivan Salvi, Wilmer Gelves, Ana Avilan, Daniel Llavaneras, Alexis Rodriguez-Acosta, Luis Navarrete, Gerardo Cordero

[1]Medical Entomology Section, Tropical Medicine Instituto, Universidad Central de Venezuela, Caracas, Venezuela, [2]Biology School, Universidad Simón Bolívar, Caracas, Venezuela, [3]Immunochemestry Section, Tropical Medicine Institute, Universidad Central de Venezuela, Caracas, Venezuela, [4]Tropical of Zoology Institute, Universidad Central de Venezuela, Caracas, Venezuela

Introduction: In Venezuela, its frequent wild triatomines introducing in the dwelling, some are able to be domiciled. *Triatoma maculata* vector of *Trypanosomas cruzi*, was capture in dwelling, bitten inhabitants and associated with the gecko *Thecadactylus rapicauda.*

Methods: In a building of three floors, next to remnant Tropical Dry Forest, 10º12'23.39N and 66º51'13.26ºW, Miranda State, at 293m high, was carried out triatomines search: direct and manually (10 hours/9 people) and in difficult access places with electric vacuum cleaner (Genie® 1.5 HP). Gecko samples were also taken. For identification of insects and reptiles, used: stereoscopic microscope and keys. The temperature and relative humidity measured. With optic microscopy and culture blood-agar of the intestinal content and feces of *T. maculata* investigated presence of *T. cruzi*, and blood meal origin establish with test-Elisa and microscopically morphological comparison.

Results: The first two floors of the building were inhabited (2Ch and 3A)**.** The discovery of colony of *T. maculata* cohabiting with population of the gecko *T. rapicauda*, was carried out in the roof, in shed (wooden and metallic sheets with abundant rust, earth and trash-from of TDF). 1448 individuals of *T. maculata* collected: 1074H (74.2%), 18NI (1.2%), 40NII (2.8%), 60NIII (4.1%), 49NIV (3.4%), 145NV (10%), 62A (4.3%). The blood meal of *T. maculata* from gecko and human determined, *T. cruzi* was absent. In the place detects feces of *Didelphys marsupialis* (opossum). The temperature was of 29.65 ºC and HR 54.21%.

Conclusion: The association *T. maculata-T. rapicauda*, is effective strategy of colonization of dwellings located in the vicinity of the habitat where are present both species.

POSTER PRESENTATION

Effects of parasitism by the ectoparasitoid *Bracon hebetor* Say (Hymenoptera: Braconidae) on host hemolymph proteins of the Mediterranean flour moth *Ephestia kuehniella* Zeller (Lepidoptera: Pyralidae)

Hülya Altuntas, Yavuz Kilic

Anadolu University, Eskisehir, Turkey

Introduction: Parasitism of lepidopteran larvae by Braconid and Ichneumonid wasps has dramatic effects on host hemolymph proteins and at the aspects of the host insect's physiology. The effects of parasitism by gregarious, idiobiont and ectoparasitoid *B. hebetor* on host hemolymph plasma proteins of the Mediterranean flour moth *E. kuehniella* last instar larvae were investigated in the present study.

Methods: Host *E. kuehniella* were selected a newly-ecydsed last instar larvae and parasitized individually by exposure to a mated *B. hebetor* females. Hemolymph samples were obtained from parasitized larvae after 24 h. and 48 h. parasitizitation as well as unparasitized host larvae on the last instar. Protein concentration of all hemolymph samples were measured to the Bradford method. The protein profiles of plasma from parasitized and unparasitized *E. kuehniella* larvae were analyzed and compared on discontinuous denaturing sodium dodecyl sulfate-polyacrylamide gel (SDS-PAGE). The gel was scanned and analyzed densitometrically in a Gel-Pro Analyzer Version 4 programme.

Results: Total amount of plasma proteins in host hemolymph were reduced gradually on 24 and 48 hours after parasitation treatment. 55.3, 39.4, 37.2, 35.6, 33.9, 29.6, 24.6, 23.1, and 14.5 kDa proteins in total 25 protein bands, which were analyzed as densitometric, reduced over the 50%, on the other hand, four bands as 52.0, 44.6, 19.0 and 24.6 kDa protein bands pointed out related to the parasitism were increased.

Conclusions: Parasitism of *E. kuehniella* by *B. hebetor* was demonstrated to cause quantitative changes in the plasma proteins of host hemolymph.

POSTER PRESENTATION

Effects of some heavy metals on the larval growth rate of *Calliphora vicina* (Diptera)

Ferhat Altunsoy, Yavuz Kilic, Caner Aydinli

Anadolu University, Eskisehir, Turkey

Introduction: Entomotoxicology is relatively new branch of forensic entomology. The potential use of insects for detecting drugs and other toxins in decomposing tissues has widely demonstrated. In death investigations, Diptera and other arthropods can be reliable altemate specimens for toxicological analysis in the absence of tissues and fluids normally taken for such purposes. *C. vicina* is one of the species which is widely used in medico-criminal investigations.

Methods: Larval development of blowfly *C. vicina* in different concentrations (0,12; 0,25; 0,50; 1 and 2 µg/g) of some heavy metals (Cd, Pb, Hg, Fe, Cu) were analyzed in the present study. Fresh *C. vicina* eggs were placed on the toxin-bovine lung mixture and reared at constant 25 ^{0}C, 70% humidity. After every 3 hours maggots and pupal samples were taken from the diets. Maggot's lengths and dry weights were measured periodically. Data entry and analysis were performed by using S.A.S. (Statistical Analysis System).

Results: All concentrations of these toxins had negative effects on larval growth and estimation of PMI (Post Mortem Interval). Growth rates of experiments and controls are significantly different. 0,50; 1 and 2 µg/g cadmium contamination had lethal effect on larvae, but other toxins had not lethal effect. 1 and 2 µg/g lead, mercury, ferric and copper contamination delayed the larval development one-three days.

Conclusions: Heavy metal pollutions in different tissues had negatively effects on the growth of insects. In this case, estimation of PMI in legal investigation is relatively difficult. In this study, effect of five toxins on maggots growth rate were declared.

POSTER PRESENTATION

Effects of some abiotic factors on the population dynamics of Tabanidae (Diptera) species in Eskişehir in Turkey

Ferhat Altunsoy, Yavuz Kilic

Anadolu University, Eskisehir, Turkey

Introduction: Tabanidae consists of about 4300 species of medium to very large biting flies; indeed, it contains some of the largest blood-sucking insects. The sheer size of tabanids and the pain their bite can cause mean they are not easily ignored. Large accumulations of flies do occur in some areas, and with their painful bite tabanids can be pests of both livestock and humans. Livestock worry can reach a level at which economic losses occur. Females of most Tabanidae species attack mammals and human. Like other blood-sucking flies, Tabanids have a negative economic effect on milk production where they commonly live. Moreover, Tabanids are known worldwide as important mechanical vectors to cause of diseases in some wild and domestic animals.

Methods: Population dynamics of the horse flies were monitored for 3 years. Fluctuations in the population were related to abiotic factors, such as maximum and minimum temperatures, rainfall, pressure and relative humidity, using Kendall's correlation coefficient test.

Results: Correlation coefficient data shown that the maximum and minimum temperatures had a significant immediate negative effect on the population ($P = 0,023$ and $P = 0,047$, respectively). Pressure and rainfall had no significant immediate or delayed effects on the population of horseflies ($P = 0,003$ and $P = 0,0025$), but relative humidity had significant immediate and delayed effect ($P = 0,035$).

Conclusions: It will be helpful for humans to know the ecology, seasonal and daily activity and chances in population density of these vector insects. In this study we discuss the yearly chances in population density of Tabanidae species.

POSTER PRESENTATION

Microorganisms isolated and identified from digestive systems of Tabanidae (Insecta: Diptera) species

Yavuz Kilic, Zerrin Tetik

Anadolu University, Eskisehir, Turkey

Introduction: The females of Tabanidae species feed on homoitherm animals and even humans by sucking their blood. For this reason they are the vectors of many diseases such as viruses, bacteria, protozoa and helminthes. In the present study 36 bacteria species were isolated from the digestive systems of 10 Tabanidae species that sucked blood from their hosts around Eskişehir province (Turkey).

Methods: Hemolysis, catalase, oxidase, indole, methyl red, Voges-proskauers, citrat, TSI, movement, DNaz, VITEK (Biomerieux),; (Microbiology reference Manual (Rev 08/2003), BIOLOG (Microstation; Microlog System Release 4.2) systems and antibiotic resistance tests were applied for the identification of bacteria.

Results: *Aeromanas caviae, A. hydrophila, A. Veronii biovar sobria, Achromobacter xylosoxidans, Alliococcus otitis, Bacillus alvei, B. mycoides, B. Pumilis, B. Subtilis, Brevundimonas vesicularis, Burkholderia mallei, Cedecea davisae, Chrysobacterium indolegenes, Enterobacter aerogenes, E. amnigenus biogrup 2, E. asburiae, E. clocea, Enterococus faecalis, E. gallinarum, Klebsiella oxytoca, Micrococcus lylae, Pseudomanas aeroginosa, P. alcaligenes, P. stutzeri, Raoultella terrigena, Serratia maecescens, S.plymuthica, Staphylococus cohnii, S. epidermidis, S. equorum, S. hominis, S. hominis ss novobiosepticus, S. pasteuri, S. saprophyticus, Sphingomonas paucimobilis Stenotrophomonas maltophila* species were identified from the investigated materials.

Conclusions: All these bacterial species have been isolated at first time from the digestive systems of horseflies. Isolation of many bacterial species from the limited number of Tabanidae species, once more indicated the importance of their properties to serve as vectors. These identified bacterial species always have potential risks on human and animal health.

POSTER PRESENTATION

Overview of personal protection measures used by the Australian Defence Force

Stephen Frances

Australian Army Malaria Institute, Enoggera, Qld, Australia

The personal protection measures used against vectors of disease by Australian Defence Force (ADF) personnel is described. Although a repellent formulation containing 35% deet in a gel is recommended, some soldiers use commercially purchased repellents, and studies comparing the protection provided by commercial repellents will be reported. The use of permethrin treated uniforms, bednets and tentage by ADF personnel will be discussed.

POSTER PRESENTATION

A synopsis of *Bracon* Fabricius species of Turkey with a description of a new species (Hymenoptera; Braconidae, Braconinae)

Ahmet Beyarslan, Ozlem Cetin Erdogan, Mitat Aydogdu

Trakya University Faculty of Arts and Science Department of Biology, Edirne, Turkey

Our studies on *Bracon* Fabricius fauna of Turkey started in 1979 and 107 species have been determined so far belonging to the subgenera *Habrobracon* Ashmead*, Asiabracon* Tobias*, Rostrobracon* Tobias *Bracon* Fahringer*, Cyanopterobracon* Tobias, *Glabrobracon* Fahringer and *Lucobracon* Fahringer. 13 new *Bracon* species were published from Turkey. With this present study *Bracon (Lucobracon) achterbergi* Beyarslan sp. nov. is described and its diagnostic characters are illustrated. The distribution of *Bracon* species are discussed according to the Euxin, Subeuxin, Mediterranean, Kseroeuxin, Iran Steppe, Anatolia Steppe, Central Anatolia Steppe and Mesopotamian Steppe phyto-geographical provinces of Turkey.

POSTER PRESENTATION

Calcium regulated fusion of yolk granules is important for yolk degradation during early embryogenesis of insects

Isabela Ramos, Kildare Miranda, Wanderley de Souza, Ana Paula Cabral de Araujo Lima, Ednildo de Alcantara Machado

Laboratório de Entomologia Médica do IBCCF da UFRJ, Rio de Janeiro, Rio de Janeiro,, Brazil

In insects the embryo development occurs totally dissociated from maternal organism. Reserve (yolk) proteins are mainly stored into organelles called yolk granules (YG), that will be degraded by activation of acidic hydrolases also stored within YGs. The hydrolases activation is mediated by proton pumps (Proton pyrophosphatases and Proton ATPases). Several works describe the presence of different YG population with different macromolecule contents. Thus, fusion of YGs could represent an interesting model of macromolecule transfer between different compartments during embryogenesis. We described the YG fusion mechanisms during early embryogenesis of two insects *Periplaneta americana* and *Rhodnius prolixus*. We showed that eggs with 0 and 3 days (in *R. prolixus*) and 0 and 5 days (in *P. americana*) contained a differential size pattern of YGs contain a greater amount of large YG (LYG) at day 3 and day 5, respectively,. Day 3/5 eggs also contain the highest [Ca^{2+}] found during early embryogenesis of these insects. *In vitro* YGs treatment with the [Ca^{2+}] found on day 3/5 eggs resulted in LYG appearance, as observed *in vivo*. We confirmed that calcium dependent LYG formation by observations of fluorescent membrane dye transfer from previously labeled small YGs (SYG) to larger ones. In addition, we showed that YGs incubation in the presence of calcium promotes the vitellins degradation *in vitro*, evidencing that YGs fusion events take part on yolk mobilization machinery. We showed that the membrane fusion of YG regulated by calcium is probably important for yolk degradation during embryogenesis of these insects.

POSTER PRESENTATION

Use of GIS to characterize areas of non-target feeding by biological control agents of invasive weeds: A case study in Tennessee, USA

Greg Wiggins, Jerome Grant, Paris Lambdin

University of Tennessee, Knoxville, Tennessee, United States

Introduction: The efficacy of two weevils (*Rhinocyllus conicus* and *Trichosirocalus horridus*) introduced in the U.S. against the Eurasian musk thistle (*Carduus nutans*) is countered by their impact on a few native *Cirsium* thistles. Non-target feeding of these weevils may impact plant reproduction and plant populations. Because the biologies of these weevils are closely linked with musk thistle, the distribution of musk thistle populations may influence non-target activity. The use of geographic information systems (GIS) could be useful in analyzing the spatial relationships among musk thistle, weevils and native thistles by characterizing suitable habitats for each thistle species over a large spatial scale.

Methods: In Spring 2004, a four-year study was initiated to identify potential areas of non-target feeding using spatial analysis. The study area (ca. 4,800 km^2) consisted of four counties in eastern Tennessee. Four thistles (native: *C. carolinianum* and *C. discolor*; introduced: *C. nutans* and *C. vulgare*) were selected as model species. Mahalanobis distance (D^2) was used to identify suitable habitats for each thistle species.

Results and Discussion: Cumulative frequency analysis indicated that threshold D^2 values of as low as 6.58 correctly classified over 65% of suitable habitats for all thistles observed in this study. Comparatively, random locations would require many more localities and greater D^2 values to correctly classify similar percentages of suitable habitats. The area of overlap of all species occupied ca. 4% of the total study area. These areas should be the focus of future model-testing efforts and non-target studies.

POSTER PRESENTATION

Arthropod abundance and diversity in commercial Bt corn farms and adjacent riparian areas in the Philippines

Edwin Alcantara[1], Maria Dulce Mostoles[2], Barbara Caoili[3], Pio Javier[3]

[1]National Institute of Molecular Biology and Biotechnology, University of the Philippines (Los Baños), College, Laguna, Philippines, [2]Camarines Sur State Colleges, Pili, Camarines Sur, Philippines, [3]Crop Protection Cluster, University of the Philippines (Los Baños), College, Laguna, Philippines

Introduction: Non-target arthropods are important trophic components of the ecosystem because they also affect the sustainability of transgenic crops. The present study would like to test the hypothesis that Bt corn does not adversely affect non-target arthropod abundance and diversity in corn and riparian ecosystems.

Methods: Arthropod abundance data were obtained by sampling plots selected within commercial farmers' fields and adjacent riparian areas. Significant effect of Bt corn MON 818 YieldGard™ on both the non-target predatory insect *Micraspis discolor* abundance and overall arthropod diversity was determined by repeated measures ANOVA. Principal response curve (PRC) analysis was used to determine significant differences in species composition at every sampling date in Bt- and non-Bt corn arthropod communities. Similar studies were conducted in adjacent riparian areas.

Results: There was no significant difference between Bt and non-Bt corn in the abundance of the predatory insect *M. discolor* within the 2006 (P= 0.436) and 2007 (P= 0.254) cropping seasons. Statistical analysis of the calculated Simpson and Shannon indices revealed no significant difference in arthropod diversity within all experimental sites in both the same period. Similarly, PRC analyses indicated no significant difference in species composition in all the arthropod communities.

Conclusion: Bt corn MON 818 YieldGard™ sustains arthropod abundance and diversity in corn and riparian ecosystems.

POSTER PRESENTATION

Effect of behavior on PVY transmission efficiency of *Rhopalosiphum padi*

Yvan Pelletier, Xianzhou Nie

Potato Research Centre, Fredericton, NB, Canada

Potato virus Y is transmitted to potato in a non-persistent manner by many aphid species, some of which do not colonize this crop. The behavior of *Rhopalosiphum padi* (L.) on potato, a plant species that is not colonized by this aphid, was described and compared with that of the potato colonizing aphid, *Myzus persicae* (Sulzer). A higher proportion of winged morph of *R. padi* than *M. persicae* left the plant, but aphids that stayed in contact with the plant took the same mean time to initiate the first probe and it lasted the same mean time compared to *M. persicae*. Electronic Penetration Graph technique was used to study the probing behavior of the aphids during PVY transmission tests. Transmission rate decreased from 29% to 8% when the acquisition time decreased from 5 minutes of continuous probing to one hour with *M. persicae*, but remained low (2% and 1%) with *R. padi*. Most of the difference in transmission rate between acquisition time with *M. persicae* and between aphid species was related to the change in the time and behavior taking place between the last cell puncture of the acquisition phase to the first cell puncture of the inoculation phase. Results presented here clearly demonstrated the importance of host-plant selection and probing behavior in the transmission of non-persistent plant viruses. They also stress the need to consider the behavior of the aphid in the design of laboratory tests of virus vector efficacy.

POSTER PRESENTATION

Environmental stresses induce expression of cuticular protein genes in the Colorado potato beetle

Jianhua Zhang, Claudia Goyer, Yvan Pelletier

Potato Research Centre, Fredericton, NB, Canada

The deposition of cuticular proteins usually occurs during molting process. Three putative glycine-rich proteins, Ld-GRP1 to 3, were identified and characterized from the Colorado potato beetle. The Ld-GRPs contained conserved GXGX and/or GGXG sequence repeats. Ld-GRP1 also contained a conserved AAPA/V motif commonly found in cuticular proteins. The transcripts of Ld-GRP1 and Ld-GRP2 were detected in epidermal cell layer by *in situ* hybridization making them putative cuticular proteins. The Ld-GRPs were highly induced by the insecticide azinphosmethyl (organophosphorous) 2-3 weeks after adult molting. Gene expression level was higher in azinphosmethyl-resistant beetles than in susceptible beetles. Furthermore, Ld-GRP1 and Ld-GRP2 were highly induced by dry environmental conditions. These results suggested that the insect might increase cuticular component deposition in adult stage in response to the environmental stresses. This ability may allow the insect to adapt to new or changing environments.

POSTER PRESENTATION

Notes on mosquito larvae predators in the Riyadh Region, Saudi Arabia

Azzam Alahmed, Suliman Alamr

King Saud University, Riyadh, Saudi Arabia

A survey for mosquito larvae predators in Riyadh Region, Saudi Arabia, was conducted during the period June 2003 -July 2004, in which 9 different mosquito larvae predators were collected from 46 sites. The collected larvae predators consisted of the mosquito-fish *Gambusia affinis*, (Cyprinodontiformes: Poeciliidae) (4.1%), the Odonata nymphs of the families Coenagrionidae (6.6%) and Libellulidae (7.4%), the water bug *Sigara* sp. (Hemiptera: Corixidae) (31.1%), the water beetle *Agabus* sp. (Coleoptera: Dytiscidae) (22.1%), *Triops* sp (Notostraca: Triopsidae) (13.9%), the adult water beetles *Eretes stictus* (Coleoptera: Dytiscidae) (7.4%), the larvae of the beetle *Cybister tripunctatus* (Coleoptera: Dytiscidae) (3.3%) and adult water beetles *Dineutes aereus* (Coleoptera: Gyrinidae) (4.1%). The predatory efficiency of these predators was assessed in the laboratory using fourth larval instars of *Culex quinquefasciatus* (Diptera: Culicidae) as prey. The highest predatory efficiency was shown by *G. affinis*, followed by *Triops* sp., *E. stictus* and Odonata nymphs of the family Libelulidae respectively.

POSTER PRESENTATION

Knockdown resistance (*kdr*) in the malaria vector *Anopheles arabiensis* from Eastern Sudan

Yousif Himeidan[1], Hong Chen[2], Fabrice Chandre[3], Martin Donnelly[4], Guiyun Yan[2]

[1]Faculty of Agriculture and Natural Resources, University of Kassala, Kassala, Sudan, [2]College of Health Sciences, University of California-Irvine, California, Irvine, United States, [3]Institut de Recherche pour le Développement, Cotonou, Benin, [4]Liverpool School of Tropical Medicine, Liverpoool, United Kingdom

Introduction: In Africa, knockdown resistance in malaria vector mosquitoes may become a major problem for malaria interventions because pyrethroids are the mainstay of vector control strategies. Regular surveillance of the susceptibility of vector populations is imperative for implementing effective insecticide resistance management strategies. This study was aim to assess knockdown resistance (*kdr*) in three populations of *Anopheles arabiensis* from eastern Sudan.

Methods: Based on field-collected anopheline larvae, insecticide bioassays for 4% DDT and 1% permethrin were performed on non-blood fed, female 1–3-day old adults using WHO protocols. DNA was extracted individually from the bioassay-tested mosquitoes, which were identified by the rDNA-PCR method. The L1014F and L1014S *kdr* alleles were screened on a Li-Cor 4300 DNA Analyzer. The results were confirmed by DNA sequencing of ~300-baspair fragments amplified by the primers AgD1 and AgD2.

Results: Bioassay mortalities ranged from 96.9-99.6% against 4% DDT and from 98.4-100% against 1% permethrin, respectively. *An. arabiensis* was the only member of *An. gambiae* complex identified in the area. The L1014F and L1014S alleles were detected in 25 out of 498 mosquitoes. L1014F allele was associated with insecticide resistance, while L1014S allele was observed only in four susceptible individuals. The overall *kdr* frequencies ranged from 7.0% in the area where insecticide-treated nets were used to 3.0% in the area with agricultural insecticide use.

Conclusion: The presence of the *kdr* alleles in *An. arabiensis* in Sudan emphasizes the need to develop appropriate resistance monitoring and management strategies for malaria vectors.

POSTER PRESENTATION

Could mosquitoes become resistant to repellents?

Nina M Stanczyk[1], Lin Field[1], James G Logan[1], John F.Y. Brookfield[2]

[1]Centre for Sustainable Pest and Disease Management, Biological Chemistry Department, Rothamsted Research, Hertfordshire, United Kingdom, [2]Institute of Genetics, The University of Nottingham, Queen's Medical Centre, Nottingham, United Kingdom

Introduction: Repellents are utilised worldwide as personal protection against many biting insects including mosquitoes. DEET is one of the most effective and commonly used repellents, however, new research has demonstrated that natural human-derived repellents could also be used to repel mosquitoes. During laboratory repellency trials a small proportion of mosquitoes still respond to human odours despite the presence of DEET or other repellent compounds.

Methods: Preliminary behavioural assays identified *Aedes aegypti* females that were insensitive to a natural human-derived repellent or DEET. The offspring of these repellent-insensitive females were then tested over three generations to determine if there was a genetic component to the trait. A further series of selection experiments using both types of repellent is being performed to obtain pure-breeding insensitive lines.

Results: In the preliminary selection experiments there was an increase in the proportion of mosquitoes that were insensitive to the repellent throughout successive generations, which shows that there is a heritable component to the trait. In future work this will allow genetic crosses to be carried out to determine the mode of inheritance, and electrophysiology and molecular techniques will be used to determine the mechanisms and gene(s) involved.

Conclusion: This research provides an insight into how insensitivity to repellents can arise and spread throughout a population when the trait is selected for, as might naturally occur in the wild. This information will aid control programmes that seek to use repellents. A more detailed understanding of the gene(s) responsible for insensitivity may lead to novel control methods.

POSTER PRESENTATION

Effects of different control programs on the populations of the lettuce aphid *Nasonovia ribisnigri* (Hemiptera: Aphididae) and its natural enemies

Patricia Larraín, Claudio Salas, Carlos Quiroz

[1]Sociedad chilena de Entomología, Santiago, Chile, [2]ESA, Maryland, United States

A study was conducted in 2007 to determine the effect of different control programs of *Nasonovia ribisnigri* on winter head lettuce, var. Cool Green. The statistical design was random bloks, with 6 treatments and four replicates, conducted in field conditions at Pan de Azúcar (30°04' South lat.; 71°55' West long.), Coquimbo Region, Chile. Treatments were: T1, Pirimicarb (pirimor 250g/ha) foliar application; T2, Chemigation withThiametoxam (actara 25 WG, 200g/ha) in seedlings; T3, Thiametoxam (actara 25 WG, 200g/ha) foliar application immediately after plantation; T4, T2 plus Pirimicarb (pirimor 250g/ha) foliar application; T5, T2 plus Thiametoxam (actara WG)foliar application ; and T6 untreated check. With exception of treatment three (T3), all foliar applications were done once *N. ribisnigri* reach an economic injury level of 1 aphid per plant per week.

The number of alive aphids (alate and apterous) and natural enemies was counted weekly in each plot until harvest.

Although at harvest head infestation levels were significant lower in plots treated with chemigation of thiametoxam in seedlings and pirimicarb foliar application, head contamination was more than likely, not commercially acceptable in any of the treatments. *Platycheirus sp.* syrphid larvae appeared as the main natural enemies responsible for aphid suppression. Its numbers were significant higher in the untreated check than in the insecticides treated plots.

POSTER PRESENTATION

Population fluctuation of Diptera Muscidae and Faniidae associated with pork production in central Chile

Claudio Salas, Patricia Larraín, Carlos Quiroz

[1]Sociedad Chilena de Entomología, Santiago, Chile, [2]ESA, Maryland, United States

From November 2006 to October 2007, a study was carried out at Longovilo (33º55' lat. Sur, 71º23' lon. Oeste), Central Chile with the aim to assess the population fluctuation of fly species belonging to the family Muscidae and Fanniidae, in farms that have approximate stock of 660.000 hogs.

Forty four Stickem traps (model BTSTICK flies I-40; BTS Intrade Laboratories) were distributed in different staffs from wean to sale, zones of irrigations with slurry, slurry stabilization lagoons, dead animal transfer units, plants of water processing, zones of composting, and restaurant located in the neighborhood of the zone of production.

After 1 years of studies, the presence of *Musca domestica, Ophyra aenescens, Psilochaeta chalybea and Stomoxys calcitrans* (Diptera: Muscidae) and *Fannia canicularis* and *Fannia femoralis* (Fanniidae) were established.

More than 67.000 specimens were collected in the course of the investigation. *M. domestica* represented 29% of the total capture, while *O. aensecens* was the 61,4%, *P. chalybea* was the 0,018%, *S. calcitrans* was the 8,6%, *F. canicularis* was the 0,02% and *F. femoralis* was the 0,88%.

Regarding captures according to zones, 82% was obtained from pork staff, 2% from zones of irrigation with slurry, 9% from slurry stabilizations lagoons, 0,97% from dead animal transfer units, 2% from plants of water processing, 3,4% from zones of composting, at the restaurant located nearby only 0,1% of the total fly population was captured.

POSTER PRESENTATION

Which island parasitoid faunas are evenly sampled? A case study using the Taxapad database on Ichneumonoidea (Hymenoptera)

Ana M. C. Santos[1], Joaquín Hortal[2], Kostas A. Triantis[3], Owen R. Jones[1], Paulo A. V. Borges[4], Donald L. J. Quicke[1]

[1]Imperial College London, Ascot, United Kingdom, [2]NERC Centre for Population Biology, Imperial College London, Ascot, United Kingdom, [3]Biodiversity Research Group, Oxford University, Oxford, United Kingdom, [4]CITA-A, Universidade dos Açores, Azores, Portugal

Introduction: Available databases of species diversity are generally biased taxonomically, geographically, or both. Several variables have been identified as effective descriptors of the processes of establishing species richness, such as body size, species abundance, geographical range size, taxonomist home range and non-random availability of expertise. Our knowledge of parasitoid species diversity is no exception, despite their importance as key components of nearly all terrestrial ecosystems. We investigated the reliability of a published database on the world ichneumonid wasps (Hymenoptera, "Parasitica") and determined which island parasitoid faunas are evenly sampled, and thus are appropriate to be used in future analysis trying to identify the underlying patterns of parasitoids on islands.

Methods: First, we used the dispersion observed on each island from the richness predicted by the species-area relationship (SAR) to determine if the archipelago falls into the same SAR as islands. After this, we applied two criteria to determine which islands are evenly sampled: a) SAR curves, and b) taxonomic information from each geographical region.

Results: Almost all the archipelagos analysed fell inside the SAR dispersion interval, demonstrating that archipelagos can be analysed as single islands when applying SARs. More islands were excluded with the taxonomic information criterion than with the SAR curves criterion. However, only the last criterion allowed us to exclude oversampled islands.

Conclusions: The method developed here can be useful in biodiversity research since it identifies some types of bias and produces comparable databases.

POSTER PRESENTATION

Effect of acetylsalicylic acid and oxalic acid on *Myzus persicae* and *Aphidius colemani*

Nikolaos Karatolos, Paul Hatcher

University of Reading, Reading, Berkshire, United Kingdom

Introduction: Plants can respond to damage by pests with both induced direct and indirect defences by the attraction of their natural enemies. Foliar application of several plant-derived chemicals, such as salicylic acid and oxalic acid can induce these defence mechanisms.

Methods: The effect of acetylsalicylic acid and oxalic acid on the aphid *Myzus persicae* Sulzer (Homoptera: Aphididae) and its parasitoid *Aphidius colemani* Viereck (Hymenoptera: Aphidiidae) was investigated. Direct application of acetylsalicylic and oxalic acids on those insects, as well as choice and no choice tests with foliar application of both chemicals on Brussels sprouts plants, *Brassica oleracea* var. *gemmifera* L., were carried out.

Results: Both chemicals have a direct effect on aphid development by increasing their mortality. Foliar application of both chemicals does not seem to induce resistance against aphids. Furthermore, foliar application of such compounds has the potential to induce indirect plant defences against aphids, by attracting parasitoids and encouraging the aphid parasitisation. Although the direct application of both chemicals on parasitoids affects negatively their development by reducing their emergence ability, foliar application does not have any negative effect. However, oxalic acid is found to reduce the number of emerged parasitoids in no-choice experiments.

Conclusion: Foliar application of acetylsalicylic and oxalic acids can be used in order to encourage aphid parasitisation, but care is needed as these chemicals can have negative effects on beneficial organisms.

POSTER PRESENTATION

Influence of the formulation matrix on repellency of IR3535® and KBR 3023 against different medically important mosquito species

Rainer Kroepke[1], Gerhard Benner[1], Jens Schulz[1], Klaus-Peter Wittern[1], Nigel Hill[2], Nicole Beyer[3], Ruediger Graf[3]

[1]Beiersdorf AG, Hamburg, Germany, [2]London School of Hygiene and Tropical Medicine, London, United Kingdom, [3]Merck KGaA, Darmstadt, Germany

The insect repellents, IR3535® (Ethyl Butylacetylaminopropionate, EBAAP) and KBR 3023 (Hydroxyethyl Isobutyl Piperidine Carboxylate, Picaridin, Bayrepel®) were evaluated in a field study at a panel of volunteers (10 male, 1 female). The testings were conducted in the Vaca Diez region, Bolivia, on field populations of medically important mosquitoes. *Anopheles darlingi, An. albitarsus, Aedes aegypti* and *Culex pedroi* were identified as the main species of the population.

Mimicking the realistic application by the consumer five proprietary repellent formulations fully marketable in composition and appearance were tested regarding their efficiency for preventing bites. The substances were applied as hydro-alcoholic spray solution or skin lotion in concentrations of 15 and 20%.

All tested samples provided lasting protection (time to first bite) over several hours with a mean of approximately 6 h. There was no significant difference in protection times between the two active substances.

Remarkably, the efficiency was more affected by the application form than by the concentration of the insect repellent itself. The applied lotion with 15% repellent led to longer protection times compared with the hydro-alcoholic spray formulation with 20%.

POSTER PRESENTATION

Effects of scabies mites on skin endothelial cells

Larry G. Arlian, B. Laurel Elder, Marjorie S. Morgan

Wright State University, Dayton, Ohio, United States

Introduction: The scabies mite, *S. scabiei*, infects millions of people worldwide and induces inflammatory and immune responses in the skin that are delayed the first time a person is infested. Venule endothelial cells of the skin microvasculature play a key role in regulating migration of inflammatory and immune cells into the site of mite infestation. The purpose of this study was to determine if the expression of cell adhesion molecules (CAMs) on endothelial cells induced by scabies mites is altered in the presence of histamine, lipid-mediators and cytokines that likely occur in scabietic lesions.

Methods: Cultured human microvascular endothelial cells were incubated with selected stimulants in the presence or absence of *S. scabiei* extracts for 6 hrs. The expression of adhesion molecules on the cells and secretion of cytokines into the medium were measured by ELISA.

Results: Scabies mite extract induced endothelial cells to express ICAM-1, VCAM-l, and E-selectin above constitutive levels. Co-stimulation with *S. scabiei* extract and histamine, prostaglandin D2, prostaglandin E2, leukotriene B4, and IL-6 did not change the level of secretion of ICAM-1, VCAM-l, and E-selectin that was induced by scabies alone. Scabies extract down regulated the TNFα induced expression of VCAM-1 but not the IL-1α, or IL-1β induced expression.

Conclusion: The expression of CAMs by human endothelial cells of the skin microvasculature in response to bioreactive substances from *S. scabiei* was not co-influenced by histamine, prostaglandins, leukotrienes, and IL-6 that likely are secreted by surrounding cells in response to scabies mites.

POSTER PRESENTATION

Comparison of natural and artificial bloodfeeding in *Anopheles stephensi*

Hassan Nasirian, Hossein Ladonni, Fatemeh Rafii

Department of Medical Entomology and Vector Control, School of Public Health and Institute of Public Health Researches, Medical Sciences/University of Tehran, Tehran, Islamic Republic of Iran

Introduction: The increasing demand for laboratory-reared haematophagous for research and control purposes makes it necessary to develop effective and standardized mosquitoes feeding methods without using live animals as hosts. Live animals have been used successfully to maintain and colonization of haematophagous insects. However, the use of animal for this purpose is expensive, inconvenient, and increasingly unacceptable in terms of animal welfare. The purpose of this study was to comparison of natural and artificial bloodfeeding in *Anopheles stephensi* (Lis.) by Guinea pig and human whole blood in insectary.

Methods: An artificial membrane and natural, bloodfeeding technique was evaluated for *An. Stephensi* using insectarium's strain in Iran. Parafilm "M" and human whole blood were satisfactory as feeding membrane and nourishing source in artificial bloodfeeding and Guinea pig as a natural bloodfeeding, respectively.

Results: Comparison of feeding rates and different ages were fluctuated in *An. stephensi* with human whole blood via membrane Parafilm "M". *An. stephensi*, a mosquito that normally requires a vertebrate blood meal to produce eggs, has been reared successfully for three generations on this substitute blood meal. Comparison between natural and artificial bloodfeeding were not observed significant differences.

Conclusions: Data showed that artificial feeding with this method, especially in the investigating projects were completely efficient and suitable, in numerous rearing and increasing populations of mosquitoes for specified time without any disadvantages include accidental disease transmission and hypersensitivity to mosquito bites that natural bloodfeeding was to have.

POSTER PRESENTATION

Monitoring of German cockroach insecticide resistance in Iran

Hassan Nasirian, Hossein Ladonni, Mansoreh Shayeghi

Department of Medical Entomology and Vector Control, School of Public Health and Institute of Public Health Researches, Medical Sciences/University of Tehran, Tehran, Iran, P.O. Box 6446-14155, Tehran, Islamic Republic of Iran

Introduction: The German cockroach, *Blattella germanica* (L.), is an important household insect pest worldwide. In addition to its economic importance, the German cockroach is a significant health hazard and acts as a mechanical vector and reservoir for pathogenic agents. Increased incidents of asthma caused by German cockroach allergens are associated with relatively high cockroach infestations and have added emphasis to the need for the control of this insect pest. Extensive use of insecticides has led to the development of resistance in German cockroach to a wide range of insecticides including organochlorines, organophosphates, carbamates and pyrethroids.

Methods: The current study was designed to monitoring of German cockroach insecticide resistance in Iran. The susceptibility level and insecticide resistance mechanisms of German cockroach to organochlorated, organophosphate, carbamate and pyrethroid insecticide groups have been studied and resistant to these insecticides.

Results and Conclusions: Since fipronil has not been used previously in Iran, German cockroach ranged from 1.5- to 2.6-fold resistant to fipronil, so this relatively low resistance could be due to cross-resistance to dieldrin. Therefore, based on the data, fipronil could not be recommended a valuable tool in resistance management of German cockroach in Iran. Management of cockroach populations in urban environments has recently shifted from the predominant use of insecticide sprays to the inclusion of baits in management programs. Studies showed that baits especially fipronil and imidacloprid baits appear to have considerable potential as a bait insecticide for insecticide resistant German cockroach infestation in Iran. I propose further studies on toxicity of novel insecticides such as avermectins acting at GABA, gama-aminobutyric acid, and glutamate receptors in proximity to chloride channels, diacylhydrazines mimicking the action of ecdysone, indoxacarb acting at a novel site in sodium channels, and imidacloprid, thiamethoxam, and spinosad acting at novel sites on the nicotinic acetylcholine receptor, several promising products acting at new target sites, which are currently not affected by resistance that will be used for pest control especially against German cockroach in Iran.

POSTER PRESENTATION

Comparison of Fipronil topical application and WHO glass jar methods, time and toxicity in *Blattella germanica* field population strains

Hassan Nasirian, Hossein Ladonni, Kamal Mashhadi Esmaeily

Department of Medical Entomology and Vector Control, School of Public Health and Institute of Public Health Research, Tehran University of Medical Sciences, Tehran, Iran, P.O. Box 6446-14155, Tehran, Islamic Republic of Iran

Introduction: German cockroaches, *Blattella germanica* (L.), are the most common urban environment cockroaches found in houses and restaurants and remain one of the most economically and medically important pest.

Methods: The duration of Fipronil topical application and WHO glass jar methods toxicity against eleven strains of feral German cockroaches, *Blattella germanica* (L.), was determined.

Results: In the topical application bioassay, the average LD_{50} of susceptible strain was 1.8, 1.3 and 0.96 ng per insect after 24 h, 48 h, and 72 h, respectively. As with the susceptible reference strain, where LD_{50} was halved from 24 to 72 h, the LD_{50} of Fipronil decreased with time in the field populations. In the WHO glass jar bioassay, the average LT_{50} of susceptible strain was 16.4, 14.3, 12.4 and 11.3 exposure minutes after 24 h, 48 h, 72 h and 96 h, respectively. As with the susceptible reference strain, where LT_{50} was halved from 24 to 96 h, the LT_{50} of Fipronil decreased with time in the feral German cockroach strains.

Conclusions: These results indicate that the Fipronil was relatively slow-acting in topical application and WHO glass jar method bioassay, with LD_{50} and LT_{50} values decreasing until 72 and 96 h and becoming stable thereafter, respectively.

POSTER PRESENTATION

Human scalp myiasis in Bandar-Abbas, Hormozgan province, south of Iran

Hassan Nasirian[1], Mussa Soleimani Ahmadi[2]

[1]Department of Medical Entomology and Vector Control, School of Public Health and Institute of Public Health Researches, Medical Sciences/University of Tehran, P.O. Box 6446-14155, Tehran, Iran, Tehran; [2]School of Public Health, Hormozgan University of Medical Sciences, Bandar-Abbas, Iran, Bandar-Abbas, Islamic Republic of Iran

Introduction: This is the second report of *Chrysomia bezziana* larvae infection in human in Iran.

Methods: A 5-year-old boy with sever headache and agitation symptoms referred to the Kodekan Hospital in Bandar-Abbas city, Hormozgan province, South of Iran. In the operating room, about 40 larvae of 3rd instar fly larvae were pulled out under the general anesthesia condition. A 30 larvae were preserved in 70% methanol and the rest were reared on ground beef placed on the top of moist soil in a mosquito net case under insectary condition at 30 ± 2 ˚C, 70 ± 5% RH. The full grown larvae crawled into the soil and developed to adult flies later on. The larvae and adult flies were identified by the available keys.

Results and Conclusions: Our precise identification indicated that the flies were the Old World screw-worm (*Chrysomia bezziana*). Physical examination showed sever extensive wound in parietal of the skull that the whole subcutaneous tissues were eaten by larvae. Endoscopy consideration revealed the presence of numerous larvae lodged inside the lateral sub marginal and the depth of the subcutaneous tissues in the wound.

POSTER PRESENTATION

Predacious mite abundance in IPM orchards in southern Quebec, Canada

Noubar J. Bostanian[1], Michael J. Hardman[2], Gaétan Racette[1], Jeffrey L. Franflin[2]

[1]Horic. Dev. Res. Centre, Agriculture and Agri-Food Canada, St. Jean-sur-Richelieu, Qc., Canada, [2]Atlantic Food and Hortic.Res. Centre, Agriculture and Agri-food Canada, Kentville , NS., Canada

Introduction: Following the withdrawal of key pesticides for biocontrol programs, many growers have adopted conservation and augmentation tactics for beneficial mites in their orchards. This evolution of pest management strategies encouraged us to re-visit several orchards to assess the presence of predacious mites in these orchards.

Materials and Methods: The field work was carried out in seven orchards, from 28 June to 28 September 1999 and from 12 July to 13 September 2000. A 5 ha block was sampled weekly in a northeast-southwest diagonal transect. The sampling was done by administering two blows to two outer branches ca. 1.5 m from the ground and collecting the displaced mites in vials. Specimens were mounted and identified according to Chant et al. (1974), Chant and Hansell (1971) and Smith Meyer and Ueckermann (1987). Repeated measures analysis of variance was used to analyze the data.

Results: Predacious mites were present in all the orchards and 13 species were identified. *Amblyseius finlandicus* and *Typhlodromus conspicuous* were identified for the first time in Quebec. *Agistemus fleschneri*, *Amblyseius fallacis* and *Typhlodromus caudiglans* were the most abundant species. Each season a complex of two to eight species per orchard were present. Repeated measures analysis showed that year had a significant effect on the counts of *A. fleschneri*, *A. fallacis* and *T. caudiglans*. It had no effect on *Anystis baccarum* or *Balaustium sp.*

Conclusion: Conservation and augmentation strategy in Quebec apple orchards in the early 1990s has had a positive impact. Prey-predator ratios have been in favour of predators and phytophagous mites have been below the action threshold for acaricide treatment.

POSTER PRESENTATION

Residual toxicity of six novel insecticides to *Anystis baccarum*

Noubar J. Bostanian, Marie-Claude Laurin

Horiculture Dev. Res. Centre, agriculture and Agri-Food Canada, St. Jean-sur-Richelieu, Qc., Canada

Introduction: In Quebec biological control programs for pest mite species in vineyards and orchards is based on the conservation and augmentation of natural enemies. *Anystis baccarun* is the key predator in vineyards. This study reports the effects of several insecticides used in vineyards.

Materials and Methods: Specimens were collected in 5L buckets from an experimental orchard where habitat management tactics are implemented. The mites were brought to the lab. in 30- ml plastic cups. In the lab. the mites were exposed individually to residues of methoxyfenoxide, spinosad, acetamiprid, imidacloprid, thiamethoxam and lambda-cyhalothrin. The label rates were calculated on the premise of applying 540 liters of sprayable material per hectare. The exposure was made in cages made from 50 mm petri dishes with a circular window . The cages were stored in a growth chamber set at 21^0C, 80% RH and a photoperid of 16:8 (L.D). Mortalty counts were made after 48 h.

Results and Discussion: All the insecticides evaluated had no toxic effects on adult *A.baccarum* except lambda-cyhalothrin. Lambda-cyhalothrin is very toxic to this predator under lab. conditions. The Canadian label rate of 0 .0184 g Ai /liter is 26-fold the LC_{50} value of 0.0007g AI / liter.

Conclusion: Imidacloprid, acetamiprid, thiamethoxam, methoxyfenoxide and spinosad are non-toxic to *A. baccarum* adults. Therefore, the effects of these compounds to *A. baccarum* fecundity, egg hatch and juveniles should be evaluated to complete our understanding of their safety. Lambda-cyhalothrin is too toxic to justify additional studies.

POSTER PRESENTATION

Kaffir lime, *Citrus hystrix* as a potential botanical insecticide to control the diamondback moth, *Plutella xylostella*.

Rita Muhamad Awang, Loh Siew Fan

[1]Universiti Putra Malaysia, 43400 UPM, Serdang, Selangor, Malaysia, [2]Universiti Putra Malaysia, 43400 UPM, Serdang, Selangor, Malaysia

Introduction: Botanical insecticides are either simply derived from natural plants parts or purified insecticidal compounds that are isolated from such plants materials. The kaffir lime, *Citrus hystrix (*family Rutaceae) is a Southeast Asian citrus plant with very pungent leaves. This study was conducted to examine the effect of *C. hystrix* dried leaves and fruit peels extracts with ethanol at different concentration on *P. xylostella* mortality

Methods:. Four concentrations of 10%, 20%, 30% and 40% for both ethanol extractions were tested and Permethrin and Neemix were used as comparisons. Cabbage leaves (*Brassica oleracea* L var. capitata) were used as substrates for the experiment. Ten third instars diamondback moth larvae were placed on the cabbage leaf treated with 1 ml extract solution in petri dishes. Eleven treatments were prepared with 10 replications. Dishes were incubated in the laboratory for 3 days. Larvae mortality was recorded every 24 hours.

Results: It was observed that kaffir lime leaves extract have slightly higher insecticidal properties as compared to the fruit peels extract. The number of larvae killed by both of the crude extracts increase over time. Their toxicity may be as good as compared to Neemix at high concentration (30% and 40%).

Conclusions: Both of the leaves and peels extract could be used as a potential botanical insecticide because of their repellent and antifeedant properties observed during the experiment.

POSTER PRESENTATION

Insecticidal action of galectin-transfected Arabidopsis on *Plutella xylostella*

Shiang-Jiuun Chen[1], Siou-Hua Wang[2], Shaw-Jye Wu[2], Ling-Long Kuo-Huang[1], Ju-Chun Hsu[3], Rong-Nan Huang[1]

[1]Department of Life Science, College of Life Science, National Taiwan University, Taipei, Taiwan, 106, Taiwan, Province of China, [2]Department of Life Science, College of Science, National Central University, Taoyuan 32054, Taiwan, Taiwan, Province of China, [3]Department of Entomology, College of Bioresources and Agriculture, National Taiwan University, Taipei 106, Taiwan, Taiwan, Province of China

Galectins (GALs) are a family of mammalian sugar-binding proteins specific for β-galactosides. Our previous studies have shown that the larvae development of diamondback moth (*P. xylostella*) was significantly disturbed when fed with galectin1 (GAL1) extract and/or recombinant GAL1 proteins purified from GAL1 over-expressed *E. coli.* In these studies, we further showed that GAL1 could interact with chitosan and chtin *in vitro*, indicating that chitosan and chitin could be a ligand of GAL1. Chitin is the structural elements of the exoskeletons and peritrophic membranes in various insects, and could be utilised as a potential target for selective bio-insecticide. To further explore the potential of GAL1 as a bio-insecticide, we established a galectin-transfected stable clone of *Arabidopsis* (GAL1-*Arabidopsis*) for further investigation of insecticidal activity. The results showed that GAL1 were successfully expressed in GAL1-*Arabidopsis* clone. The survival and body weight of *P. xylostella* fed on GAL1-*Arabidopsis* clone were significantly decreased in a time-dependent manner. The ultrastructural studies further showed that the midgut of GAL1-*Arabidopsis*-fed insect was distorted. In view of GAL1 having a carbohydrate-recognition domain recognized the structural motif N-acetyllactosamine (Gal β 1-4GlcNAc) that is similar to that of chitin (β-1,4 N-acetyl-D-glucosamine), we proposed that the insecticidal mechanism of GAL1 involves direct binding with chitin, the main component of insect exoskeleton as well as peritrophic matrices lining the gut epithelium.

POSTER PRESENTATION

Occupation of bird-nest-boxes by invertebrates: is there an inter-taxa competition?

José Pablo Veiga[1], Vicente Polo[1], Wanyoike Wamiti[2]

[1]Museo Nacional de Ciencias Naturales, CSIC, Madrid, Spain, [2]National Museums of Kenya, Nairobi, Kenya

Introduction: Little is known about the propensity of insects and other invertebrates to occupy nest-boxes (usually targeted to birds). Competition for these places as suitable breeding sites or shelters may be potentially strong both among invertebrate taxa and between harmful arthropods and birds or other vertebrates that can use the boxes. We investigated the frequency of occupation of wooden nest-boxes by invertebrates and vertebrates in five study sites representing three ecosystem types (savanna, montane forest and tropical rain forest) in Kenya.

Methods: One hundred and eighty wooden-boxes were placed in five different localities in Kenya in Sept and October 2006. The boxes were checked during the long rains (April-June) and the short rains (September-October) in 2007. We did not collect specimens so the identification of invertebrates was made *in situ* and by inspecting photographs. With the exception of honeybees *Apis mellifera*, classification of other invertebrates was only possible at the level of genus, family or even upper.

Results: Hymenoptera species were the most frequent occupant of nest boxes. In 4.1% of the boxes during spring and 14.0% during fall, we found active hives while in 3.0% either the bees had abandoned the boxes or the honey had been harvested by humans. In 9.2% of the checkings, the box had nesting wasps or their old nests. 4.5% of the boxes had ant nests. All these kind of insects, together with some other venomous arthropods (e.g. arachnids) also found occupying boxes, may represent a serious threat for potential competitors. Only in 14 out of 84 boxes occupied by invertebrates, we found two or more different taxa. The proportion of boxes with arthropods increased markedly from spring to fall suggesting that occupation rates is likely going to increase following our last control.

Conclusions: A relatively high proportion of nest boxes were occupied by arthropods, many of them potentially harmful for other holders, either vertebrate or invertebrate. This implies that inter-taxa competition (even invertebrates vs. vertebrates) for suitable nesting places or shelters may be an important factor affecting population density and structure in hole-nesting-sheltering species.

POSTER PRESENTATION

Oviposition preference by the vine weevil (*Otiorhynchus sulcatus*) in relation to raspberry (*Rubus* spp.) cultivars

Katy Clark[1], Scott Johnson[1], Sue Hartley[2]

[1]Scottish Crop Research Institute, Dundee, United Kingdom, [2]University of Sussex, Brighton, United Kingdom

Introduction: The vine weevil (*Otiorhynchus sulcatus*) is a highly polyphagous insect herbivore and a destructive pest in many production systems. The survival and reproductive success of *O. sulcatus* can be influenced by the status of their host plant, but it is unclear how different plant cultivars affect oviposition behaviour of adults living aboveground. We investigated adult feeding and oviposition behaviour on nine raspberry cultivars.

Methods: Nine cultivars were used; Glen Ample, Glen Clova, Glen Rosa, Glen Magna, Glen Moy, Malling Jewel, Octavia, Tulameen and a wild variety. An adult choice experiment was conduced in 20 large arenas that allowed the weevil to move freely between the plants choosing where to eat and oviposit. In the adult no-choice experiment, individual weevils were caged on a single plant of each variety. In both cases, leaf consumption and number of eggs laid were quantified after 21 days.

Results: Egg laying on or around each plant ranged from 0 to 64 and 0 to 148 for the choice and no-choice experiments respectively. There was no statistically significant difference in the number of eggs laid upon the different cultivars for either experiment. However, weevils laid the least number of eggs on Glen Moy and the most on Glen Ample in both experiments. In the choice experiment, less than 1% of the total cultivar leaf area available to the weevils was consumed.

Conclusion: No oviposition preference for adult vine weevils was found between different raspberry cultivars.

POSTER PRESENTATION

First record of the endoparasitoid *Dolichogenidea (Apanteles) anarsiae* (Hymenoptera: Braconidae) in Greece

Petros T. Damos, Matilda Savopoulou-Soultani

Aristotle University of Thessaloniki, Faculty of Agriculture,Laboratory of Applied Zoology and Parasitology, Thessaloniki, Greece

Parasitoids of the family Braconidae are widely distributed and recorded throughout Europe, the Indian subcontinent and parts of Africa. Despite the fact that a number of individuals of the genus *Dolichogenidea* have been recorded around the Mediterranean (mostly France and Italy), this is the first record of the species *Dolichogenidea anarsiae* in the wide Balkan Peninsula and east Mediterranean area. Although usually listed as a species of the genus *Apanteles* (Foerster 1862), following the breaking up of this genus, which is proposed by a number of taxonomists, *A. anarsiae* (Faure and Alabouvette 1924) should be included in the genus *Dolichogenidae*. The species is considered as an important endoparasitoid of the peach twig borer *Anarsia lineatella*, but is also recorded as an endoparasite in a great variety of Tortricidae members. A significant number of *D. anarsiae* individuals were found in overwintering *A. lineatella* larvae. Hibernacula samples, with overwintering larvae, were collected from peach trees in northern Greece (40.32^{o}N). In addition, the presence of *D. anarsiae* was very high throughout the winter and especially in orchards where no pesticides were applied during the previous years. Sampling sites, habits and morphology of the solitary parasitoid wasp *D. anarsiae* are illustrated.

POSTER PRESENTATION

Content of Pb, Cd, Zn, Cu and Mn in bodies of field ground beetles (Coleoptera, Carabidae) with respect to selected ecological factors – case study from Central Europe

Lubos Purchart[1], Emanuel Kula[2], Vladimir Hula[3]

[1]Mendel University of Agriculture and Forestry, Institute of Forest Ecology, Brno, Czech Republic, [2]Mendel University of Agriculture and Forestry, Department of Forest Protection and Game Management, Brno, Czech Republic, [3]Mendel University of Agriculture and Forestry, Department of Zoology, Brno, Czech Republic

The concentration of heavy metals in the bodies of invertebrates is dependent on their physiological equipment and prevalent environmental factors. To verify the effect of some of these factors on the content of metals (Pb, Cd, Zn, Cu, Mn) we analysed and then tested (using RDA, t-test) ten species of field ground beetles (Coleoptera, Carabidae).

A significant effect of Cu and Cd was discovered in terms of the sex; the males accumulated more Cu (27.520 mg kg^{-1}) than females (18.297 mg kg^{-1}) (P<0.01), which, on the contrary, accumulated more Cd (1.495 mg kg^{-1}) than males (0.663 mg kg^{-1}) (P<0.02). The content of all the metals differed significantly (P<0.03) according to the species, unambiguously showing species-specific models of accumulation. The effect of the feeding ecology was evident only on the essential elements; carnivores (Zn – 222.596 mg kg^{-1}, Cu – 27.211 mg kg^{-1}, Mn – 71.929 mg kg^{-1}) had a significantly (P<0.03) higher contents than omnivores (Zn – 168.198 mg kg^{-1}, Cu – 21.116 mg kg^{-1}, Mn – 58.452 mg kg^{-1}). Although there were differences (P<0.01) in the concentrations of Zn and Cu between the spring (Zn –163.749 mg kg^{-1}, Cu – 19.998 mg kg^{-1}) and autumn (Zn – 202.373 mg kg^{-1}, Cu – 25.496 mg kg^{-1}) species, the effect of the type of reproduction is considered to be only partial. At the same time the time of sampling affected the Zn and Mn (P<0.02) content. An important positive correlation was determined between the contents of Cu-Zn, Mn-Zn and Mn-Cu.

Acknowledgement: The project was supported by Research plan of the Czech Ministry of Education MSM 6215648902.

POSTER PRESENTATION

Metagenomics of glassy-winged sharpshooter, *Homalodisca vitripennis* (Hemiptera: Cicadellidae)

Wayne Hunter[1], Scot Dowd[2], Kent Shelby[3], Catherine Katsar[4], Phat Dang[5], Laura Hunnicutt[6]

[1]USDA, ARS, Fort Pierce, FL, 34945, United States, [2]USDA, ARS, Lubbock, TX, 79403, United States, [3]USDA, ARS, Columbia, MO 65203, United States, [4]USDA, APHIS, Fort Lauderdale, FL 33316, United States, [5]USDA, ARS, Dawson, GA 39842, United States, [6]North Carolina State University, Raleigh, NC, United States

The microenvironment of leafhoppers was exposed by using a Metagenomics approach to identify unknown organisms which live in association with the glassy-winged sharpshooter, 'Homalodisca vitripennis' (Hemiptera: Cicadellidae). Metagenomics is described as "the comprehensive study of nucleotide sequence, structure, regulation, and function". The production of cDNA libraries from the GWSS resulted in the identification of multiple organisms associated with these leafhoppers. Three newly discovered single-stranded RNA viruses, along with three bacteria, and one potential fungi and a bacterial phage were identified, along with plant material ingested by the insects. The viruses are undergoing full genome sequencing and may provide new biological control agents against leafhoppers. Species comparison to all available data on NCBI provided insights into the homologous nature of leafhopper genomics. The number of sequences returning a top homology match to other species provide more matches to 'D. melanogaster', (~12,500) followed by 'A. aegypti',(~9,600), 'T. casteum',(~9,000), 'A. gambiae',(~8500), 'N. vitripennis', (~8,000), 'A. mellifera', (6,000) and then 'H. sapiens' (~4,500). The dataset is being further mined for enzymes which may aid in post processing of cellulosic waste materials, or animal waste streams. Ultimately the information can then be applied to solve problems in agriculture to create healthier human populations which will use environmentally friendly technologies. Metagenomics is a new and exciting field of molecular biology that is growing into the standard technique for understanding biological diversity.

POSTER PRESENTATION

Pentatomidae (Hemiptera) associated with rice crops in south-eastern Australia

Mark Stevens[1], Jianhua Mo[1], Fred McDonald[2]

[1]E H Graham Centre for Agricultural Innovation (NSW Department of Primary Industries and Charles Sturt University), Yanco Agricultural Institute, Yanco NSW, Australia, [2]School of Integrative Biology Insect Collections, St Lucia Campus, The University of Queensland, Brisbane Qld, Australia

Introduction: Pentatomid bugs cause reductions in rice crop yield and quality throughout the world, but have not been regarded as pests in south-eastern Australia until relatively recently. We surveyed rice crops to determine the species composition of the fauna, and conducted glasshouse experiments on the most common species, *Anaxilaus vesiculosus* (Herrich-Schaeffer), to confirm its pest status.

Methods: Sweep-net sampling was conducted in 38 rice crops in the Murrumbidgee and Murray Valleys during maturation of the 2005/6 and 2006/7 crops. Adult *A.vesiculosus* were placed on caged rice plants, where reproduction and development were monitored. Grain from exposed and controlled plants was hulled, milled and assessed for damage.

Results: Seven pentatomid species were recorded, however three species accounted for approximately 97% of the bugs collected. The native species *A.vesiculosus* dominated the fauna (84% of captures). Bug densities were too low to fully account for the level of damage observed, suggesting that fungal infections and/or physiological disorders may also be involved in grain damage. Field-collected *A.vesiculosus* adults placed on caged rice plants survived for up to 20 days. Nymphs that emerged from eggs laid on the plants were reared through to adulthood without any alternate food sources, and grain from the exposed plants showed the characteristic blemishes associated with stink bug feeding.

Conclusions: This is the first record of *A.vesiculosus* feeding and developing on rice. Further research is needed to determine the relative contributions of pentatomids, fungal infections, and physiological disorders to rice grain damage in south-eastern Australia.

POSTER PRESENTATION

Which is the most suitable approach to determine the invaded range of Argentine ant at local scales?

Núria Roura Pascual[1], Josep M. Bas[2], Wilfried Thuiller[3], Rainer Krug[1], Lluis Brotons[4]

[1]*Centre for Invasion Biology, University of Stellenbosch, Stellenbosch, South Africa,* [2]*Departament de Ciencies Ambientals, Universitat de Girona, Girona, Catalonia, Spain,* [3]*Laboratoire d'Ecologie Alpine, UMR-CNRS 5553, Université J. Fourier, Grenoble, France,* [4]*Centre Tecnològic Forestal de Catalunya, Solsona, Catalonia, Spain*

Introduction: Determining the geographical extent and ecological suitability range of an invasive species is a challenge for most ecologists concerned about management practices. In the absence of detailed data on the real distribution of species, distributional models offer the opportunity to estimate the geographic extent of an invasion and also to better understand the ecological processes acting at different spatial scales.

Methods: Herein, several modelling approaches (correlative and mechanistic) are used to determine the distribution of the Argentine ant (*Linepithema humile*), a highly widespread invasive species native to South America. Occurrence data mostly obtained from two different sampling strategies were combined with environmental data at different resolutions in order to predict the geographical extent of the ant invasion in Catalonia (NE Iberian Peninsula) across spatial scales.

Results and conclusions: Comparisons between models suggest that the species is still expanding at the northeastern area of the Iberian Peninsula, where the Argentine ant is not in equilibrium with its environment. Special attention should be paid at the Costa Brava, where the species seems to present highly suitable conditions along the whole coast and also in inland areas. In this sense, long-distance jumps are the ultimate responsible for the expansion and should receive special attention in order to establish efficient measures to control the invasion spread.

POSTER PRESENTATION

Semiochemicals involved in termite raiding by the Ponerine ant *Pachycondyla analis*: Observations on raiding behaviour

Abdullahi Ahmed Yusuf[1], Ian Gordon[1], Robin M. Crewe[2], Peter G. N. Njagi[1], Christian W. Pirk[2], Ahmed Hassanali[1]

[1]International Centre of Insect Physiology and Ecology (icipe), Nairobi, Kenya, [2]Department of Zoology and Entomology, University of Pretoria, Pretoria, South Africa

Introduction: The termitophagous ant *Pachycondyla analis* (Latreille) organises coordinated raids on termites. Understanding the cues mediating the raiding behaviour of this ant and its semiochemical interactions with its termite prey could offer potentials in the control of termite pests.

Methods: Thirty four nests of *P. analis* were studied at Mpala central Kenya. Time of raids, duration of different activities during raids, termite species taken, number of ants in the raid and number of ants carrying termites were recorded. Ground temperature and RH at the time of departure for raids were also recorded.

Results: Out of the 330 raids observed, 56% occurred in the morning (0700-1100 hr), 42% in the evening (1600-1930 hr), and 2% entirely nocturnal (2000-2400 hr). The minimum and maximum foraging distances during a raid were 1.5 and 39.8 m respectively, temperatures during raids were between 18.4-36.4 ℃ and 26.6-69.0 % RH. Duration of raids ranged between 4-99 minutes. Foraging parties contained between 22-800 ants with 10-720 ants carrying termites back from raids. Number of termites captured per foraging party increased from the month of April to May, decreasing in June with a further increase in July and decreasing in August and September respectively. Average number of termites carried per ant ranged from 1.0 to 7.0, while predation rates were 1.063 termites per nest per m^2 and 959.1 termites per nest per day, with preferences of *Microtermes* and *Odontotermes* species.

Conclusion: These results will open opportunities for studies directed at understanding the chemical interaction between these ant raiders and the termites.

POSTER PRESENTATION

Why do striders fly? Inferring evolutionary causation from genetic, environmental and geographic variation in wing dimorphism.

Daphne Fairbairn, Elizabeth King

University of California, Riverside, California, United States

Introduction: In this paper, we take advantage of wing dimorphism in the waterstrider, *Aquarius remigis* (Hemiptera-Heteroptera, Gerridae) to measure genetic and phenotypic variation in dispersal capability within and among populations from across a California. We then use these patterns to deduce the evolutionary mechanisms responsible for the unusually high frequency of macropters in this region of North America.

Methods: (1) A half-sib mating design split across two temperatures is used to estimate the heritability of wing morphology and the genetic correlations between sexes and environments. (2) Three populations are reared under two temperature regimes to measure genetic differentiation among populations. (3) Field samples from 37 Californian populations are used to detect correlations between proportion macropterous and environmental and geographic variables.

Results: (1) In both environments, wing morphology is highly heritable and shows very high genetic correlations between males and females. The genetic correlations between environments are significant but somewhat lower than those between sexes. (2) Both mean proportion macropterous and its reaction norm with temperature differ significantly among the three populations, indicating strong genetic differentiation. (3) Patterns of geographic variation reveal no correlation between proportion macropterous and stream size, rainfall or latitude, but a strong positive correlation with altitude.

Conclusions: Wing dimorphism in *A. remigis* has a high potential to respond to selection within populations and has clearly diverged genetically among populations. The geographic pattern of variation suggests that the high proportion macroptery in California is an adaptation to altitudinal gradients rather than to seasonal lowland drought, as previously thought.

POSTER PRESENTATION

Effects of snowdrop lectin (GNA) on the development of beet armyworm, *Spodoptera exigua* (Lepidoptera: Noctuidae)

M Naghdi, Ali R. Bandani, Kh Talebi

Plant Protection Department, Faculty of Agriculture, University of Tehran, Karaj, Islamic Republic of Iran

Introduction: In order to control this pest emphasis has been placed on using pesticides. However, problems associated with pesticide usage have resulted in greater interest in the potential for exploiting plant defensive proteins such as lectin to control insect pest. GNA (*Galanthus nivalis* agglutinin; Snowdrop lectin) is toxic toward a number of insect species including Homopteran, Coleopteran and Lepidopteran species. So, the aim of the current study is to investigate the effects of GNA on beat armyworm larval growth and development.

Materials and Methods: Larvae of the beet armyworm, *Spodoptera exigua*, were collected from the field and reared on a wheat germ-based artificial diet (Bio-Serv) in a growth chamber (16:8 hrs light: dark, 50% relative humidity and 25 ± 1 ℃. GNA incorporated in artificial diet at 0 Control), 0.1, 0.2, 0.5, 1 and 2 % of total dietary protein.

Results: Larvae in the control grew normally while in the GNA treatments percentages of larval mortality varied in the different treatments. Fore example percentages of mortality in the first instar larvae in the 0.1, 0.25, 0.5, 1 and 2% GNA treatment were 16.6, 30, 33, 36 and 50, respectively. Only larvae in the o.1% lectin treatment grew up to adult stage while in the other treatments all larvae died before reaching pupal stage. Also, larvae and pupae in the control weighed consistently more than those in the GNA treatments.

Conclusions: Current study showed that the main effects of the GNA treatment on beet armyworm were reduction in larval survivorship and larval and pupal weight suggesting that GNA can play an important role in reduction of population and damage levels of the pest in the field.

POSTER PRESENTATION

Control of codling moth through post-harvest fruit removal

R.A. Van Steenwyk, C.F. Fouche, S.C. Welter, C.A. Ingels, L.G. Varela, R.B. Elkins

University of California, Berkeley, United States

Pears, *Pyrus communis* (L.) 'Bartlett' are harvested in California from mid-July through mid-August. After commercial pear harvest, it is common to find a large number of unharvested fruit remaining on the trees. Since insecticide use is terminated two or more weeks before the completion of harvest, the unharvested fruit serve as excellent sites for codling moth, *Cydia pomonella* (L.) (CM) oviposition and allow for a rapid increase in the CM population. CM larvae that complete their development in the unharvested fruit before the end of July will enter the pupal stage and emerge as adults. However, CM larvae that complete their development by the end of August will enter the overwintering stage. If the CM population can be controlled before mid-August, then the overwintering population would be largely eliminated. Studies with post-harvest fruit removal or post-harvest insecticide applications have demonstrated that post-harvest control can reduce the overwintering CM population by approximately 75%. During the course of our studies, it was observed that CM larvae that infest ripe pears do not complete their larval development. The pears rot faster than the larvae can complete their development. It was determined that an application of ethephon shortly after harvest promotes early ripening and fruit drop with a resulting reduction in the overwintering CM population. Plant growth regulators can substitute for post-harvest hand stripping of fruit or post-harvest insecticide applications at a reduced cost to the grower and with less environmental impact. Ethephon was registered in California for post-harvest use in 2007.

POSTER PRESENTATION

Studies on different populations of *Aphis gossypii* in transmission of citrus tristeza virus (CTV) to some citrus cultivars in Mazandaran Province

A Hadizadeh[1], Gh. Reza Rassoulian[1], Gh Mosahebi[1], H Rahiamian[2]

[1]Department of Plant Protection, Faculty of Agriculture, University of Tehran, Karaj; [2]Department of Plant Protection, Faculty of Agriculture, University of Mazandaran, Sari, Islamic Republic of Iran

Introduction: Citrus tristeza virus (CTV) is a phloem – limited aphid transmitted pathogen that causes the most economically important disease of citrus worldwide. The virus appears to be steadily spreading to new sites by melon aphids. Sour orange is the only rootstock used in Mazandaran province that seriously affected by citrus tristeza virus.

Methods: Experiments were conducted to investigate the role of different populations of *Aphis gossypii* in transmitting of the virus to the different citrus cultivars. MIS isolate of CTV maintained on Rangpour lime seedlings were used for determination and transmission efficiencies. Populations of *A. gossypii* were collected from different citrus species. Aphid populations were collected from related host plants in the field. Aphid colonies of cotton and citrus trees were reared on the same host plants in greenhouse conditions and were used directly in transmission tests. Apterous aphids were transferred onto different citrus cultivars after acquisition feeding from donor plants. Approximately 20-25 aphids were used per test seedling and 5 seedlings were used for each plant. The results were assessed three months after inoculation by ELIZA tests.

Results: The M1S isolate of CTV in Rangpour lime were transmitted to different citrus cultivars by cotton and euonymus populations of *A. gossypii* at 8 and 13% respectively. CTV in mandarin was transmitted by cotton populations of aphids at 16%. The cotton and weeping fig aphid populations have transmitted the CTV 7.6% and 51.50%, respectively. Mean transmission rate obtained was 19% for this isolate on different citrus cultivars.

Conclusions: Our investigations have shown that all population of melon aphids in Mazandran Province can transmit the CTV. Therefore it seems that the virus in this area spread rapidly.

POSTER PRESENTATION

Resistance of phytophagous mites as an evidence of the unfavourable changes in biocenose of apple orchard

Elena Moontean, Victoria Sumencova, Elena Iordosopol, Mihai Batko, Igor Yazlovetsky

Institute for Plant Protection and Ecological Agriculture, Kishinev, Europe, Republic of Moldova

Introduction: One of the main problems of pest apple orchards control is excessive reliance on chemicals leading to biocenose destabilization. The influence of the insectoacaricide treatment of apple orchard upon the structure of acarifauna and upon the level of resistance in population of phytophagous mites was studied.

Methods: The median lethal concentrations of insecticide were determined by probit analysis and the rates of resistance were calculated.

Results: In the first orchard (7 insectoacaricide treatments per year during 15 seasons) the acarifauna complex was represented by 8 phytophagous and 4 predatory species. *Tetranychus viennensis* and *Aculus schlechtendali* were dominant, with spots of propagation of *Panonychus ulmi*. The mites were resistant more than x 1000 to Dimethoate, Zolone, Malathion, Chlorpyriphos. *P. ulmi* and *T. viennensis* began to develop form resistance to acaricides Brompropylate (x 3,5) and Propargite (x 4,0). In the second orchard (4 treatments) 5 phytophagous and 20 predatory species of mites were detected. *P. ulmi* was not found. *T. urticae* and *T. viennensis* had low resistance to Dimethoate (x 23 and x 2) and to Zolone (x 10 and x 7) respectively.

Conclusions: The reduction of useful acarifauna under the influence of insectoacaricides occurs together with the formation of acaricide resistance by phytophagous mites. Besides, mites present constantly in the agrocenose, slowly migrate and form quickly a high resistance to insectoacaricides. Therefore, the level of phytophagous mites resistance to insectoacaricides can serve as a criterion for evaluation of the current biocenose status of apple orchard.

POSTER PRESENTATION

On South African diversity of Pterophoroidea (Lepidoptera)

Petr UstJuzhanin[1], Vasily Kovtunovich[3], Mike Mostovski[2]

[1]Siberian Zoological Museum, Institute of Animal Systematics and Ecology, Russian Academy of Sciences, Novosibirsk, Russian Federation, [2]Natal Museum and School of Biological & Conservation Sciences, University of KwaZulu-Natal, Pietermaritzburg, South Africa, [3]Moscow Society of Nature Explorers, Moscow, Russian Federation

Introduction: Research of southern African plume moths was commenced in mid-19th century. This region became the best studied part of sub-Saharan Africa, with almost 90 pterophorid species recorded from here (Gielis, 2003). The pterophorid fauna of South Africa is rather specific, with a number of endemic species and certain links with other parts of the world. Recent survey of museum collections and extensive field work demonstrated that the state-of-art is far from being satisfactory.

Results: The family Macropiratidae (genus *Agdistopis*) is recorded in South Africa for the first time; this is also the first record of this hitherto Australasian family in the Afrotropical Region. The following genera represent South African Pterophoridae (with number of species): *Adaina* (4), *Agdistis* (42–47), *Amblyptilia* (2), *Antarches* (1), *Buckleria* (1), *Cosmoclostis* (2), *Eucapperia* (1), *Exelastis* (9–10), *Gypsochares* (4–5), *Hellinsia* (20–25), *Marasmarcha* (5), *Megalorhipida* (3), *Merrifieldia* (1), *Oxyptilus* (6–7), *Paulianilus* (1), *Picardia* (1), *Platyptilia* (16–18), *Pselnophorus* (2–3), *Pterophorus* (7–8), *Sphenarches* (2), *Stenodacma* (2), *Stenoptilia* (6–7), *Titanoptilus* (2), *Trichoptilus* (10), *Walsinghamiella* (4–5). Some 50 to 60 species of South African Pterophoridae can be recognised as new, with over 20 of them belonging to the genus *Agdistis*. Seven genera and over 20 species are recorded as new to the South African fauna; five species were previously known as endemics of Madagascar. With 155–174 pterophoroid species altogether (excluding alucitids), South Africa can be considered a centre of diversity for *Agdistis* (also Mediterranean and Central Asia), *Exelastis* and *Trichoptilus*.

POSTER PRESENTATION

The impact of fungicides on the predatory mite *Anystis baccarum* in apple orchards in Northern Ireland

Andrew Cuthbertson[1], Archie Murchie[2]

[1]Central Science Laboratory, York, United Kingdom, [2]Agri-Food and Biosciences Institute, Belfast, United Kingdom

Introduction: Apple scab (*Venturia inaequalis*) is the most serious disease in Bramley's Seedling apple orchards in Northern Ireland. As a result, as many as 14 fungicide sprays can be applied each season to control the disease. These fungicide sprays have an impact on both pest populations (*Aculus schlechtendali*) and non-target species (*Anystis baccarum*) populations.

Methods: Three commonly used fungicides (captan/penconazole, mancozeb and dithianon) were selected for investigation. Treatments were applied to individual trees arranged in six randomized blocks using an electric Berthoud Vermorel 2000 knap-sac sprayer to each tree at ten-day intervals. Three litres of spray solution were applied at recommended dose rates to each tree. Control trees were sprayed with water.

Results: On mancozeb treated trees there were fewer *A. baccarum* and more *A. schelcthendali* compared to the other treatments. Dithianon had no detrimental effect on *A. baccarum*. Mancozeb treated trees gave satisfactory scab control.

Conclusion: *Anystis baccarum* has shown a level of compatibility with various chemical fungicides commonly used for apple scab control. Therefore, there is potential for its incorporation into IPM programmes for the control of invertebrate pest species. Apple growers should be encouraged to recognise this beneficial mite and work to conserve its populations and apply only chemical applications that are compatible with the mite.

POSTER PRESENTATION

Impact on abundance of surface active non-target arthropods following soil fumigation with 1,3-Dichloropropene

Andrew Cuthbertson[1], Helen Thompson[1], Mark Miles[2]

[1]Central Science Laboratory, York, United Kingdom, [2]Dow AgroSciences, European Development Centre, Abington, United Kingdom

Introduction: The potato cyst nematode, *Globodera pallida*, is a widespread problem throughout England and Wales. A large scale field study was initiated in North Yorkshire with the aim of investigating the effects of soil fumigation with Telone II, 97.5% w/w 1,3-dichloropropene, for nematode control on carabid, spider and collembola populations.

Methods: Treatments were made by soil injection to a depth of 20 cm of 1,3-dichloropropene, in the autumn prior to cultivation of potatoes in the spring of the following year. Pitfall trapping commenced prior to fumigation and continued for 12 months.

Results: A reduction in arthropod numbers was noted immediately post-application. Carabid and linyphiid populations were noted to exceed the levels in the control 8 months after treatment before returning to untreated levels 10 months after treatment. Collembola populations had recovered within 1 year and were the most sensitive arthropods sampled.

Conclusion: The findings indicated that although effects were apparent post-application in the autumn/winter samples all arthropod populations had recovered within an ecologically relevant time scale. Overall effects on each taxa appeared to be related to their position in the field at the time of application (which determined their exposure) and recovery rate related to reproductive and dispersive capacity.

POSTER PRESENTATION

Efficacy of the entomopathogenic nematode, *Steinernema feltiae*, against sweet potato whitefly, *Bemisia tabaci*, under laboratory and glasshouse conditions

Andrew Cuthbertson, Keith Walters, Phil Northing, Weiqi Luo

Central Science Laboratory, York, United Kingdom

Introduction: The potential of using the entomopathogenic nematode *Steinernema feltiae* to control the sweetpotato whitefly, *Bemisia tabaci* has been well established. However, laboratory studies can overestimate the level of control achieved by biocontrol agents in the glasshouse.

Methods: Controlled laboratory and glasshouse trials were undertaken to confirm the efficacy of *S. feltiae* as a control agent against *B. tabaci*. The nematodes were applied using a hand held applicator. Mortality was assessed following 72 hours. The efficacy of the biocontrol agent at various application rates was also investigated.

Results: Under both controlled laboratory and glasshouse conditions high mortality of second instar *B. tabaci* (>90% and >80% respectively) was recorded after application of *S. feltiae*. Halfing the application rate of *S. feltiae* application (5000 IJ/ml) caused no significant reduction in *B. tabaci* mortality on tomato foliage.

Conclusion: *Steinernema feltiae* has shown much potential for incorporation into integrated pest management strategies for the control of *B. tabaci* in UK glasshouses.

POSTER PRESENTATION

Status quo of honeybee (*Apis mellifera* L.) pests and diseases in Sudan

Mogbel El-Niweiri, Abdalla Satti

Environment and Natural Resources Research Institute, National Centre for Research, Khartoum, Sudan

Introduction: Honeybees are found naturally in Sudan since ancient time and traditional beekeepers are present. Recently, modern beekeeping has been flourished using imported colonies, so the threat of spreading exotic pests and diseases was expected. Since few data is available in this field, it was aimed by this work to recognize important pests, predators, diseases and parasites of honeybees and their incidences in different parts of the country.

Methods: Data were collected through intensive surveys and questionnaires covering nine bee areas (States) in Sudan during the period 2003 - 07. Different modern and traditional apiaries and wild colonies were inspected, where the percentages of affected colonies by major pests or diseases were indicated in most areas. Samples taken included 122 local colonies and 350 Carnio-Egyptian colonies plus 30 colonies of *Apis florea*. Detected insects were mostly identified at the Insect Collection of the Agricultural Research Corporation (ARC), Sudan, whereas vertebrate species identified either at the Wild Life Research Centre, ARC or Sudan Institute for Natural Sciences. Suspected diseases were confirmed through laboratory culturing and biochemical tests followed at the Department of Microbiology, Faculty of Veterinary Sciences-University of Khartoum.

Results: Lists of more than 35 pests and predators of honeybees were recorded at variable levels in different areas. They include mainly insect and vertebrate species and few spiders. Among these, twenty species were new records e.g. the hive beetles, bee wolves, squirrel and honey badger. However, many species were found causing serious problems such as *Galleria* moth (86.3% infested colonies), ants and two predatory birds (*Merops* spp.). On the other hand, all areas were found free of most bacterial and fungal diseases, except the bacterial brood disease, *Serratia marcescens*, found in 2.6% of Khartoum colonies. Moreover, the parasitic mite, *Varroa jacobsoni*, was found firstly infecting 75% of colonies in Khartoum State as new record, thenceforth detected in Sennar and Kordofan States.

Conclusions: Various indigenous pests of honeybees were found in Sudan and some exotic pest and disease species were introduced through commercial beekeeping.

POSTER PRESENTATION

Regressive evolution: ontogenetic study on wing reduction in the bagworm moths (Lepidoptera, Psychidae)

Shuhei Niitsu

Tokyo Metropolitan University, Hachioji-shi, Tokyo, Japan

Winglessness has evolved many times in neopteran insects in a response to a change according to ecological conditions. Females of bagworm moths show phased-reduction of wings: Males are winged while females have frequently the vestigial wings or completely wingless form. Studying processes of wing reduction in Psychidae possibly helps understanding the evolution of wing reduction in insects. Using light and electron microscopy, I studied the process of wing development in the period from larval instar to pupal stages. In the study, histological analysis revealed that the females of the bagworm moths express two ontogenetic patterns of wing reduction. The female adults of *Taleporia trichopterella, Bacotia sakabei,* and *Proutia* sp. have atrophied wings. The wingless-legged state of these species (usually called wingless-legged bagworm moths) has been hypothesized as the intermediate condition between two extremities of females with normal wings and those with absolutely no wings. In these species, wing disc degeneration caused by apoptosis occurs in two steps: in the prepupal stages and pupal stages. In contrast to three species described above, *Eumeta variegata* female adults are vermiform lacking wings and legs. This vermiform state of the females has been hypothesized as the most derived condition in the evolution of Psychidae. In this study by using this species, a sac-like wing rudiment was formed by invagination of the epidermis in the last instar. The wing rudiment disappears through apoptosis on the prepupal stages. These processes of wing reduction have probably evolved secondarily during the course of evolution.

POSTER PRESENTATION

Bt crop effects on functional guilds of non-target arthropods: A meta-analysis

L. LaReesa Wolfenbarger[1], Steven Naranjo[2], Jonathan Lundgren[3], Royce Bitzer[4], Lidia Watrud[5]

[1]University of Nebraska at Omaha, Department of Biology, Omaha, NE 68182, United States, [2]USDA-ARS Arid Land Agricultural Research Center, Maricopa, AZ 85238, United States, [3]USDA-ARS North Central Agricultural Research Laboratory, Brookings, SD 57006, United States, [4]Iowa State University, Department of Entomology, Ames, IA 50011, United States, [5]US Environmental Protection Agency, National Health and Environmental Effects Research Laboratory, Western Ecology Division, Corvallis, OR 97333, United States

Uncertainty persists over the environmental effects of genetically-engineered crops producing the insecticidal Cry proteins of *Bacillus thuringiensis* (Bt). We perform meta-analyses to synthesize current knowledge about the effects of Bt cotton, maize and potato on the abundance and interactions of arthropod non-target functional guilds. We compare the abundance of predators, parasitoids, omnivores, detritivores and herbivores under scenarios in which neither, only the Bt crops, or both Bt and non-Bt crops received insecticide treatments. Predators were less abundant in Bt cotton compared to unsprayed non-Bt controls. Fewer specialist parasitoids of the target pest occurred in Bt maize fields compared to unsprayed non-Bt controls, but no general effects on parasitoids existed. Predators and herbivores increased in Bt crops compared to sprayed non-Bt controls. Type of insecticide influenced the magnitude of increases in predators. In maize, higher abundances of detritivores in insecticide-treated controls were associated with reductions of their predators in sprayed non-Bt maize. Predator-to-prey ratios were unchanged by either Bt crops or the use of insecticides; ratios did increase in Bt maize relative to the sprayed non-Bt control.

Overall, we find no systematic effects of Bt crops on the functional guilds of non-target arthropods. Use of and type of insecticides influenced the magnitude and direction of effects; insecticide effects were much larger than those of Bt crops. These meta-analyses underscore the importance of using controls not only to isolate the effects of a Bt crop but also to reflect the replacement of existing agricultural practices.

POSTER PRESENTATION

Evaluating integrated pest management strategies for managing bed bugs

Timothy Gibb, Changlu Wang

Purdue University, W. Lafayette/ IN, United States

A recent surge of bed bug infestations in the USA is posing a major concern to citizens as well as to Professional Pest Managers who are asked to control them. Elimination of bed bugs currently relies heavily upon chemical sprays or dusts. Exclusive reliance upon pesticides alone presents three serious challenges: 1) none of the registered chemicals have the desirable residual efficacy; 2) there is evidence of wide-spread resistance to insecticides; and 3) treatment of bedding materials causes immediate risk of pesticide exposure to humans. These challenges underscore a need to investigate Integrated pest management (IPM) strategies that will decrease dependence upon pesticides alone, reduce the risk of human-insecticide exposure, and at the same time, improve the efficacy of bedbug management programs.

This summary reports the development and implementation of two IPM strategies to manage bed bugs and compares both their cost and effectiveness in actual bedbug infested residences. These strategies include; 1) non-chemical methods only; and 2) non-chemical methods plus a residual insecticide. Both IPM strategies included resident education and cooperation as components in implementation.

POSTER PRESENTATION

Occurrence of storage pests of kolanuts across the kola-growing belt of Nigeria

E.U Asogwa, T.C.N Ndubuaku, I.U Mokwunye

Cocoa research Institute of Nigeria, Ibadan, Oyo, Nigeria

Introduction: In Nigeria, *Cola acuminata* and *Cola nitida* are important economic crops cultivated in the rainforest zones of the South and riverine areas of the savannah region. Kolanuts play a significant role in the culture and ceremonies of the people, but are attacked by the kolanut weevils, which can cause appreciable damage between 30% - 70%. The distribution and frequency of occurrence of these insect pests was studied with a view of developing standard integrated packages for their control.

Methods: Random samples of matured kola pods and cured kolanuts were procured from across the kola belt and assessed using parameters such as percentage nut infestation, total number of emerged larvae and adult weevils; mean number of exit holes and colour change.

Results: The weevil distribution cuts across all the sampled locations but at different levels of infestations. The mean number of weevils (*Balanogastris kolae* and *Sophrorhinus spp*.) sampled at the various locations were not significantly different, however, *B. kolae* was significantly more abundant than *Sophrorhinus spp*. Weevil infestation level of 100% was recorded after 3 months of storage of nuts selected from kola pods from different zones as compared to the highest infestation level of 21.7% recorded for cured nuts.

Conclusions: It is evident that kolanut weevils, especially *B. kolae* are more abundant and widely distributed in Nigeria at varying degrees and such infestation normally starts on the field. The low infestation level on cured kolanuts could be as a result of application of some control measures by the kola vendors.

POSTER PRESENTATION

Geographic variation in the susceptibility of *Thaumatotibia leucotreta* (FCM) populations to a granulovirus (CrleGV-SA)

John Kwadwo Opoku-Debrah, Sean Douglas Moore, Peter Retief Celliers

Nelson Mandela Metropolitan University; Citrus Research International, Port Elizabeth, Eastern Cape, South Africa

Introduction: The false codling moth (FCM), *Thaumatotibia leucotreta* is a serious pest of citrus and other crops in sub-Saharan Africa. The use of biological control agents such as *Cryptophlebia leucotreta* granulovirus (CrelGV–SA, CRYPTOGRAN®) has proven to be very useful in the control of FCM. Markedly lower susceptibility of some codling moth populations to a granulovirus have been reported in Europe. Genetic variation between FCM populations in South Africa has been reported. It is therefore possible that differences in the susceptibility of geographically distinct FCM populations to CrelGV-SA might exist.

Methods: Firstly a benchmark for pathogenicity was established. Surface dose-response bioassays were conducted with laboratory reared FCM larvae of all five instars with CrelGV-SA. Dose-response relationships were calculated. Bioassays were also conducted with FCM larvae collected from infested fruit from a range of geographic regions.

Results: LC_{50} values were calculated to be 4.095×10^3, 4.516×10^4, 1.581×10^5, 2.205×10^6 and 2.678×10^7 OBs/ml, respectively. The LC_{90} values for the five larval instars were also calculated to be 1.185×10^5, 4.287×10^6, 1.113×10^7, 1.661×10^8 and 9.118×10^9 OBs/ml respectively.

Conclusions: A protocol for conducting bioassays with field collected FCM larvae was established. It was therefore possible to compare the susceptibility of larvae from different regions with laboratory reared FCM.

POSTER PRESENTATION

Cameraria ohridella Deschka and Dimic (Lepidoptera: Gracillariidae) host trees and potential host range expansion of the moth in Greece

Nikolaos Avtzis, Dimitrios Avtzis

[1]Technological Education Institute of Kavala - Branch of Drama - Dept. of Forestry and Natural Environment Management, Drama, Greece, [2]Institute of Forest Entomology, Forest Pathology and Forest Protection - BOKU, Vienna, Austria

Introduction: *Cameraria ohridella* is a new pest in Europe, that was first detected near Ohrid-Lake by Deschka & Dimic (1985). In 1998 Skuhravy found the insect in Greece for the first time, whereas in 2001 started its study within the framework of Controcam Project.

Methods: The distribution of the moth was investigated either by on-site observations as well as through the application of pheromone traps made by the Institute of Organic Chemistry and Biochemistry (Czech Republic), which were installed in various places of Greece. Besides distribution, Controcam included the study of host trees and potential host range expansion of the moth in Greece, something that is still being investigated.

Results: The insect is observed until now in 80 different places, both on wild (39) and ornamental (41) *Aesculus hippocastanum* trees.

The observations made by pheromone traps (2001-2004) and leaf sampling (2001-2007) did not report the moth on the following *Acer* species: *Acer sempervirens, Acer platanoides, Acer monspesulanum, Acer campestre, Acer tataricum, Acer pseudoplatanus, Acer creticum, Acer obtusatum, Acer hyrcanum, Acer heldreichii* and *Acer negundo*. These species were not infected by the moth even when growing near heavily infested horse chestnut trees (greater than 86.3% of the total assimilating surface).

Conclusion: The unique host tree attacked by *C. ohridella* in Greece was found to be *Aesculus hippocastanum,* an endemic species of the Balkans (Polutin, 1997). This result is incongruent with the findings of other researchers, which report the complete development of this insect on *Acer* species, f.e. *Acer pseudoplatanus* (Jona, 2001).

POSTER PRESENTATION

Otiorhynchus sulcatus F. – a pest of ornamental plants

Elda Vitanović, Sonja Kačić, Miro Katalinić

Institute for Adriatic Crops and Karst Reclamation, Split, Croatia, Croatia

Introduction: The genus of *Otiorhynchus* is represented in Croatia by 228 species. *Otiorhynchus sulcatus,* as a pest, has been known in Europe for quite a while, while in Croatia it has been causing significant damages since 2004. It attacks ornamental bushes and flowering plants grown indoors, but also those cultivated outdoors. Presence of this destructive species in glasshouses can cause loss of the whole production of flower species under attack.

Methods: The first control measure is mechanical by all means, i.e. hand-collection of adults and their destruction, as well as use of Rincho-trap strips applied in three ways. Further on, larvæ have to be controlled by chemical protective measures. Chemical preparations based on chlorpyrifos-ethyl, dimethoate, imidachlopride, alphacipermetrine, biphentrine and physical preparation have been used in our facilities. Plants in pots were treated with 1.5 dl of prepared solution.

Results: The mechanical measures reduced the number of females, and thus the number of eggs from which destructive larvæ could have emerged. The used preparations chlorpyrifos-ethyl, and dimethoate were 100% effective in destruction of larvæ as early as two to three days after application, while the other preparations were less effective six days later.

Conclusion: Control of *Otiorhynchus sulcatus* is difficult. Namely, larvæ, which cause damage, are resistant to chemical preparations, so that effectiveness of treatments with various preparations is not always satisfactory. Only rapid-action and 100% effective preparations should be used in control of this weevil's larvæ, because a single surviving larva in a pot causes decay of the plant.

POSTER PRESENTATION

Determintion of efficient dosage of Spirodiclofen Sc240 and Emidakavprid pesticides against *Aganoscenae pistasia* in Damghan, Iran

Mohammad Ali Oshaghi, Alireza Amir-Ahmadi, Saeed Seyfi Keshtgar

Islamic Azad University, Damghan Branch, Damghan, Semnan Province, Islamic Republic of Iran

Introduction: Pistachio is one of the most important agricultural products of Damghan, Iran which has been exported extensively to abroad. Pistacho psylla (*Aganoscenae pistasia*) is one of the main pests which has got great influence on the quantity and quality the products. In this study, we try to test the efficiency of two pesticides (Spirodiclofen Sc240 and Emidakavprid) against the psylla.

Methods: The study was carried out in 10 ha. pistachio garden where was heavily infected by the pest. The trees were of Shahpasand and Abasali cultivars, where the former is very susceptible to psylla. A complete random blocks with eight treatments each involved three replicates was designed. Each replicate included two trees. A day prior to spraying, sampling from trees was done and number of the pest was estimated. Spraying was performed by a 300 litter spraying machine in a sunny day without wind blowing. Sampleing was done in first, third, 7^{th}, 14^{th}, and 25^{th} day post spraying. Five leaves from tips of stems was selected randomly and the number of psylla was counted. The data (mean) were analysed by Donken-test.

Results: Results of this study showed that there were a significat differences between the treatments and control, but no significant variation within treatment. It is shown that both Spirodiclofen Sc240 and Emidakavprid pesticides with 0.2 per thousand dosage without oil are efficient to control of the pistachio psylla.

Conclusion: Two pesticides of Spirodiclofen Sc240 and Emidakavprid can be recommend for control of the psylla in the region.

POSTER PRESENTATION

Sweetpotato weevil, *Cylas formicarius elegantulus* (Summers) in North Carolina, USA

Kenneth Sorensen

North Carolina State University, Raleigh, North Carolina, United States

Introduction: Sweetpotato weevils are the most destructive insect pests of sweetpotato, *Ipomoea batatas. Cylas formicarius elegantulus (Summers)* is one of many species of sweetpotato weevils (SPW) which occur worldwide, but is the only one in the United States (US). In North Carolina (NC), SPW is restricted to barrier islands of the southern coast, where it feeds on alternate host, seaside morning glory (*Ipomoea sagitata*). NC ranks first in US production of sweetpotatoes with over 40,000 acres and well over $80,000,000 and the introduced SPW remains a serious threat.

Methods: Literature and media were reviewed and new information resources prepared to increase awareness of SPW impact and to enforce quarantines throughout the US. Sex pheromones evaluated in NC were placed in unitraps and boll weevil traps and monitored at 2 sites in southeastern NC from 1990-2007.

Results: Illustrations of SPW damage and life stages, of traps, and population graphs from 1990-2003 are shown. Populations since 2003 dropped significantly and are not included. US and worldwide SPW distribution are illustrated. Best management practices sheets, pocket guides, and powerpoint and poster presentations were shared with growers and extension workers throughout the US.

Conclusions: SPW monitoring technology, statewide application and preventive education effort has helped keep the weevil in abeyance. Future research using DNA fingerprinting will help understand taxonomic relations of SPW on wild and cultivated hosts and elucidate pathways of movement. Geographical and spatial collections and DNA analysis will help with SPW source identification, movement and introduction.

POSTER PRESENTATION

Integrated pest management (IPM) of *Helicoverpa armigera* using *Helicoverpa* nuclear polyhedrosis virus on chickpea in Bangladesh.

Svetlana Micic, Abu M Musa, Chris J Johansen

[1]*Department of Agriculture and Food, Western Australia, Albany, Western Australia, Australia,* [2]*People's Resource Orientated Voluntary Association, Rajshahi, Bangladesh,* [3]*Independant Consultant, Perth, Western Australia, Australia*

Helicoverpa armigera (Pod borer) is a major yield reducer of chickpea (*Cicer arietinum*) throughout south Asia. The main control technique for this pest has focused on the use of insecticides. However, *H. armigera* has developed resistance to several insecticides and their field efficacy is now greatly reduced. Previous trials have shown that *Helicoverpa* nuclear polyhedrosis virus (HNPV) can be an effective alternative, or at least a supplement to chemical insecticides. Multiplication of HNPV was initially attempted at village level but poor sanitary techniques prevented the production of HNPV of high titre with low contamination. The first stage in the commercialization of HNPV in Bangladesh has been to assess the field efficacy of high titre HNPV produced in India with that produced by Rajshahi University, Bangladesh and compared to conventional chemical controls. Results suggest that applications of HNPV and chemicals provide adequate control of *H. armigera* relative to unsprayed plots. Monitoring crops for *H. armigera* in Bangladesh can be difficult, especially if larvae are 1st or 2nd instars and difficult to see. It is at this stage that HNPV applications are most effective. Hence, early detection of *H. armigera* leads to better control measures. The traditional technique of assessing *H. armigera* numbers infield by counting larvae per square metre was compared to sweep netting. The comparative efficiency of these methods to monitor *H. armigera* numbers is also discussed.

POSTER PRESENTATION

Evaluation of new pyrethrin synergists for use against the cotton bollworm *Helicoverpa armigera* (Hübner) (Lepidoptera: Noctuidae)

Tanya Joffe[1], Geoff Allen[1], Robin Gunning[2], Graham Moores[3], Matthew Greenhill[4]

[1]University of Tasmania, Hobart, Australia, [2]NSW Department of Primary Industries, Tamworth, Australia, [3]Rothamsted Research, Harpenden, United Kingdom, [4]Botanical Resources Australia, Ulverstone, Australia

Introduction: The cotton bollworm, *Helicoverpa armigera* (Hübner) (Lepidoptera: Noctuidae), is a major pest in many agricultural systems, capable of causing great economic damage if not effectively controlled. The use of pyrethrum is being investigated for control of *H. armigera* in field crops in Australia, however, a substantial problem hampering effective control of these insects is the presence of pyrethroid/pyrethrum resistance. Resistance is metabolic and has been shown to be esterase mediated. The use of a synthetic synergist, such as piperonyl butoxide (PBO), inhibits esterase activity sufficiently so as to allow pyrethrum to take effect. This study aims to determine the efficacy of various natural synergists in combination with pyrethrum to enable synthetic PBO to be replaced with a natural synergist suitable for use in agriculture and the organic crop market.

Methods: Efficacy of the various putative pyrethrum synergists were tested in the laboratory using topical application bioassays on *H. armigera*. Biochemical techniques were used to asses the esterase inhibiting potency of these compounds.

Results: Some natural synergists have shown potential in the laboratory for use with pyrethrum by inhibiting esterases in *H. armigera*, thus temporarily lowering resistance in these insects sufficiently to allow death by pyrethrum.

Conclusions: Some natural synergists are potent esterase inhibitors, and pyrethrum synergists, in the laboratory but further work will be required to determine efficacy in the field.

POSTER PRESENTATION

Comparison of residual effects of Lambdacyhalothrin WP10% and Lambdacyhalothrin SC10% at 25 mg/m2 on various surfaces against *Anopheles stephensi* (Diptera: Culicidae), in southeastern Iran, 2006 – 2007

Kamran Akbarzadeh[1], Ahmad Raeisi[2], Mohammad-Reza Abai[1], Abdolghaffar Hassanzehi[3], Mehdi Nateghpour[4]

[1]Department of Medical Entomology, School of Public Health, Tehran University of Medical Sciences, Tehran;, [2]Center of Management of Diseases, Ministry of Health, Tehran; [3]Public Health Center of Sistan and Baluchestan Province, Zahedan; [4]Dept. of Medical Parasitology, Tehran University of Medical Sciences, Tehran, Islamic Republic of Iran

Introduction: Indoor residual spraying (IRS) is one of the primary vector control intervention for reducing and interrupting malaria transmission. Lambdacyhalothrin (Icon®) WP 10% has used successfully during 1993 - 2000 for IRS in Iran. The aim of this study was comparison of the residual effects of two formulations of Icon® WP and Icon® SC (as a new formulation introduced in Iran) at 25 mg/m2 on various surfaces in Iranshahr district, where is the endemic area for malaria in the country, during 2006 - 2007.

Methods: The lab-strain of *Anopheles stephensi mysorensis* was used for bioassays. Each formulation was sprayed separately on various surfaces. Spraying process and bioassay tests were carried out according to the method recommended by WHO.

Results: Both tested adulticides, Icon® SC 10% and Icon® WP 10%, showed statistically similar residual activity about 50, 140, 140 and 140 days on cement, plaster, mud and wood surfaces respectively ($p>0.05$). There is a significantly difference between mortality of the mosquitoes between various surfaces ($p<0.05$).

Conclusions: This is the first study on residual effects of SC formulation of Lambdacyhalothrin in Iran. Previous studies on its WP formulation showed residual effects about 90 days on various surfaces in other parts of Iran. The SC formulation simply dissolves in water and doesn't leave any sediment in equipments. Due to noticeable residual duration, this insecticide could be recommended for continuing the study in large village scale trial in southeastern Iran.

POSTER PRESENTATION

Using a new artificial feeding apparatus for infecting *Anopheles stephensi mysorensis* (Diptera: Culicidae) with *Plasmodium vivax*

Kamran Akbarzadeh[1], Hamid Reza Basseri[1], Soghra Doosti[1], Mehdi Nateghpour[2]

[1]Department of Medical Entomology and Vector Control, School of Public Health, Tehran University of Medical Sciences, Tehran;, [2]Dept. of Medical Parasitology, Tehran University of Medical Sciences, Tehran, Islamic Republic of Iran

Introduction: The new designed portable artificial feeding apparatus has been made first for routine rearing of mosquitoes in insectry of Tehran University of Medical Sciences. This cylinder shape apparatus has a 2.5 ml. volume feeding chamber. It safely works with an electrical heater (6 - 12 v. 3 - 4 a.) and a thermostat. Based on literature this system can be used for various scientific subjects such as infecting parasites to blood feeding arthropods for biological and physiological studies. This study has conducted with the aim of determining the capability of the apparatus for infecting *An. stephensi mysorensis* with *Plasmodium vivax*.

Methods: The parasites were obtained from malaria patients harboring gametocytes of *P. vivax* which were referring to health centers of Iranshahr County, southeastern of Iran, during Oct. to Dec. 2004. The apparatus equipped with Parafilm "M" as feeding membrane. All experiments have fulfilled in insectry condition with lab-bred Iranshahr strain of *An. stephensi* in Iranshahr Station of Public Health Research. Double walled cages used for preventing the escape of infected mosquitoes.

Results: In this study total numbers of 164 mosquitoes were fed successfully on infected blood. About 10.22 p 2.88% of them had developed oocysts on their midgut and about 9.68 p 4.95% had sporozoite in their salivary glands.

Conclusions: This study demonstrates that this apparatus can be easily employed for infecting the mosquitoes to malaria parasites. Natural infection of *An. stephensi Mysorensis* had recorded in Iran but this experimental infection provides an outline for further studies in laboratory.

POSTER PRESENTATION

Some observations on the distribution, behavior and hosts of the acacia bagworm *Auchmophila kordofensis* R. (Lepidoptera: Psychidae) in Kordofan, Sudan

Yasir G. A. Bashir[1], Mubarak O. Eljepori[2], Mohammed E. Abd Elrahman[2], Abbas A. Elshiekh[1]

[1]Agricultural Research Corporation, Wad Medani, Sudan, [2]University of Kordofan, Elobeid, Sudan

Introduction: The acacia bagworm *Auchmophila kordofensis*, was first identified in the year 1906 based on type specimens collected from Kordofan, Sudan. This pest remained for long time as a pest of no economical importance attacking only *Acacia nubica* trees. Recently, it emerged as a major pest defoliating many shrubs and tree species in western Sudan. This study investigated some aspects of its relative abundance, feeding behavior as well as it host range.

Methodology: Field surveys were conducted during 2001-2003 to determine the relative abundance of *A. kordofensis* larvae on different hosts. The number of larvae was expressed as number per m twig. Observations on feeding, movement as well as occurrence on different host plants were also monitored.

Results: Field surveys indicated that *Acacia nubica* was the most populated host plant followed by *A. seyal* and *A. tortilis*. The mean number of larvae/m twig during season 2001/2002, was 11.6, 5.3 and 1.3 larvae for *A. nubica*, *A. seyal* and *A. tortilis*, respectively. While during season 2002/2003, the number of larvae/m twig was increased to 18.9, 11.4 and 2.6 for the three hosts, respectively. Newly hatched larvae crawl out of the old bag, attach it self to a host branch and start feeding and constructing a cocoon. During feeding, the head and thorax projected from the case and attachment to branches was done by the thoracic legs. As the larva grows, its bag expands to comfortably accommodate the larva while molting takes place inside the bag. The list of host plants includes *A. seyal*, *A. tortilis*, *A. nilotica*, *Zyziphus spina-christi*, *Prosopis chilensis*, *Cassia senna*, baobab beside its principle host *A. nubica*.

POSTER PRESENTATION

Study of the entomofauna and biodiversity in an urban park in Madrid (Spain)

Laura Del Fresno, Luis Castresana, Antonio Vives, Pedro Ros, Antonio Notario

[1]Universidad Politécnica de Madrid, Madrid, Spain, [2]Sociedad Hispano Luso Americana de Lepidopterología, Madrid, Spain, [3]Asociación Española de Entomología, León, Spain, [4]Sociedad de Entomología Aplicada, Madrid, Spain

Introduction: This dissertation is realized in the Vicálvaro Forest Park (Madrid). The overall objective is to provide the necessary information to help make better management of the Vicálvaro Forest Park, as well as serve as a starting point for comparison and possible entomological studies of biodiversity within urban parks.

Methods: It has been in use traps with attractive of light and food.

Results: It is realized an exhaustive list of the species found, establishing its curves and flight detected which of these species are potentially harmful and which are not. At this point it is determined definitively biodiversity in the park, offering values of indices of biodiversity which serve as a reference for comparison in studies of another parks. It has been captured 157 species, belonging to 67genus and 66 Families. 54 of these species have identified accurately. A specimen belonging to the genus *Scythris* (Lepidoptera, Scythrididae) can be treated as a new species. The values of indices of biodiversity at level of Family and level of species are similar, so we recommend realizing, in this kind of works, the study to level family. The observed Species Richness is minor that the estimated Species Richness. The diversity of the Park is lower-middle; the index of Shannon is approximately 40 % of the maximum possible value for our case.

POSTER PRESENTATION

Laboratory and field investigations of pestiferous Chironomidae (Diptera) in man-made wetlands in central Florida, USA

Arshad Ali, Robert Leckel, Naphtali Carandang

Department of Entomology and Nematology and Mid-Florida Research and Education Center, University of Florida, Apopka, Florida, United States

A one-year population survey of pestiferous Chironomidae was conducted in four man-made wetlands in Florida. Benthic samples were randomly collected each month from each habitat. Geocoordinates, water depth, and substrates physical composition at each sample location were noted. Adult midge populations in the area were assessed by using New Jersey light traps monitored weekly. Chironominae and Tanypodinae occurred in the larval and adult samples; a few Orthocladiinae were also noted. Among Chironominae, Chironomini (mostly *Polypedilum* spp., *Cryptochironomus* spp., *Glyptotendipes paripes,* and *Goeldichironomus carus*) and Tanytarsini (mostly *Tanytarsus* spp.), and some other Chironomidae were recorded. Tanypodinae were quantitatively not important. Annual mean larval density and range of total chironomids amounted to 1,128/m^2, range: 0-12,332/m^2. The total larvae were most abundant in May. *Tanytarsus* spp. and *Polypedilum* spp. were the most predominant spatially as well as temporally. Monthly mean number of total adults per trap night ranged from 23 in February to 211 in October. Mean water depth at the sampled locations was 1.83 m; 47% of the total larvae occurred at < 1 m and 53% at > 1 m water depths. Of all the sampled locations, 51, 28, and 22% predominated with sand, mixed, and muck substrates, respectively. The predominance of sand and mixed substrates was conducive to supporting the numerically dominant *Tanytarsus* spp. and *Polypedilum* spp. In laboratory bioassays, *Tanytarsus* spp., *Polypedilum* spp., *G. carus*, and *G. paripes* were highly susceptible to temephos and to *s*-methoprene. *Bacillus thuringiensis israelensis* was most effective against *Tanytarsus* spp. and least against *G. carus*.

POSTER PRESENTATION

Distribution of neuropeptides in the cephalic nervous system of the Mediterranean flour moth, *Ephestia kuehniella*

Silvie Fexova[1], Radka Zavodska[2], Ivo Sauman[3]

[1]Faculty of Science, University of South Bohemia, Branisovska 31, 370 05 Ceske Budejovice, Czech Republic, [2]Pedagogical Faculty, University of South Bohemia, Jeronymova 10, 371 15 Ceske Budejovice, Czech Republic, [3]Biology Centre ASCR, Institute of Entomology, Branisovska 31, 370 05 Ceske Budejovice, Czech Republic

Introduction: Insect neurohormones influence many physiological processes and some have been proved to be associated with circadian timing as well. Both spatial and temporal localization of seven candidate neuropeptides (allatostatin, allatotropin, eclosion hormone, prothoracicotropic hormone, diuretic hormone, pigment-dispersing factor and corazonin) have been determined in the brain of *Ephestia kuehniella* (Pyralidae, Lepidoptera) in order to explore their possible connection to the circadian clock system.

Methods: Immunocytochemical methods on paraplast sections as well as the whole mount preparations were used to investigate the distribution of immunoreactive neurons in the brains of both sexes.

Animals were kept under 12:12 LD regime and brains were dissected at two time points, ZT 4 and ZT 16.

Results: All the antibodies reacted with a restricted population of cells within the cephalic ganglion-retrocerebral complex of *Ephestia kuehniella* and each produced a distinct staining pattern. The number as well as the localization of the immunopositive cells seemed to be the same in both sexes and does not vary between the night and day samples. The immunoreactive material was always confined to the cytoplasm.

Conclusion: The distribution pattern of some of these neuropeptides, particularly that of corazonin and pigment-dispersing factor, indicates their possible connection to the circadian clock system as the immunoreactive cells seem to correspond both in number and position to neurons that were previously recognized as hosting the circadian clocks in other lepidopterans. It seems that the expression of none of the investigated neuropeptides oscillate throughout the day.

POSTER PRESENTATION

The corazonin- and PDF-immunoreactivities in the brain of termites do not differ among the castes and show no circadian fluctuations

Radka Zavodska[1], Chih-Jen Wen[2], Ivo Sauman[3]

[1]Pedagogical Faculty, University of South Bohemia, Jeronymova 10, 371 15 Ceske Budejovice, Czech Republic, [2]Department of Entomology, National Taiwan University, Taipei, Taiwan, [3]Biology Centre AV CR, Institute of Entomology, Branisovska 31, 370 05 Ceske Budejovice, Czech Republic

Introduction: The neuropeptides pigment-dispersing factor (PDF) and corazonin (Crz) are tentative components of the output pathway of circadian clocks in insects.

Methods: Antibodies to [His^7]-corazonin and to the pigment-dispersing factor were used for immunocytochemical detections of neurons in the central nervous systems of workers and soldiers of seven termite species.

Results: Slight variance between workers and soldiers was found in *Coptotermes formosanus* in which the soldiers lacked 4 Crz-immunoreactive (Crz-ir) perikarya in the *pars intercerebralis* and consistently possessed 4 central perikarya in the labial neuromere, whereas some workers had 6 perikarya in this position. Comparison of the pseudergates, soldiers, and replacement reproductives in *Prorhinotermes simplex* also did not disclose any caste-specific differences. The PDF-immunoreactivity (PDF-ir) occurred in all castes in 3 cells at the base of each optic lobe and in a single cell in the soboesophageal ganglion. The Crz-ir was confined to three lateral clusters in each protocerebral hemisphere. Diurnal changes in PDF-ir and Crz-ir were examined in *P. simplex* kept under a long day (18 hr light and 6 hr darkness) or a short day (10:14 hr light: darkness) photoperiods. No circadian fluctuations in the distribution or the intensity of immunostaining were found in the pseudergates that were sacrificed in 4 hr intervals. No differences were also revealed in 6 hr intervals in the male and female replacement reproductives.

Conclusions: The corazonin- and PDF-immunoreactivities in the central nervous system of termites did not revealed differences among the castes and demonstrated no circadian fluctuations

POSTER PRESENTATION

Systematics and co-evolution of insect herbivores on the Casuarinaceae

Gary Taylor[1], Andy Austin[1], John Jennings[1], Matthew Purcell[2], Nancy Schellhorn[3]

[1]Australian Centre for Evolutionary Biology & Biodiversity, The University of Adelaide, Adelaide, South Australia 5005, Australia, [2]USDA-ARS Office of International Research Programs, Australian Biological Control Laboratory, CSIRO Entomology, Indooroopilly, Brisbane, Queensland 4068, Australia, [3]CSIRO Entomology, Indooroopilly, Brisbane, Queensland 4068, Australia

Introduction: The Casuarinaceae are a significant component of the Australian flora that represents a relict lineage of Gondwanan origin. They possess a unique combination of morphological characters dominated by xeromorphic reductions such as drooping twigs with an apical whirl of reduced scale-like leaves, reduced wind-pollinated flowers, woody 'cones' and wind-dispersed 'samaras' as seeds. Three Australian species, *Casuarina equisetifolia, C. glauca* and C. *cunningamiana* have become serious invasive weeds in southern Florida, including the Everglades National Park. With its rapid growth, dense coverage and thick litter accumulation, *Casuarina* dramatically alters the habitat of infested areas inhibiting growth of native plants and associated herbivores.

Methods: In Australia, the Casuarinaceae has a unique complex of associated insect herbivores that are generally poorly documented. Nor are there any comprehensive studies on the evolutionary events that have driven speciation. In this study the molecular phylogenies of selected taxa will be generated, and compared with the phylogeny for the Casuarinaceae, to test whether insect herbivores and their hosts have co-evolved. It will refine the selection process for identifying suitable biological control agents by utilising a molecular basis for assessing host specificity and host range.

Results: Surveys conducted primarily in eastern Australia have yielded a number of herbivores groups amenable to comparative phylogenetic analysis. These include granivorous micro-Hymenoptera (Torymidae), narrowly host-specific psyllids (Triozidae), *Cylindrococcus* and other eriococcid gall and scale insects, and a major radiation of *Misophrice* weevils (Curculionidae).

Conclusions: It is hypothesised that phylogenies synchronous between herbivore and host would indicate a close evolutionary association that would confer considerably safer options as potential biological control agents than in a group that may have radiated on many host taxa.

POSTER PRESENTATION

Mixed cropping and intercropping as cultural means of control for some cucurbit pests

Abdalla A. Satti

Environment and Natural Resources Research Institute, National Centre for Research, Khartoum, Khartoum State, Sudan

Introduction: Both mixed cropping and intercropping can be defined as growing different crops simultaneously on the same land, but intercropping is characterized by having a base crop and one or more associated crops planted within. Apart from their agronomical merits, they sometimes perceived as cultural means of pests and/or diseases control. However, these cropping systems were attempted in this study for the purpose of mitigating damage of some cucurbit pests.

Methods: The study included five field experiments carried out at Shambat, Khartoum-North, Sudan. A mixed cropping of *Cucumis melo*, *Abelmoschus esculentus*, *Solanum melongena*, *Vigna unguiculata* and *Lablab purpureus* was conducted during late autumn (Sep.-Nov.) where the distribution of *Bemisia tabaci* and *Jacobiasca lybica* were studied. Similarly, five cucurbit species were screened against *B. tabaci*, *Aphis gossypii* and *Epilachna elaterii* during winter season (Nov.-Feb.). Moreover, the effects of intercropping either fenugreek or coriander with cucumber on the *E. elaterii* were evaluated, each in a separate winter experiment.

Results: Results of the first experiment showed that the population mean of *B. tabac*i was significantly higher on *L. purpureus*, whereas *J. lybica* was significantly higher on *S. melongena*. Since the two pests were drastically suppressed on muskmelon (*C. melo*), intercropping either of these crops with muskmelon (or other cucurbits) should be emphasized separately depending on each pest infestation. However, comparing cucurbit species muskmelon was almost lied among the highly infested crops by *B. tabaci*, *A. gossypii* and *E. elaterii*. In this sense *Citrullus colocynthis* was detected as the most repellent plant for the two former pests, but attractant for the latter one. On the other hand, fenugreek and coriander significantly reduced infestation and damage by *E. elaterii* on intercropped cucumber.

Conclusions: Mixed cropping and intercropping were proved effective in controlling some important cucurbit pests particularly *B. tabaci*, *J. lybica* and *E. elaterii*. *L. purpureus*, *S. melongena* and *C. colocynthis* showed attractant effect to the three pests, respectively. Hence, they can be checked as trap crops.

POSTER PRESENTATION

Chalcidoid wasps associated with galls on southern African plants: records from a specimen-based database

Ottilie Neser

ARC-Plant Protection Research Institute, Pretoria, South Africa

Databasing of the chalcidoid specimens at the National Collection of Insects, Pretoria, began in 2001 and the database currently contains details of specimens with host data of all the large families (with the exception of some Encyrtidae and Aphelinidae). The more than 11000 records in the database reflect the wealth of taxonomic, biological and distributional information present in the drawers of the collection. Most specimens have been identified to generic level, but a large proportion remains unidentified at species level. The great diversity of chalcidoids associated with (but not necessarily causing) galls on southern African plants is strikingly brought home by the captured data, with over 850 entries reflecting chalcidoids that emerged from galls. The database should greatly aid further collection and study of galls and their associated parasitoid faunas, by making the mostly unpublished information more readily accessible to the research community. A list of the chalcidoid families, genera and species that are associated with or emerged from galls, is provided. Plant families, genera and species as well as plant parts affected by the galls from which chalcidoids emerged, are recorded. Details of insect and other arthropod hosts present in the galls, and a map showing the collection sites in southern Africa are included. Some interesting examples of galls, the possible or known gall formers and their associated parasitiod complexes are highlighted. Unfortunately very little is known about the biology of many species developing inside these galls – 'who does what' often remaining a mystery.

POSTER PRESENTATION

Status quo of honeybee (*Apis mellifera* L.) pests and diseases in Sudan

A. A. Mogbel El-Niweiri, Abdalla A. Satti

Environment and Natural Resources Research Institute, National Centre for Research, Khartoum, Khartoum State, Sudan

Introduction: Honeybees are found naturally in Sudan since ancient time and traditional beekeepers are present. Recently, modern beekeeping has been flourished using imported colonies, so the threat of spreading exotic pests and diseases was expected. Since few data is available in this field, it was aimed by this work to recognize important pests, predators, diseases and parasites of honeybees and their incidences in different parts of the country.

Methods: Data were collected through intensive surveys and questionnaires covering nine bee areas (States) in Sudan during the period 2003 - 07. Different modern and traditional apiaries and wild colonies were inspected, where the percentages of affected colonies by major pests or diseases were indicated in most areas. Samples taken included 122 local colonies and 350 Carnio-Egyptian colonies plus 30 colonies of *Apis florea*. Detected insects were mostly identified at the Insect Collection of the Agricultural Research Corporation(ARC), Sudan, whereas vertebrate species identified either at the Wild Life Research Centre, ARC or Sudan Institute for Natural Sciences. Suspected diseases were confirmed through laboratory culturing and biochemical tests followed at the Department of Microbiology, Faculty of Veterinary Sciences-University of Khartoum.

Results: Lists of more than 35 pests and predators of honeybees were recorded at variable levels in different areas. They include mainly insect and vertebrate species and few spiders. Among these, twenty species were new records e.g. the hive beetles, bee wolves, squirrel and honey badger. However, many species were found causing serious problems such as *Galleria* moth (86.3% infested colonies), ants and two predatory birds (*Merops* spp.). On the other hand, all areas were found free of most bacterial and fungal diseases, except the bacterial brood disease, *Serratia marcescens*, found in 2.6% of Khartoum colonies. Moreover, the parasitic mite, *Varroa jacobsoni*, was found firstly infecting 75% of colonies in Khartoum State as new record, thenceforth detected in Sennar and Kordofan States.

Conclusions: Various indigenous pests of honeybees were found in Sudan and some exotic pest and disease species were introduced through commercial beekeeping.

POSTER PRESENTATION

Comparative analysis of larval developments of *Lucilia sericata* Meigen (Diptera: Calliphoridae) from different geographic populations at constant temperatures

Matthias Gosselin[2], Yves Braet[1]

[1]National institut of Criminology and Criminalistics, Brussels, Belgium, [2]University of Mons-Hainaut, Mons, Belgium

Introduction: *Lucilia sericata* Meigen (Diptera, Calliphoridae) is a very common forensic fly in the temperate area of the northern hemisphere but is also widespread throughout the major zoogeographical regions. Available publications show that its development depends of the geographical origin of the population. This variation could be driven by local adaptation (intrinsic factors).

Methods: Two modelling methods (linear and non-linear) were used to estimate the developmental constants (Development Minimum Threshold, Thermal Constant) for a Belgian population of *L. sericata* at different constant temperatures. The developments periods (in days) of this population and from previously published studies were compared to verify if larval development is subject to geographical variation. The percentage of pupae emerging successfully was counted at the same temperatures.

Results: New development periods were recorded for extreme temperatures and new developmental constants have been estimated. The developmental periods were observed to be longer than those published before. This difference could be caused by variation of development between different populations of blowflies. It emphasizes that there are large variations in developmental data that have been measured across the temperature range between different publications. The minimal, optimal and maximal temperature for survivorship have been calculated and compared with the former publications.

Conclusions: The variation in developmental rates emphasizes the importance of using local developmental data to estimate PMI in forensic cases. Thermal data coming from the same or a nearby population are important to give a best PMI estimation.

POSTER PRESENTATION

Insect growth regulator novaluron to control Nitidulidae sap beetles in strawberries

James Price, Curtis Nagle

University of Florida, Wimauma, Florida, United States

Introduction: Strawberries valued at 210 million USD were produced on 3,200 ha. in Florida, USA during 2006-2007. Main arthropod pests include the twospotted spider mite (*Tetranychus urticae*), cyclamen mite (*Phytonemus pallidus*), southern and fall armyworms (*Spodoptera eridania* and *S. frugiperda*), strawberry root and melon aphids (*Aphis forbesi* and *A. gossypii*), flower thrips (*Frankliniella bispinosa* and *F. occidentalis*), and sap beetles (principally *Lobiopa insularis* and *Haptoncus luteolus*). Sap beetle adults enter fields in late winter, chew holes in ripe fruit and reproduce there. The presence of small numbers of adults or their larvae in fresh fruit can inflict significant economic damage. Growers largely depend on their removing all ripe fruit from the field and applying the pyrethroid insecticides, bifenthrin and fenpropathrin, but find these tools insufficient to manage the problem adequately. The pyrethroids disrupt natural and applied biological control of other arthropods.

Methods: Two experiments were conducted in 2006 and one in 2007 to determine the usefulness of aqueous sprays of novaluron, the benzoylurea inhibitor of chitin biosynthesis insecticide, for management of sap beetles in strawberries. Novaluron was applied at 87 g/ha. with and without bifenthrin applied at 168 g/ha. twice at 1 week intervals.

Results: Novaluron provided excellent control for sap beetles with or without bifenthrin.

Conclusions: The insect growth regulator, novaluron, can be useful to control sap beetles in strawberries and additionally contribute a new mode of action to the control options. The additional mode of action can enhance programs that reduce probabilities of resistance to chemical control measures.

POSTER PRESENTATION

Life-history and phenology of the non-native *Halyomorpha halys* (Stål) (Hemiptera: Pentatomidae) in the United States

Anne Nielsen[1], Gary Bernon[2], George Hamilton[1]

[1]Rutgers University, New Brunswick, NJ, United States, [2]USDA-APHIS CPHST, Cape Cod, MA, United States

The brown marmorated stink bug, *Halyomorpha halys* (Stål) (Hemiptera: Pentatomidae), is an Asian species that was accidentally introduced into the United States in the mid 1990's into Allentown, PA. We conducted weekly beat samples on ornamental trees and shrubs from 2005-2007 to determine its seasonal phenology and population dynamics as well as the relative abundance of native species of stink bugs. Several host plants were identified as being able to support nymphal development, including *Paulownia tomentosa*, one of its known host plants in its native range. However, despite being univoltine, degree-day accumulations and female ovarian development indicate that a proportion of first generation females become reproductively mature. A small increase in temperature could lead to a second generation in the Mid-Atlantic States. On the host plants we sampled, *H. halys* was the most predominant stink bugs species, far outnumbering native species.

POSTER PRESENTATION

Calreticulin expression and endoplasmic reticulum organization during ovulation and early embryogenesis of *Rhodnius prolixus*

Isabela Ramos[1], Claudia Campos[3], Marcos Sorgine[2], Francisco Nobrega[3], Marina Nobrega[3], Kildare Miranda[1], Wanderley Souza[1], Ednildo Machado[1]

[1]IBCCF, UFRJ, Rio de Janeiro, Brazil, [2]IBqM, UFRJ, Rio de Janeiro, Brazil, [3]IPD, UNIVAP, Sao Paulo, Brazil

Endoplasmic reticulum (ER) is the most important intracellular compartment involved in calcium storage and release, and calreticulin is a multifunctional ER resident chaperone that buffers calcium with high capacity. Egg activation is a complex process that triggers events necessary for the egg to support the early development, including extensive transient rises in intracellular free calcium. This work reports calreticulin expression levels and endoplasmic reticulum organization during ovulation, fertilization and early embryogenesis of the bug *Rhodnius prolixus*. Calreticulin was cloned and its coding sequence was obtained. Real time PCR evidenced that during ovulation and fertilization, calreticulin expression remains at low levels when compared to laid fertilized eggs. Immunohistochemistry showed that this protein is mainly located in the periphery of the eggs, and transmission electron microscopy revealed the existence of a thin differential peripheral ooplasm, external to the yolk granules-filled central ooplasm. It was showed that ovulated oocytes present alterations in the peripheral ooplasm, chorion and permeability, thus suggesting that ovulation triggers the initiation of egg activation. Immunoelectron microscopy evidenced that during ovulation and fertilization the ER (calreticulin labeled) is presented as dispersed lamellae and vesicles, and transmission electron microscopy showed that only after oviposition an organized rough ER is found, filling the peripheral ooplasm. Thus, it was reported that ovulation might trigger initiation of the egg activation, and that even though this process is marked by extensive events of Ca^{2+} release it does not involve alterations or organization of the ER.

Parasitoids complex of *Trioza erytreae* (Del Guercio) (Homoptera:Triozidae), african citrus psyllid, in Cameroon.

Tamesse Joseph Lebel

University of Yaounde I, Ecole Normale Supérieure, ; Laboratory of Zoology, P.O Box 047 Yaounde, Cameroon

In Cameroon, citrus is under the permanent attacks of *Trioza erytreae*, african citrus psyllid; this insect is the vector of the greening disease of citrus. In this country, chemical control against *Trioza erytreae*, does not abate the high level of the pest populations in citrus orchards. Biological control would be the most promising way to limit these populations in the country. The psyllid parasitism was studied on attacked citrus plants. Mummified larvae were collected in a citrus orchard in the area of Yaounde (Cameroon), and on isolated citrus trees and *Clausena anisata* trees, one endemic Rutaceae in Cameroon. These mummies were observed in the laboratory and the hymenoptera which emerged were identified. The total parasitism level was approximately 15%. The inventory of the parasitoïd species of *T. erytreae* showed the presence of primary parasitoids: *Psyllaephagus pulvinatus* (36.3%), *Tamarixia dryi* (3.5%), *P. secus* (3.3%), *Psyllaephagus* sp. (0.6%), *P. chiangamus* (0.6), *Dilyta* cf *camerounensis* (0.4%) and *Coccophagus pulvinariae* (0.03%); and hyperparasitoids: *Aphidencyrtus (Syrphophagus) cassatus* (45.3%), *Tamarixia* sp. (6.8%), *Tetrastichus* sp. (1.5%), *Marrieta javensis* (0.2%), *Physcus* sp. (0.2*%), Aphanogmus* sp. (0.2%) and *Cheiloneurus cyanonotus* (0.1%). The parasitoïd fauna of *T. erytreae* is diversified in Cameroon. Certain species are cited on this psyllid for the first time: *Aphanogmus* sp., *Tamarixia* sp., *Psyllaephagus chiangamus*, *Psyllaephagus* sp., *Psyllaephagus secus* and *Dilyta* cf *camerounensis*. The conservation of the biodiversity of these parasitoids of *T. erytreae* is an interesting advantage in initiating biological control against this important citrus pest in the country.

POSTER PRESENTATION

Parasitoids complex of *Trioza erytreae* (Del Guercio) (Homoptera: Triozidae), the African citrus psyllid, in Cameroon

Tamesse Joseph Lebel

University of Yaounde I, Yaounde, Cameroon

Introduction: The position of termites among the Dictyoptera has long been disputed. I present molecular evidence to show conclusively that termites are cockroaches. However, termites have diverged from cockroach traits in many ways, particularly through the greater phenotypic plasticity that eusociality has provided.

Methods: I will present two phylogenetic datasets, one for Dictyoptera (five genes) and a larger one for termites (three genes) as well as data on gut structure and function.

Results:.Termites are eusocial cockroaches. However, termite eusociality has allowed for an extraordinary range of behavioural, anatomical and physiological traits to evolve. One good example is trophic ecology - a wider variety of feeding substrates can be consumed by termites than by other closely related cockroaches. This has been made possible through the development of specialised castes that have freed workers to evolve gut structures not possible, for intrinsic design-cost reasons, in other cockroaches. These changes are not just observed between *Cryptocercus* and other termites, but also found in other parts of the tree: the general trend being from mid-gut detritivory to hind-gut fermenting. I will discuss the evolutionary and ecological consequences of these changes.

Conclusions: Eusociality has allowed termites to become a very sophisticated sort of cockroach.

POSTER PRESENTATION

Development of *Chrysomya marginalis* Wiedemann 1830 (Diptera: Calliphoridae) at different temperatures for the estimation of post mortem interval

Philip S. R. Weyl, Martin H. Villet

[1]Rhodes University, Grahamstown, South Africa, [2]Rhodes University, Grahamstown, South Africa

Chrysomya marginalis is a carrion-breeding fly, which gives it the potential of being important in forensic investigations to determine post mortem interval (PMI). The developmental curves were established for eight different constant temperatures using length and developmental landmarks and actual age. The thermal summation constants (K) and developmental threshold (D_0) were calculated for five developmental landmarks using the method described by Ikemoto & Takai (2000). Isomorphen and isomegalen diagrams were also constructed for the purpose of PMI. *Chrysomya marginalis* had an average developmental threshold (D_0) of 14.04 ºC (SE = 0.70 ºC, n = 4), and the thermal constant (K) was 74.25 hºC (SE = 2.23) at 1st ecdysis, 566.64 hºC (SE = 42.77) at 2nd ecdysis, 1007.66 hºC (SE = 81.71) at the wandering stage, 1489.91 hºC (SE = 128.37) at pupariation and 3299.53 hºC (SE = 183.99) for eclosion. *Chrysomya marginalis* has a preference for larger carcasses, which makes the results from this study valuable for wildlife management and poacher control.

POSTER PRESENTATION

Preliminary molecular phylogenetics and inferred historical biogeography of three African cicada genera of the Platypleurini (Hemiptera: Cicadidae)

Tarryn Goble, Benjamin Price, Nigel Barker, Martin Villet

Rhodes University, Grahamstown, South Africa

Cicadas provide interesting models for mechanistic studies of biogeography because they are often habitat-specific and their present distributions may reflect past geological history. Representatives of 14 African platypleurine genera were included in this study. Of particular interest were the arid-adapted cicada genera, *Munza*, *Severiana*, and *Soudaniella* that all have biogeographic ranges which include the Kalahari Desert system in southern Africa. Separate phylogeographic analyses of these genera using two mitochondrial genes, *Cytochrome oxidase* I (*COI*) and the large ribosomal subunit *16S* rRNA revealed some discrepancy in the resolution of cicada clades. The separate *COI* and *16S* analyses resolved *Munza* as a well-supported monophyletic group with the genus *Severiana* forming its sister group, but in the combined analysis *Munza* was no longer monophyletic. Molecular dating analyses, calibrated using published *COI* and *16S* substitution rates typical for related insects, showed that the *Munza, Severiana*, *Soudaniella* and *Capcicada* lineages probably date back to the late Miocene or early Pliocene (4.4-8.1 MYA) with a second diversification occurring within *Munza* during the Pleistocene (1.0-2.7 MYA). These diversifications coincide with both the development of the Kalahari Desert at about 5 MYA and the subsequent movement of alluvial sands that have been active since the Pliocene-Pleistocene transition.

POSTER PRESENTATION

Implications of a preliminary molecular investigation of four African cicada genera in the tribe Parnisini (Hemiptera: Cicadidae)

Tarryn Goble, Benjamin Price, Nigel Barker, Martin Villet

Rhodes University, Grahamstown, South Africa

The Cicadidae of southern Africa have not been systematically revised since the publication of Distant's *Insecta Transvaalensia* in 1906, leaving a confusing account of their classification, particularly the poorly-studied tribe Parnisini. Approximately 772 base pairs of mitochondrial DNA from the *Cytochrome oxidase* subunit 1 (*CO1*) gene, from 44 samples, representing the parnisine genera *Koranna*, *Masupha*, *Neomuda*, *Oudeboschia*, *Quintilia*, *Zouga*, were sequenced. Analysis of the sequences revealed that the type species of *Quintilia*, *Q. rufiventris*, appeared to be phylogenetically isolated, implying that the genus *Quintilia* was currently not a monophyletic group, but a taxonomic dumping ground for many cicada species and that its revision was required. All analyses provided good evidence that *Quintilia walkeri* and the *Q. carinata* species-group formed a monophyletic clade. The genus *Masupha* was recognised as a distinct clade. The formation of a clade of *Quintilia* species around the type species of *Koranna* was supported by a strong pattern of common biogeographic distribution, suggesting that many *Quintilia* species should be transferred to *Koranna*. The genera *Neomuda*, *Oudeboschia* and *Zouga* appeared to have little in common with the other Parnisini.

POSTER PRESENTATION

In vivo pathogenicity of *Beauveria bassiana* and *Metarhizium anisopliae* on *Chrotogonus trachypterus* (Orthoptera: Pyrgomorphidae)

Ali Mirshekar, Aziz Kharazi-Pakdel

Department of Plant Protection, Faculty of Agriculture, University of Tehran, Karaj, Tehran, Islamic Republic of Iran

Introduction: Concerns over the environmental and human health impacts of chemical control of grasshoppers have led to considerable interest in developing of alternative control methods e.g. using entomopathogenic fungi.

Methods: Effects of two native isolates of the fungus *Beauveria bassiana*, a native isolate of *Metarhizium anisopliae* a long with Green Muscle™, a commercialized formulation of *M. anisopliae* var. *acridum*, were investigated on the sugarcane grasshopper and some other short and long-horned native grasshoppers. LD_{50} and LD_{99} were separately calculated for male and female adults also without regarding their sex.

Results: The results showed the pathogenicity of all isolates of *M. anisopliae* and *B. bassiana* against the studied grasshopper. The lowest LD_{50} obtained as 187 spore/insect for female insects treated with the native isolate of *Metarhizium anisopliae* and the highest was calculated as $2/06\times10^5$ spore/insect for biologically-treated male insects. Comparison between LD_{50} and LD_{95} off all isolates were demonstrated that native isolate of *Metarhizium anisopliae* had the lowest LD_{50} ; Other native isolates had high pathogenicity rather than commercialized product. The results indicated that insect susceptibility was decreased with increasing of age.

Conclusions: These results indicate that more studies is essential in order to isolation of native strains of entomopathogenic fungi and determination of their effectiveness on insect pests.

POSTER PRESENTATION

Stored pests control by cineole essential oil

Vlatka Rozman[1], Zlatko Korunic[2], Irma Kalinovic[1], Anita Liska[1]

Faculty of Agriculture, University of J.J. Strossmayer in Osijek, Osijek, Croatia[1], Diatom Research and Consulting Inc., Guelph, Canada[2]

Introduction: Laboratory research to control *Sitophilus oryzae* L., *Rhyzopertha dominica* F., *Cryptolestes ferrugineus* L. and *Tribolium castaneum* Herbst. by cineole essential oil aimed to find out potential source of new fumigants.

Methods: Three experiments with cineole were done: first, to test efficacy of cineole against different developmental stages of insects; second, to test effective concentration of 50, 100, 150, 200, 250 µl/L; and third, to test effective cineole concentration in spaces differently occupied with wheat (empty space, 50% and 95% filled up).

Results: Developmental stages of *C. ferrugineus* in wheat grain were more sensitive to cineole in comparison to the remaining tested species. By testing 5 concentrations of cineole, 100% mortality of *C. ferrugineus* was obtained with 50 µl/L. However, 100% mortality of *R. dominica* was obtained with concentration of 150 µl/L, with *S. oryzae* and *T. castaneum* at concentration of 250 µl/L.Concentration of cineole of 50µl/L in empty space induced nearly 100% mortality in all four tested insect species, while results of fumigation of space occupied with wheat (50% and 95%) did not prove to be successful and acceptable.

Conclusion: Cineole proved to have fumigant effect *in vitro*, but it would be needed to apply high concentrations relative to phosphine or methyl bromide to gain satisfactory results.

POSTER PRESENTATION

Ecological niche and potential geographic distribution of the invasive fruit fly *Bactrocera invadens* (Diptera: Tephritidae)

Marc De Meyer[1], Mark Robertson[2], Mervyn Mansell[3], Sunday Ekesi[4], Kenji Tsuruta[5], William Mwaiko[6], Jean-François Vayssières[7], A. Townsend Peterson[8]

[1]Royal Museum for Central Africa, Entomology Section, Tervuren, Belgium, [2]Department of Zoology and Entomology, University of Pretoria, Pretoria, South Africa, [3]United States Department of Agriculture, APHIS, Pretoria, South Africa, [4]International Centre of Insect Physiology and Ecology, Nairobi, Kenya, [5]Moji Plant Protection Station, Nishikaigan, Moji-ku, Kitakyushu, Japan, [6]Ministry of Agriculture and Food Security, Plant Health Services, Dar es Salaam, Tanzania, United Republic of, [7]CIRAD, UPR Production Fruitière, Montpellier, France, [8]Natural History Museum and Biodiversity Research Center, University of Kansas, Lawrence, Kansas, United States

Two correlative, evolutionary-computing solutions to the challenge of ecological niche modeling techniques (genetic algorithm GARP, maximum entropy Maxent), were used to predict the potential distribution of the invasive fruit fly, *Bactrocera invadens* based on known occurrence records and a set of environmental predictor variables. The two models yield similar potential ranges, largely corresponding to Equatorial climate classes with high precipitation. Maxent may be more conservative in its evaluation of suitability (depending on the threshold levels taken into account), excluding areas with distinct dry seasons, while GARP models indicate that climate class as partly suitable. Field observations in Benin and Tanzania confirm relationships between seasonal occurrences and the abiotic factors of humidity and temperature.

POSTER PRESENTATION

Host range and partitioning of fruit-infesting pestiferous fruit flies (Diptera: Tephritidae) in Central Tanzania

Maulid Mwatawala[1], Marc De Meyer[2], Rhodes Makundi[3], Amon Maerere[1]

[1]Department of Crop Science and Production, Sokoine University of Agriculture, Morogoro, United Republic of Tanzania, [2]Royal Museum for Central Africa, Entomology Section, Tervuren, Belgium, [3]Pest Management Centre, Sokoine University of Agriculture, Morogoro, United Republic of Tanzania

The host range of major fruit fly pests in Central Tanzania was evaluated from October 2004 to October 2006. Samples of 48 potential hosts were collected and incubated for fruit flies emergence. *Bactrocera invadens* was the dominant species, both in host plant range, incidence expressed as the ratio of infested to total number samples collected, as well as infestation rate expressed as number of flies emerging per unit weight. Nine new host fruits are reported for this invasive species. Infestation by native fruit fly pests, such as *Ceratitis capitata* and *C. cosyra* was minor compared to *B. invadens*. *Ceratitis rosa* was the dominant species in temperate fruits, and Cucurbitaceae were mainly infested by *Bactrocera cucurbitae*, a specialized cucurbit feeder. Among commercial fruits, high infestation incidences were observed in mango and guava, but they decreased throughout the fruiting season. Low infestation incidences were observed in all *Citrus* species sampled and in avocado indicating these fruits as poor hosts for the studied fruit fly pests in this region. Fruit species studied here provide suitable hosts for year-round breeding of *B. invadens*, while this is not apparent for the other fruit fly pests studied. Seasonal infestation differs with mango being the most important host in October to January, while guava being important from February to August. Tropical almond showed very high incidence and infestation rate for *B. invadens* and might act as an important reservoir host bridging the fruiting seasons of mango and guava. Soursop acts as an important host for *C. cosyra* after the mango season. *Ceratitis capitata* is a pest of minor importance of the commercial fruits studied in this region.

POSTER PRESENTATION

Management of *Sitophilus oryzae* and *Tribolium castaneum* in stored rice by traditional parboiling as practiced in Guinea

Aïssata Camara[1], Charles Vincent[2], Michel Raymond[1]

[1]Institut des sciences de l'environnement (ISE), Université du Québec à Montréal (UQAM), C.P. 8888, succursale Centre-Ville, Montréal, Qc, Canada, [2]Horticultural Research and Development Center, Agriculture and Agri-Food Canada, 430 Gouin Blvd., Saint-Jean-sur-Richelieu, Qc, Canada

Introduction: In Guinea, traditional methods are used to manage insect pests of stored grains. However, the entomological effect of such traditional methods is often unknown.

Methods: We quantified the effect of parboiling as a procedure to manage two bruchid pests, *Sitophilus oryzae* L. and *Tribolium castaneum* Herbst, over a period of three months. Three types of rice (i.e. white, red and paddy) were used in two experiments conducted with the collaboration of peasants from the surroundings of Conakry (Guinea). In experiment 1, *S. oryzae* was used as a sole pest to infest the rice. Parboiled paddy rice had the lowest level of infestation after 15 days, as determined by the number of emerged adults.

Results: Oviposition was significantly lower in parboiled paddy, white and red than in respective control rice types. In experiment 2, the lowest levels of infestations were found in parboiled paddy rice and parboiled white rice. Trends similar to those of experiment 1 were determined regarding oviposition.

Conclusions: We conclude that traditional parboiling is efficient to manage the two insect pests in post-harvest situations akin to guinean peasantry. The next challenges are to foster greater usage of this traditional method to the peasants and to verify its effect on other major post-harvest pests.

POSTER PRESENTATION

Educational programs for indoor pest control in the United States

Susan King, James Fredericks

University of Delaware, Newark, Delaware, United States

From September 2006 to September 2007, eight educational workshops for homeowners were delivered in Delaware, USA through the Cooperative Extension System. The workshops were attended by 129 individuals. All attendees received informational packets that included two magnetized color plates for attaching to their refrigerators: “Indoor Pest Control Decisions - Ants” and “Indoor Pest Control Decisions - Pantry Pests.” Post workshop surveys showed that 83% of attendees planned to use Integrated Pest Managements techniques the next time they had pest insects in their homes. In November 2007, Home Paramount Pest Control provided 100 of their customers with the same magnetized color plates. These individuals were not offered educational workshops. Attitude and behavioral comparisons will be made between homeowners who attended workshops and those who did not.

POSTER PRESENTATION

The seasonal occurrence, soil distribution and flight characteristics of the lesser chestnut weevil, *Curculio sayi* (Coleoptera: Curculionidae) in Mid-Missouri

Ian Keesey, Bruce Barrett

Entomology Program Area, Division of Plant Sciences, University of Missouri, Columbia, Missouri, United States

Introduction: Following the chestnut blight in the early 19th century, the overall range of the American chestnut tree (*Castanea dentata*) was greatly reduced. As interest in the restoration of this tree increases, and as commercial production of chestnut fruit is being developed in the Midwest, multiple aspects of commercial production, such as pest management of key chestnut pests, need to be addressed. This study examined some basic biological aspects of the lesser chestnut weevil, *Curculio sayi* (Gyllenhal) in mid-Missouri: adult seasonal occurrence, soil distribution of immature stages, and adult flight characteristics.

Methods: Three trap types were used to monitor adult activity: ground-based cone traps, circle-trunk traps and pyramid (or Tedder's) traps. Soil containers were buried and mature larvae placed in them to ascertain larvae burrowing depth and time spent underground per developmental stage. A laboratory flight mill was used to examine adult flight characteristics.

Results: Adult weevils had distinct spring (usually May) and fall (August-September) emergence periods (not previously reported in the literature). Peak adult activity within the trees occurred during the fall emergence period (which coincided with nut production). Periodic removal of the buried soil containers over a two-year period revealed that the minimum duration of the underground larval stage was 17 months, and that the depth most larvae burrowed to was 7.5 to 15 cm. Preliminary data from the flight-mill study revealed that the average single flight times of adults lasted about 10 minutes, and that the distance was about 0.25 km for both sexes.

POSTER PRESENTATION

Biodiversity and key insect fauna on wheat agro ecosystem in Romania

Ioan Rosca, Rada Istrate, Constantin Popov

[1]*University of Agricultural Sciences and Veterinary Medicine; Bucharest, Bucharest, Romania,*
[2]*University of Agricultural Sciences and Veterinary Medicine; Bucharest, Bucharest, Romania,*
[3]*Agricultural Research and Development Institute - Fundulea, Fundulea, Romania*

Introduction: It is done a comparative study between useful and pest fauna from wheat agrocoenosis, taking into consideration Heteroptera insect from wheat, as an indicator of agro ecosystem biodiversity.

Methods: Researches referring biodiversity of insect fauna from wheat were done in field, by insect collecting from 10 to 10 days in the whole vegetation period, through pitfall traps, pheromone traps, Yellow sticky traps, entomological net and plant analysis for presence of insects on and in stem.

Results: There were registered species of insects from main insect orders (14133 specimens), and spiders (982 specimens) in wheat agro ecosystem, the most numerous insects were Homoptera (8502, especially aphids), followed by Hymenoptera (2138) and Diptera (1935). From order Heteroptera, there were identified representatives from 11 families, the most numerous being species from families Miridae and Nabidae. From raping Heteroptera, in wheat agro ecosystem the most important key species were representative of family Anthocoridae (*Anthocoris nemorum* L., *A. nemoralis* Fabr.) and Nabidae (*Nabis pseudoferus* Rm., *Nabis feroides* Rm., *Nabis rugosus* L. and *Nabis ferus* L.,), with regulating function in ecosystem. It has to underline the role of species *O. niger* as predator. It is discussed role of these insects in wheat agrocoenosis. The data collected allow to conclude that eventualy adverse effects on the biodiversity could be identified through data obtained regarding whole insect fauna from wheat and Heteroptera insect from wheat, as an indicator of agro ecosystem biodiversity, and Carabidae and Staphylinidae fauna captured in pitfall traps, calculating *Sorensen* index.

POSTER PRESENTATION

Studies of heteroptera insects from Romania: A case study of Heteroptera from wheat and corn, as an indicator of agro ecosystem biodiversity

Ioan Rosca, Constantin Popov

[1]*University of Agricultural Sciences and Veterinary Medicine; Bucharest, Bucharest, Romania,*
[2]*Agricultural Research and Development Institute Fundulea, Fundulea, Romania*

Introduction: Interest of more people jointed in actions referring to protect environment conservation, made to increase interest for study of useful fauna from different agrocoenosis. Heteroptera structure could be an indicator of biodiversity.

Methods: Zoogeographic analysis of whole Heteroptera fauna from Romania, was done on basis of Heteroptera species recorded in literature. The Heteroptera fauna from wheat and corn was analysed as an indicator of agro ecosystem biodiversity, being discussed role of these insects in these two agrocoenosis.

Results: There were registered species of insects from main Heteroptera families with 695 species signalled in Romania, 6 species (0,86%) – cosmopolitan; 48 species (6,90%) – Holarctic; 46 species (6,62%) – Palaearctic; 115 species (16,54%) – Euro-Siberian; 158 species (22,73%) – European; 230 species (33,12%) – Mediterranean; 57 species (8,20%) – Ponto-Mediterranean; 25 species (3,59%) – Turanian and only 10 species (1,44%) endemics.

A number of 80 species (11,51%) are useful of human economy because through their feeding way are limiting pest species populations. From order Heteroptera, there were identified representatives from 11 families, the most numerous being species from families Miridae and Nabidae. From raping Heteroptera, in wheat and corn agro ecosystem the most important key species were representative of family Anthocoridae and Nabidae, with regulating function in ecosystem. It is discussed role of these insects in wheat and corn agrocoenosis. The data collected allow to conclude that eventualy adverse effects on the biodiversity could be identified through data obtained regarding Heteroptera insect, as an indicator of agro ecosystem biodiversity.

POSTER PRESENTATION

IRAC International: Approaches to resistance management for insect-protected Biotech crops

Nicholas Storer[1], Graham Head[2], Jonathan Holloway[3], Ryan Kurtz[4], Elizabeth Owens[5]

[1]Dow AgroSciences LLC, Indianapolis, IN, United States, [2]Monsanto Co., St. Louis, MO, United States, [3]Bayer CropScience, Lubbock, TX, United States, [4]Syngenta Seeds, Inc., Research Triangle Park, NC, United States, [5]Pioneer Hi-Bred International, Johnston, IA, United States

In 2006, IRAC (Insecticide Resistance Action Committee; www.irac-online.org) established a Project Team to address resistance management issues with international significance related to insect-protected biotech crops. Maize and cotton varieties containing *cry* genes from *Bacillus thuringiensis* (*Bt*) are being commercially cultivated on 26.3 million hectares across 17 countries (2005 figures). This represents nearly 25% of the global cotton area and 12% of the global maize area. This area of cropland protected by *Bt* is rapidly increasing and the types of crops involved are broadening. It is in the interest of industry, in partnership with growers, universities, and governments, to preserve the long-term benefits of *Bt* crops by taking proactive resistance management measures that maximize the utility of the technology. Bt crops present some unique challenges to insect resistance management (IRM) since many of the measures taken to protect the durability of sprayable chemicals are not applicable to in-plant protection. The IRAC International Biotech Team is charged with globally advancing guidelines for designing locally-workable resistance management measures. We develop and distribute educational materials to help technology providers, seed companies, and growers appreciate the need for IRM and understand how to implement IRM programs. The group also assists country-level organizations develop specific resistance management programs for insect-protected biotech crops geared to local conditions, cultivation practices and pest spectra. We recommend sound scientific principles to be the foundation of these plans while recognizing the commercial and infrastructure realities in each geography.

POSTER PRESENTATION

Olfactory memories acquired during trophallaxis affect the odor choice at the food source in carpenter ants

Yael Provecho, Roxana Josens

Grupo de Estudio de Insectos Sociales, Departamento de Biodiversidad y Biología Experimental. Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, Buenos Aires, Argentina

Introduction: A few social insect species are known to establish olfactory memories at the food source associating an odour cue with the reward stimuli (nectar). We studied whether the carpenter ant *Camponotus mus* is able to learn an olfactory cue *during the mouth-to-mouth food exchange (trophallaxis)* and tested the role of this memory in a Y-shaped food source.

Methods: Pairs of ants were isolated under controlled conditions. After a given period, one of them (donor ant) was fed with aromatised sucrose solution and then put back again with her partner (receiver ant). After the first trophallaxis, the response of receiver ant was evaluated on a Y-shaped food source without any reward by presenting two different odours: in one branch, the solution odour and in the other, a new scent.

Results: In non-reinforced tests, receiver ants consistently chose the branch with the odour presented in the sucrose solution and spent more time searching therein. Olfactory learning occurred independently of the duration of trophallaxis.

Conclusions: These results thus show for the first time that individual nectivorous ants perceive and learn odours during trophallaxis and that this memory influences the subsequent search behaviour at the food source. These results will be discussed in light of recent evidence of similar olfactory learning patterns in other eusocial insect species.

POSTER PRESENTATION

Insects: friend, foe or fifty-fifty? Density-dependent pollination and fruit predation in a self-incompatible legume

S.R. Simpson, C.L. Gross

University of New England, Armidale, NSW, Australia

Introduction: Populations are often thinned by habitat fragmentation. Processes such as pollination and predation can be influenced by habitat modification. Self-incompatible species that rely on pollen vectors to set seed may be particularly vulnerable to fluctuations in local population density.

Methods: The Australian endemic *Dillwynia sieberi* (Fabaceae) is reliant on insects for seed set, but its seeds are often consumed by coleopteran larvae. To determine the impact of density on this species, focal plants in 5 dense and 5 sparse plots in each of three populations were monitored in 2004 and 2005 for floral visitation, fruit and seed production and fruit predation.

Results: Bee visitors to *D. sieberi* included *Apis mellifera* and species from *Exoneura, Lasioglossum* and *Leioproctus*. Floral visitation, fruit to flower ratios and fruit predation were often higher in dense plots. However, density effects on seed production were less straight-forward. In the absence of predation, seed to fruit ratios were similar between densities, indicating that 1) fruit to flower ratios are not always good indicators of reproductive success and 2) net seed set is moulded by factors other than pollination. When fruit predation was factored into seed to fruit ratios and when percent reduction of seed due to predation was assessed, seed attrition was often higher in dense plots.

Conclusion: Although we detected density-dependent floral visitation, potential benefits are neutralised at the seed interface by density-dependent predation. Thus, plants in sparse populations may experience better fitness outcomes than conspecifics from dense populations.

POSTER PRESENTATION

Repellents and attractants as push-pull strategy for potato moth control

Maria Isabel Gomez[1], Teja Tscharntke[2], Katja Poveda[2]

[1]Universidad Nacional de Colombia, Bogotá, Colombia, [2]Georg-August University, Göttingen, Germany

Introduction: Push-pull strategies are based on the behavioral manipulation of insect pests by the simultaneous use of repellent stimuli that make the crop unattractive (push) and attractive stimuli to areas where direct control is facilitated (pull). One of the main pests in potato crops is the Guatemalan potato moth (T*ecia solanivora*) whose larvae are specialized on potato tuber feeding. This pest is able to destroy up to 100% of a potato crops in Latin America.

Methods: In greenhouse experiments we tested the oviposition deterrency of eight aromatic plants intercropped with potato plants and the trap capacity of eight potato varieties as oviposition stimulants for *T. solanivora* adults. In a 2 x 2 factorial designed field experiment we tested the effectiveness of the combined use of attractive (trap plant) and repellent stimuli (garlic-pepper extract) on the insect community, herbivory, and tuber production of potato plants.

Results: *T. solanivora* had a higher oviposition rate on one of the potato varieties (Roja Nariño) variety, while none of the aromatic plants tested affected the ovipostion rate on neighboring potato plants. In the field experiment, potato plants growing in plots where we combined the application of attractive and repellent stimuli had less damaged tubers and a higher productivity than any other treatment, including the conventional application of insecticides.

Conclusions: Results suggest that the simultaneous use of garlic-pepper extracts and the intercropping with the Roja Nariño potato variety could be used as an effective and ecologically sound push-pull strategy for the management of *T. solanivora* in the Colombian Andes.

POSTER PRESENTATION

Landscape scale diversification of Andean crop systems: enhancing biological control of potato pests

Katja Poveda[2], Eliana Martinez[1], M.A. Bonilla[1], Teja Tscharntke[2]

[1]Universidad Nacional de Colombia, Bogota, Colombia, [2]Georg-August University, Göttingen, Germany

Introduction: Current agricultural practices have caused serious ecological problems that affect agricultural sustainability by reducing ecological functions and biodiversity. There is evidence that the density of natural enemies of crop pests is related to high biodiversity. Although in temperate zones landscape-scale management practices (augmenting landscape complexity) have been studied, results are very controversial, and their applicability to tropical systems is still unknown. In order to contribute to the development of sustainable and ecologically sound management methods for potato cultivation in the Colombian Andes we evaluated landscape complexity on the insect community associated with potato plants and their effect on tuber production.

Methods: We choose potato fields along a gradient of landscape complexity; complex landscapes characterized by a higher percentage of native forest and shrubs while simpler landscapes are dominated by potato crops and pastures. For each of the 17 plots we determined insect composition, foliar and tuber herbivory, as well as final tuber production.

Results: Landscape complexity (less potato production) increased the abundance and family richness of natural enemies of potato pests. Simultaneously the amount of tubers damaged per plant increased with increasing potato abundance in the landscape.

Conclusions: Landscape complexity has a remarkable effect augmenting the natural enemies of potato pests in potato plantations in the Colombian Andes. Furthermore, the positive effect of complex landscape on tuber quality should be considered in landscape wide management practices of future potato cultivation schemes.

POSTER PRESENTATION

Vibratory signals and mating behavior of the predatory stink bug, *Eocanthecona furcellata* (Heteroptera: Pentatomidae)

Hsiao-Yung Ho, Yu-Ting Su, Ding-Hsuan Chang

Institute of Cellular and Organismic Biology, Taipei, Taiwan

Substrate-borne vibrational signals (songs) were recorded from both sexes of the predatory stink bug species, *Eocanthecona furcellata*. Males initiate substrate borne vibrational communication and produce four different songs. Females sing two different songs. A unique rubbing behavior in copulation of *E. furcellata* is reported and the possible function of the behavior is discussed.

POSTER PRESENTATION

Relationships between defoliating insects and predators in some Romanian oak forests

Constantin Ciornei[1], Catalin Rang[2], Constantin Netoiu[1], Roxana Voicu[2]

[1]Forest Research and Management Institute, Bucharest, Romania, [2]University of Bacau, Faculty of Biology, Bacau, Romania

Introduction: The paper deals with oak forests infested with defoliating insects from Southern and Eastern Romania. Defoliating insects and their main predators are assessed (invertebrates of epigean fauna and birds).

Methods: Classic methods of defoliating insect population density assessment were applied. The diversity of the epigean fauna assemblage was assessed using the captures from Barber traps. The bird communities were analyzed from quantitative and qualitative point of view, based on sound emissions and food diet (stomach content) of adults.

Results: During 2000 – 2007 period, the infestation level with defoliating species (*Lymantria dispar*, *Tortrix viridana*, Geometridae, Noctuidae, Tenthredinidae) in oak forests (*Quercus robur*, *Q. petraea, Q. cerris*, *Q. fraineto*, *Q. pedunculiflora*) fluctuated since very low to very high, in some stands treatments with biological products with *Bacillus thuringiensis* or metamorphosis inhibitors were adopted. In these forests, were detected predators from Carabidae (*Carabus coriaceus, Calosoma sp., Molops piceus, Pterostichus oblongopunctatus*), Staphilinidae, Formicidae families. Nesting birds are important in these forests as defoliating insects' predators, because the food of the brood, during the postembryonic development in the nest, consists in defoliating larvae. The most important bird species belong to Paridae, Sitidae, Fringilidae, Corvidae families. The food range depends on the abundance of defoliating insects.

Conclusions: Predator species in epigean fauna and nesting birds in oak forests may contribute to defoliating insect population decrease in forests with adequate structure.

POSTER PRESENTATION

Varietal susceptibility of potato to the black cutworm, *Agrotis ipsilon* (Hfn.)

Faiza E. Salah[1], Abdien M. Zein Elabdien[2], Salah El –Tom[2], A. Azrag[2]

[1]Dept. of Crop Protection, University of Gezira, Medani, Sudan. P.O. Box 20; [2]Dept. of Crop Protection, University of Khartoum, Sudan

The black cut worm (BCW) *Agrotis ipsilon* (HFN) (Lepidoptera: Noctuidae) is a highly polyphagous pest of several wintry crops and became a major potato pest in lighter soils of Khartoum state. BCW inflicted serious damage on the tubers, resulting in drastic yield losses annually. Despite its economic importance, little attention has been directed to this pest in the Sudan.

Field experiments were conducted for two seasons at Karari, Khartoum state, central Sudan, to evaluate 10 potato varieties (lines/accessions) for resistance to BCW damage. The percent damaged tubers numbers (%DTN) and weight (% DTW) as parameters were used for evaluation. Differences in both parameters were very highly significant, due to varieties and seasons ($P < 0.001$ for both parameters). The interaction between the varieties and seasons was also very highly significant ($P < 0.001$). Two parameters were found to correlate strongly and significantly ($r = 0.83$). The 10 potato varieties (lines/accessions) were also subjected to a series of no – choice test in the laboratory for two seasons. The tests included testing the larval and pupal developmental rates on fresh potato foliage, potato tubers and synthetic potato leaf diet. Significant differences were noted in larval weight gains (LWGs), due to differences in potato varieties across the various feeding tests. Alpha, Lesita, Bright varieties showed higher levels of resistance both in the field and in the laboratory, while Desiree and Spunta showed highest level of susceptibility. Factors governing the causes for resistance were discussed.

POSTER PRESENTATION

Transmission of fungal communities by *Tyrophagus putrescentiae*

Wojciech Wakulinski[1], Ewa Szlendak[2], Agata Domoslawska[1]

[1]Department of Plant Pathology, Warsaw University of Life Sciences SGGW, Warsaw, Poland, [2]Department of Applied Entomology, Warsaw University of Life Sciences SGGW, Warsaw, Poland

Introduction: Fungi are principal decomposers of organic matter but for some organisms, including mites, are also food sources**.** Mites ingest fungi sporadically; however, their migration to places previously colonized by fungi is strictly oriented as a result of specific micro conditions created by the fungi**.** By moving to new places, mites may serve as vectors and transmit fungal colonies. The aim of our study was quantitative and qualitative analyses of this process.

Methods: The ability of *Tyrophagus putrescentiae* to transmit fungi commonly occurring on stored grain (*Fusarium culmorum, F.avenaceum, Alternaria alternata, Penicillium verrucosum* and *P. chrysogenum*) was assayed. The test was performed on arenas containing seven small plugs of fungi, cut of from 10-day-old axenic cultures. Mites were left for 24 hours on these arenas, and the assortment and frequencies of fungal species found on their body surface and in whole-body homogenates were determined.

Results: Five fungal species were transmitted by *T.putrescentiae*: *F.culmorum, A.alternata, A. flavus, P.chrysogenum,* and *P.verrucosum*. The last species occurred most frequently and constituted 47% of the total number of fungal cultures derived from mites. It was isolated with higher frequency from the surface than from the inner parts of mite bodies.

Conclusions: Quantitative and qualitative spectra of fungal species isolated from *T. putrescentiae* indicated that their transmission by mites is not random. The dominance of particular fungal species may reflect trophic preferences of *T. putrescentiae* or the existence of specific mechanism(s) for transferring only particular species.

POSTER PRESENTATION

Honeybee (*Apis mellifera*) serotonin receptors – characterization of full length receptors and truncated splice variants

Markus Thamm, Wolfgang Blenau

University of Potsdam - Institute for Biochemistry and Biology, Potsdam, Germany

The honeybee, *Apis mellifera*, is a model organism for studying learning, memory and division of labor. The biogenic amine serotonin (5-hydroxytryptamine, 5-HT) has been implicated in the control and regulation of these phenomena. Pharmacological and functional studies have indicated, that serotonin can activate various receptor subtypes. These receptors belong primarily to the protein family of G protein-coupled receptors (GPCRs), which in turn are coupled to different intracellular second-messenger pathways.

By screening the honey bee genome, we found four candidate genes encoding for putative serotonin receptors. One of them, Am5-HT_7, was already characterized (Schlenstedt et al. 2007). The sequence information was used to generate a PCR-based strategy to isolate the cDNAs encoding for the three remaining receptors. The deduced amino acid sequence of one putative honeybee serotonin receptor shows the highest homology to the 5-HT_1 receptor of the spiny lobster, *Panulirus interruptus.* Two additional receptor sequences likely represent - 5-HT_2 receptor isoforms, whose closest relatives where found in *Drosophila melanogaster* and *Panulirus interruptus*, respectively. Therefore, we tentatively named them Am5-$HT_{2\alpha}$ and Am5-$HT_{2\beta}$.

The genomic structures of the two honeybee 5-HT_2 receptors show interesting details. Both genes have very large introns of several kB in length. Furthermore, we found alternative splice variants of both Am5-$HT_{2\alpha}$ and Am5-$HT_{2\beta}$. In case of Am5-$HT_{2\alpha}$, the truncated mRNA can potentially be translated into a protein, which is similar to the full-length variant but lacks two transmembrane domains. In contrast, the Am5-$HT_{2\beta}$ splice-variant possesses a frameshift that produces an early stop codon.

In order to clarify the functional properties of the cloned receptors and their splice variants, we are currently studying HEK 293 cell lines which heterologously express the receptor proteins. In addition, we are analyzing the tissue distribution of the native receptor proteins.

POSTER PRESENTATION

Food selection preferences of *Tyrophagus putrescentiae* acarid mites among wheat kernels infested by fungi

Ewa Szlendak[1], Wojciech Wakuliński[2]

[1]*Department of Applied Entomology, Warsaw University of Life Sciences, Warsaw, Poland,*
[2]*Department of Plant Pathology, Warsaw University of Life Sciences, Warsaw, Poland*

Introduction: The suitability of mycelium of a particular fungal species for mites grazing on stored products probably depends on its attractiveness or repellence to mites, on the specific mite species, and on the mites' feeding ability. The aim of our study was to determine whether the species of fungus inoculated on wheat kernels, and the duration of kernel pre-infestation by fungi, influence mite choice of these kernels as potential food.

Methods: Wheat kernels inoculated 1, 5 or 10 days previously with *Fusarium culmorum, F. avenaceum, Alternaria alternata, Penicillium cyclopium = verrucosum, P. notatum = chrysogenum, Aspergillus ochraceus, A. flavus* were distributed on Petri dishes, which served as test arenas, to determine the infested kernels' attractiveness to *Tyrophagus putrescentiae* mites. The number of mites attracted by each species of fungus growing on wheat kernels was recorded at 0.5, 1, 4 and 24 hours after their release into the test arenas.

Results: Similar percentages of mites preferentially selected usually more than one (from 1 to 4) types of inoculated wheat kernel. Kernels inoculated with *Fusarium avenaceum* produced volatiles that attracted numerous mites in almost all experimental combinations. Depending on the test combination, large numbers of mites were also attracted by kernels inoculated with *Alternaria alternata, F. culumorum, Penicillium cyclopium* and *P. notatum.*

Conclusions: Our data show that mites select food among wheat kernels inoculated by particular species of fungi, and that both the selection period and the degree of kernel predigestion by fungi have a strong influence on mite choice.

POSTER PRESENTATION

Determining dispersal patterns of *Planococcus ficus* (Hemiptera: Pseudococcidae) among South African vineyards using RAPD markers

Marna Ferreira[1], Gerhard Pietersen[1], Eugenia Barros[2], Kerstin Kruger[1]

[1]University of Pretoria, Pretoria, South Africa, [2]CSIR, Pretoria, South Africa

Introduction: The vine mealybug *Planococcus ficus* is regarded as a key agricultural pest of grapevine (*Vitis vinifera*). It causes damage to vines through direct feeding, honeydew excretion and transmission of plant viruses. Mealybugs can spread rapidly throughout wine growing areas, e.g. through human contact, farming equipment, nursery stock, insects or birds. By understanding how mealybugs disperse specific control strategies can be implemented. We tested randomly amplified polymorphic DNA (RAPD) markers to differentiate amongst individual mealybugs from different vineyards to deduce possible dispersal patterns in South Africa.

Methods: *Planococcus ficus* individuals were collected from six vineyards in the Western Cape. DNA yield and quality from three DNA extraction methods were compared. RAPD - PCR conditions were optimized by varying final concentrations of PCR components including five sources of *Taq* polymerase and comparing the generated fingerprinting profiles. Twenty-seven 10-mer primers from University of British Columbia (UBC) were tested for polymorphisms.

Results: The three extraction methods yielded DNA concentrations ranging from 35 ng/ul (Roche kit) and 425 ng/ul (STE buffer) to 1704 ng/ul (Nylon membrane). The Roche kit consistently yielded high molecular weight DNA and was used for DNA extractions. Different final concentrations of PCR components and different sources of *Taq* polymerase generated different fingerprinting profiles. BIOTAQ™ DNA polymerase was selected and an optimal set of PCR conditions was determined. Four polymorphic primers revealed genetic differences among vineyards in a preliminary RAPD study.

Conclusions: RAPD markers can be used successfully to determine genetic differences among *P. ficus* individuals from South African vineyards.

POSTER PRESENTATION

The first finding of *Wolbachia* in thelytokous seed chalcids (Hymenoptera : Torymidae, *Megastigmus* sp.)

Thomas Boivin[1], Jean-Noël Candau[1], Alain Roques[2], Marie-Anne Auger-Rozenberg[1]

[1]Institut National de la Recherche Agronomique, Avignon, France, [2]Institut National de la Recherche Agronomique, Orléans, France

Introduction: In haplodiploid insect species, thelytokous parthenogenesis may be associated with bacterial endosymbionts that manipulate their host reproduction. Such an association was tested in the highly invasive genus *Megastigmus*, within which thelytokous parthenogenesis is much less frequent than arrhenotoky, which is the classical way of reproduction in chalcid insects.

Methods: Specific primers were used for the screening of *Wolbachia*, *Cardinium*, *Rickettsia* and *Arsenophonus* endosymbionts in three arrhenotokous and seven thelytokous *Megastigmus* species. Both *Wolbachia* infection and progeny sex ratios were compared between non- and antibiotic-treated females of *M. pinsapinis*. The phylogenetic relationships of the different thelytokous *Megastigmus* species and their infecting *Wolbachia* were compared to assess the evolutionary trajectories of such an association.

Results: PCR amplification with *Wolbachia* primers (*wsp*) was successful in all of the seven thelytokous *Megastigmus* species while no reaction occurred using *Cardinium*, *Rickettsia* and *Arsenophonus* primers. None of the three tested arrhenotokous species allowed amplification whatever the primer. Antibiotic treatments of *M. pinsapinis* females resulted in a loss of their *Wolbachia* infection and in a return to an arrhenotokous mode of reproduction. Molecular phylogeny of *Wolbachia* variants paralleled the observed radiation of *Megastigmus* species with respect with host-plant families (Pinaceae, Rosaceae and Anacardiaceae), but no significant divergence in *Wolbachia* sequences was found within host-plant families.
Conclusions: Thelytokous parthenogenesis in *Megastigmus* species may be associated with *Wolbachia* infection. Phylogenetic constructions suggest that horizontal transfers of *Wolbachia* occurred between insect species exploiting closely related host-plants. This may raise critical questions within the context of biological invasions in this insect genus, which frequently generate novel cases of sympatry.

POSTER PRESENTATION

Preliminary identification of P450 genes of the *CYP4*, *CYP6, CYP9* and *CYP12* Families in *Aspidiotus nerii* Bouché (Hemiptera: Diaspididae)

Jin Wu, Benjamin Normark

University of Massachusetts, Amherst, MA, United States

Aspidiotus nerii Bouché (Hemiptera: Coccoidea) is an extraordinarily polyphagous insect species, attacking plants from 110 families. *A. nerii* is an economically important pest and includes both sexual lineages and *Cardinium*-bacteria-infected parthenogenetic lineages. Given that plant allelochemicals are diverse among these hosts, genes involved in allelochemical metabolism in *A. nerii* are expected to play a critical role in adaptation to such a wide host range. Cytochrome P450 monooxygenase (P450) families *CYP4*, *CYP6, CYP9* and *CYP12* are the most studied metabolic enzymes that have been shown to be involved in detoxification of plant xenobiotics in polyphages. To isolate related cytochrome P450s in *A. nerii*, conserved regions in the alignment of insect *CYP4*, *CYP6, CYP9* and *CYP12* proteins served as a guide for the design of degenerate oligonucleotide primers for reverse transcription–polymerase chain reaction (RT-PCR) amplification of mRNA from adult female *A. nerii*. The RT-PCR products were cloned, sequenced, and then used as probes to screen a cDNA library. Full-length cDNA of selected clones from the cDNA library screening were sequenced, aligned and classified according to the nucleotide and amino acid identity with the other insect cytochrome P450s. To further identify and characterize those genes, phylogenetic analysis was conducted including all Cytochrome P450s from Hemiptera and Lepidoptera.

POSTER PRESENTATION

Phylogenetic relationships of Ciidae (Coleoptera: Cucujiformia)

Christin Grossmann, Gerda Buder, Anna Hundsdoerfer, Klaus-Dieter Klass

Museum of Zoology Dresden, Dresden, Saxony, Germany

Introduction: Cucujiformia is the largest coleopteran subgroup (207.000 species), classified into Lymexyloidea, Cleroidea, Cucujoidea, Tenebrionoidea, Chrysomeloidea, and Curculionoidea. Ciidae (Tenebrionoidea) comprise ca. 600 species in 40 genera, have a cylindrical body 0.5–7 mm long, and live in tree-fungus basidiocarps.

Methods: To study relationships in Ciidae, test its monophyly, and resolve its position within Cucujiformia, we sampled 20 species from 11 genera of Ciidae, 27 species from 20 other families of Cucujoidea and Tenebrionoidea, 2 species from the cleroid family Trogossitidae (all Cucujiformia), and *Bostrichus* (Bostrichiformia: Bostrichidae). We analysed 18S, COI, and – for Ciidae – COII sequences according to maximum parsimony (fixed alignment and partial direct optimization), maximum likelihood, and Bayesian methods, applying these to three subsets of the taxon sample.

Results: Ciidae appear as monophyletic. We find non-monophyly for the huge genus *Cis*, *Sulcacis*, and the tribe Orophiini. Different analyses suggest either *Rhopalodontus*, or *Sulcacis fronticornis* + *Xylographus* + *Octotemnus*, or *Sulcacis fronticornis* + *Xylographus* alone as sister group of the remaining Ciidae. Apart from a clade *Sulcacis fronticornis* + *Xylographus* the results for inter-generic relationships in Ciidae vary strongly with analyses and sampling. Different analyses place Ciidae sister to Nitidulidae or far basally and isolated in the cucujoid-tenebrionoid assemblage. Resolution of the phylogeny of the cucujoid-tenebrionoid assemblage is poor and conflicting. Monophyly is supported for Sphindidae, Cryptophagidae, Tenebrionidae, Coccinellidae + Endomychidae, and Tetratomidae + Anthicidae + Monotomidae. Altogether, families from Cucujoidea and Tenebrionoidea are fairly mixed up in our trees, and the cleroid Trogossitidae falls within the cucujoid-tenebrionoid assemblage.

POSTER PRESENTATION

The tentorium and anterior head sulci in Dictyoptera and Mantophasmatodea (Insecta)

Klaus-Dieter Klass, Ute Eulitz

Museum of Zoology Dresden, Dresden, Saxony, Germany

Introduction: The head capsule in insects has a complicated pattern of internal ridges (sulci), which serve for mechanical strengthening. Inside the head there is a cuticular tentorium, which is composed of 2 pairs of tubular invaginations fused in the center of the head. These structures were studied in Mantophasmatodea and various Dictyoptera and explored regarding their phylogenetic information content.

Methods: The tentorium, the anterior head sulci (epistomal, subgenal, subantennal, circumantennal, and circumocular sulci), and the extension of the anterior tentorial pit were studied in 26 species of Blattaria (representing most principal lineages), 4 species of Mantodea (including the basal *Mantoida schraderi*), and 1 species each of Isoptera (the basal *Mastotermes darwiniensis*) and Mantophasmatodea (*Austrophasma caledonense*). The morphology of these head structures was compared with literature data on other insect orders, mainly Phasmatodea, Orthoptera, Dermaptera, Embioptera, and Plecoptera, and partly Odonata and Zygentoma. Characters were defined, presented in a matrix, and evaluated with regard to phylogenetic implications and homoplastic evolution.

Results: The structural relationships of the subantennal sulcus to the subgenal, circumocular, and circumantennal sulci were found highly variable; the patterns are strongly homoplastic and depend much on the size of the compound eyes. Several types of subantennal sulci are defined. The presence of an anterior transverse bridge in the tentorium ("perforated tentorium") of all Dictyoptera here studied confirms the monophyly of this group. Mantophasmatodea lack this element. Various details of the sulci and tentorium confirm the monophyly of Mantodea.

POSTER PRESENTATION

Effects of desiccation and immersion on the third instar larvae of oriental fruit fly

Xinfeng He, Qi Xie

Institute of Entomology, Zhongshan University, Guangzhou, Guangdong Province, China

Introduction: Many studies have focused on the effects of different temperatures on the development, survival, and fertility of oriental fruit fly. Less attention is paid to the effects of humidity on the pupae of this fly. Humidity is expected to be a major limiting factor on the pupation of the mature larvae.

Methods: Prior to experimentation, soils were sifted through a 1-mm-mesh metal sieve and dried at 100℃ for 48h in an oven. Eight durations (2, 4, 6, 8, 10, 12, 14, and 16 h) were set in the desiccation experiment, each with 40 larvae for testing. Forty larvae were weighed on an electronic balance and placed in desiccation conditions as described above. Following a defined desiccation time (2, 4, 6, 8, 10, 12, 14, and 16 h), the larvae were screened from the soils and reweighed rapidly. Healthy and active mature larvae were immersed simultaneously in still water at 25 ± 1℃. Forty larvae were removed randomly from the water and transferred to moist sand after immersion of 0.5, 1.0, 1.5, 2.0, 2.5, 3.0, 3.5, and 4.0 d, respectively. All samples were held at 25 ± 1℃ and 75% RH under a 12:12 (L:D) h photoperiod for emergence. The number of newly emerged adults was recorded and removed daily.

Results: Third instar larvae desiccated in dry soils did not survive beyond 12 h, nor submerged under water beyond 3.5 d. The time to 50%, 90%, and 99% mortality (LT_{50}, LT_{90}, and LT_{99}) were 5.67, 8.60, and 10.99 h respectively in desiccation condition, and 1.81, 2.49, and 3.06 d in immersion test. The average eclosion time of survived flies was not significantly affected by the desiccation time, while that increased linearly with increasing immersion time. Cumulative weight loss of larvae increased curvilinearly with desiccation time, and the rate of weight loss was greatest during the first 2 hours. It was estimated that when the percentage of cumulative weight loss was 29.1%, 36.7%, and 43.0% respectively, the mortality rates was 50%, 90%, and 99% correspondingly.

Conclusions: Flooding would be an effective control method in pupa stage of oriental fruit fly.

POSTER PRESENTATION

Arthropod fauna associated with Southern African sugarcane in relation to sugarcane thrips, *Fulmekiola serrata* control

Mike Way

SASRI, Mt Edgecombe, South Africa

Monitoring techniques provided information on faunal complexes within sugarcane leaf spindles in South Africa that might include natural enemies of the serious pest thrips, *Fulmekiola serrata* (Kobus) (Thysanoptera: Thripidae).

During the 2005/06 seasons extensive surveys were carried out. Twenty-eight thysanopteran taxa from 3 families were identified, namely Thripidae, Phlaeothripidae, Aeolothripidae were distinguished. *F. serrata* was clearly predominant. Genera recovered were: *Fulmekiola, Allelothrips, Anaphothrips, Arhipidothrips, Arorathrips, Chirothrips, Elaphrothrips, Exothrips, Frankliniella, Haplothrips, Megalurothrips, Phibalothrips, Podothrips, Stenchaetothrips and Thrips*. Many taxa were scarce.

The following associated arthropod taxa were recovered: Anthocoridae: possibly *Orius* sp.; Staphylinidae: Oxytelinae; Chrysomelidae: Alticinae: *Chaetocnema* sp.; Curculionidae: Scolytinae; Coccinellidae: Scymninae: *Nephus* cf. *voeltzkowi* Weise and *Scymnus* sp.; Corylophidae, Formicidae: *Anoplolepis* sp.; indeterminate Lepidoptera; Cicadellidae: *Cicadulina niger* Ghauri; Laelapidae: Mesostigmata: *Ololaelaps* sp. (soil predatory mite); Araneae: Clubionidae: *Clubiona* sp.; Thomisidae: *Firmicus* sp.

The South African Sugarcane Research Institute (SASRI) is researching an Integrated Pest Management (IPM) strategy against this pest. Cognisance of this faunal complex is paramount to the long-term success of any recommendation.

POSTER PRESENTATION

Acoustic detection of freshwater insects and other invertebrates

Jaroslava Frouzova[1], Jan Kubecka[1], Josef Matena[1], Jan Frouz[2]

[1]Instutute Hydrobiology, Ceske Budejovice, Czech Republic, [2]Institute of Soil Biology, Ceske Budejovice, Czech Republic

Introduction: Observation activity of aquatic insect in open water of large water bodies is difficult task. Hydroacustic may be new valuable tool to solve this problem.

Methods: This contribution reviews the hydroacustic records of freshwater invertebrates from 14 studies using frequencies between 100 and 500 kHz.

Results: The highest target strength (TS) >-52 dB of common freshwater pelagic invertebrates was recorded for water bugs (Hemiptera, Insecta). In the TS interval of –58 to –75 dB, well defined targets of dipteran insects. Larger crustacean like Amphipoda and Mysidiacea fall into the TS range of –74 to –85 dB. Freshwater jellyfish, Craspedacusta sowerbii was found to be acoustically unidentifiable in most situations; despite quite large size 1-2 cm its TS was under of threshold –95 dB.

Conclusion: Invertebrates with gas filled organs in the body are likely to give strong echoes. Also other invertebrate organisms with exoskeleton give relatively stronger echo than completely soft body organisms.

This review show that water insects and other invertebrates as small as 2-3 mm can be successfully detected by hydroacustic techniques which can be powerful approach for study of many aspects of their biology in water column.

POSTER PRESENTATION

Non-intentional inoculation of earthworms during forest reclamation of post mining sites change soil development and arthropod diversity

Jan Frouz

Institute of Soil Biology, Ceske Budejovice, Czech Republic

Introduction: Soil restoration in post mining sites is an important part of ecosystem reconstruction. Here we studied effect of earthworm on development of soil biota in chornosequences of post mining sites.

Method: Two chronosequences of sites, covered by alder plantations and the second unreclaimed, both covering age from 1-41 years were studied.

Results: Macrofauna namely earthworms were abundant in reclaimed sites due to better litter condition and unintentional colonisation by earthworm during tree planting. In non-reclaimed sites macrofauna abundances were lower and appear in higher densities in 25-30 years old sites. In the contrary Meso and macrofauna density and diversity were higher in unreclaimed sites namely Testacea amoebae and oribatid mites, densities were high, similar as in natural forest. Mesofauna and microfauna densities decreased after 30 year of succession when unreclaimed sites were colonised by earthworms, which resulted in more intensive soil mixing, rapid formation of humus layer and fast removal of litter and fermentation layer from soil surface.

Conclusion: Soil macrofauna alter composition of soil meso and microfauna due to modification in topsoil physical structure.

POSTER PRESENTATION

What is the source of CO_2 production in wood ant nests ant or microbial respiration

Jan Frouz

Institute of Soil biology, Ceske Budejovice, Czech Republic

Introduction: Wood ant nests are hotspot of CO_2 production. Here we partionate ant and microbial respiration of the nest.

Methods: In two dry nest, moisture less that 15% and two wet nest with moisture more than 25% were embedded two plastic cylinders one with holes the second closed with net on the top. Both were filled by nest material in closed cylinder the ants were hand sorted out in cylinder with holes ants remain. CO_2 production both cylinders, and surrounding soil was measured by SR1000. In one dry and one wet nest CO_2 production was also measured on longitudinal transect across the nest.

Results: Respiration in wet nets was higher than in dry one. In dry nests higher CO_2 production (7-15µL/m2 min) was found in center of the nest. In wet nest the highest values was also found in the nest center (50 µL/m2 min) but increase from nest periphery was more gradual. In dry nest the respiration values in ant free cylinder was near control soil value. In wet nest ant free cylinder still keep about half of respiration of ant accessible cylinder. Ant based respiration was higher in wet than dry nest due to higher ant density.

Conclusion: both ant and microbial respiration take part on CO_2 production from wood ant nest, its proportion depends on nest moisture.

POSTER PRESENTATION

Metabolic rate of brown locust eggs

Innocent Kambule, Shirley Hanrahan, Frances Duncan

University of the Witwatersrand, Johannesburg, South Africa

The brown locust, *Locustana pardalina* (Walker) (Orthoptera: Acrididae), is found in the semi-arid regions of the central Karoo, South Africa. Diapause contributes to brown locust survival under arid conditions preventing immediate hatching and allowing build-up of eggs in the soil which contributes to swarming. We measured the metabolic rate of diapause and non-diapause eggs and directly linked these to embryonic development. There are two major stages in egg development, namely anatrepsis and catatrepsis. Anatrepsis is the development prior to rotation of the embryo. Diapause eggs remain in anatrepsis between 9 and 40 days. Catatrepsis begins when the embryo turns and the development process is usually completed irrespective of environmental conditions. Eggs were obtained from adult locusts collected in the Karoo and bred in the laboratory. Metabolic rate was determined measuring CO_2 output of eggs in various stages of development using Licor - 6262 analyzer. Embryonic development was examined using light microscopy. The metabolic rate of non-diapause eggs increased steadily from day 0 until hatching at day 10. Diapause eggs maintained a low constant metabolic rate 4½ times lower than that of non-diapause eggs.

POSTER PRESENTATION

Alien versus predator (and other natural enemies): can *Harmonia axyridis* be controlled?

Helen Roy[1], Marc Kenis[2], Renate Zindel[3], Michael Majerus[4]

[1]NERC Centre for Ecology and Hydrology, Cambridgeshire, United Kingdom, [2]CABI Europe-Switzerland, Delémont, Switzerland, [3]University of Fribourg, Fribourg, Switzerland, [4]University of Cambridge, Cambridge, United Kingdom

The harlequin ladybird, *Harmonia axyridis* (Pallas) (Coleoptera: Coccinellidae), is a predatory beetle native to Asia but an invasive alien species in many countries worldwide. It is considered invasive because it is a human nuisance, a grape and wine pest and a threat to native biodiversity. Many methods have been employed to control this beetle with varying degrees of success. These include: mechanically preventing adult beetles from entering buildings in autumn or removal of beetle aggregations inside buildings; the use of insecticides on buildings or in vineyards to prevent aggregation in houses or on grapes; cultivation practices in vineyards to lower the impact of the ladybird on grape production and wine quality and remedial treatments for wine tainted by the ladybird. However, other methods are under development and these include: the use of deterrent or attractant semiochemicals and the manipulation of natural enemies. Candidate natural enemies include: an insect pathogenic fungus, (*Beauveria bassiana*), a predator (the predatory bug *Deraeocoris ruber*), a hymenopteran parasitoid (*Dinocampus coccinellae*), a dipteran parasite (*Phalacrotophora fasciata*), two sexually transmitted ectoparasites (a mite, *Coccipolipus hippodamiae*, and a laboulbenialean fungus, *Hesperomyces virescens*), and a variety of male-killing bacteria (*Wolbachia*, *Spiroplasma*, *Rickettsia*). We consider the potential of these natural enemies as biological control agents of *Harmonia axyridis* and conclude that only the sudden adaptation of a native natural enemy or the, potentially risky, importation of an Asian natural enemy may ultimately lower population densities.

POSTER PRESENTATION

Molecular studies on *Baetis harrisoni* (Ephemeroptera, Baetidae), using two mitochondrial genes, CO1 and 16S, to distinguish species level differences between populations

Lyndall Pereira da Conceicoa[1], Helen James[2], Benjamin Price[1], Nigel Barker[1], Martin Villet[1]

[1]Rhodes University, Grahamstown, South Africa, [2]Albany Museum, Grahamstown, South Africa

Introduction: *Baetis harrisoni* Barnard (1932) is found in fast flowing streams and rivers throughout Africa south of the Sahara. To date, identifications of *B. harrisoni* have relied on external morphological features. These vary subtly with regards to the gill size, abdominal patterns and length of caudal filaments; which has raised the question of whether *B. harrisoni* in South Africa is a single species or a species complex.

Methods: Genetic variation between nymphs from populations from 11 rivers in different areas of South Africa was quantified using statistical molecular analyses of the CO1 and ribosomal 16S rRNA mitochondrial genes.

Results: The preliminary phylogenetic results for *B. harrisoni* strongly indicate the presence of two clades: a south western (winter rainfall) clade and a north eastern (summer rainfall) clade. A brief morphological examination of the two main clades further supports the phylogeny.

Conclusions: This report has highlighted distinct genetic differences that suggest that this African baetid may be comprised of more than one species. This study has set the foundations for a larger, more in-depth project that will finally resolve the true taxonomy of the *Baetis harrisoni* species complex.

POSTER PRESENTATION

Trait-mediated effects of predatory mites on thrips and its host plant

Andreas Walzer, Peter Schausberger

University of Natural Resources and Applied Life Sciences, Institute of Plant Protection, Vienna, Austria

Introduction: The concept of top-down trophic cascades is the fundament of biological control theory. Despite the increasing knowledge that trait-mediated effects are as important in triggering top-down trophic cascades as density-mediated effects, the occurrence of trait-mediated interactions between predators, prey and plant has been largely ignored in biological control. Here we show that trait-mediated interactions in an agro-ecological food chain can generate top-down trophic cascades.

Methods: The study system consisted of the predatory mites *P. persimilis* and *N. californicus*, the herbivorous non-target prey western flower thrips *F. occidentalis* and the host plant bean. Three experiments were conducted on (1) foraging behaviour of larval prey, (2) survival and development of prey larvae and (3) foraging and oviposition behaviour of female prey in the presence and absence of predator cues.

Results: Irrespective of predator species and risk posed to prey, the presence of predator eggs led to increased ambulation, increased mortality and decreased oviposition of thrips. The presence of predator eggs reduced leaf damage caused by thrips. To our knowledge this is the first experimental evidence for a positive trophic cascade triggered by trait-mediated interactions between predators and non-target prey in an augmentative biological control system.

Conclusions: Our study indicates the potential importance and strength of trait-mediated effects of predators on a non-target herbivorous pest and its host plant. It hopefully stimulates further research on this topic to find out how widespread trait-mediated predator effects are in biological or natural control of arthropod pests and how important they are relative to density-mediated predator effects.

POSTER PRESENTATION

Monitoring of anatomical changes within the bird cherry shoots evoked by *Rhopalosiphum padi* L. (Hemiptera: Aphididae)

Hubert Sytykiewicz, Bogumil Leszczynski

University of Podlasie, Siedlce, Poland

Introduction: The bird cherry-oat aphid, *Rhopalosiphum padi* L. (Hemiptera, Aphididae) is a heteroecious species that life-cycle is characterized with occurrence of holocyclic development. Its primary host is a tree or shrub of the bird cherry (*Prunus padus* L.), whereas a wide spectrum of secondary hosts embraces plants belonging to *Cyperaceae*, *Juncaceae, Poaceae* and *Typhaceae*. The purpose of the study was to define the anatomical damages within primary host tissues caused by *R. padi* feeding.

Methods: Plant material was collected during the peak density of *R. padi* occured on bird cherry shrubs in central-eastern Poland. Infested shoots were incubated in FAA solution - 50% ethanol, acetic acid, 40% formaldehyde /18:1:1, *v:v:v*/. Subsequently, series of transverse sections through stems, petioles and midveins of leaf blades were taken and examined under light microscopy.

Results: Salivary exudates of the bird cherry-oat aphid contained enzymes which depolimerised ultrastructural compounds of middle lamella and cellular wall of the primary host tissues. The bird cherry-oat aphid damaged and hydrolysed large areas within mesophyll tissue of stems and leaf stalks. It was also shown that when bird cherry-oat aphid inserted its stylets directly into phloem bundle, disruption of peripheral tissues was more restricted.

Conclusions: The bird cherry-oat aphid penetrated tissues of its primary host mostly intracellularly and the aphid stylets piercing the bird cherry shoots were generally located within phloem bundle and/or parenchyma cells.

POSTER PRESENTATION

Toxic effects of phytohemagglutinin (PHA) on development and fecundity of rose grain aphid, *Metopolophium dirhodum* Walker

Iwona Sprawka, Bogumil Leszczynski

University of Podlasie, Siedlce, Poland

Introduction: Recent progress in plant breeding for insect resistance has increased interest in potential toxicity of plant proteins towards herbivorous insects. Lectins are class of the entomotoxins considered as potential biopesticides that might be used against polyphagous aphids. Hemagglutinin (PHA) the lectin from *Phaseolus vulgaris* is tetrameric protein with a molecular weight of 120 kDa and sugar specificity for D-galactose/ N-acetyl-D-galactosamine residue. The toxic effects of PHA on Lepidoptera is well documented but little is known on its toxicity to aphids.

Methods: Effect of the PHA on survival, development and fecundity of *M. dirhodum*, was studied in laboratory conditions. Several concentrations (10-1500 μg per ml) of the lectin were incorporated into artificial liquid diets. Fifty adult aphids were used for each treatment and control (without PHA).

Results: The obtained results showed that presence of the PHA in the diet decreased fecundity of the adult *apterae* up to 50% compared to aphids fed on the control diet. Aphids exposed to PHA also showed reduction of weight by about 25% and total mortality at concentration 1000 μg per ml incorporated into the sucrose diet.

Conclusions: The data presented here, sugest that PHA showed a high insecticidal activity towards the rose-grain aphid and might be considered as protein biopesticide towards the insect pest.

.

POSTER PRESENTATION

Influence of grain aphid (*Sitobion avenae* F.) feeding on arginase activity within winter triticale seedlings

Cezary Sempruch, Bogumil Leszczynski, Izabela Wojtas

University of Podlasie, Siedlce, Poland

Introduction: Arginase (EC 3.5.3.1) is an enzyme that catalyses biodegradation of L-arginine to L-ornithine and urea. This enzyme is quite important in plant-insect chemical interactions since it reduces nutritive value of plant tissues for herbivorous pests. The aim of the study was to determine changes in arginase activity within seedlings of winter triticale caused by *S. avenae* feeding.

Methods: Seven days old seedlings of winter triticale cultivars: Tornado (susceptible) and Witon (less susceptible) were artificially infested in climatic chamber with five wingless females per seedling. Infested and control (without aphids) seedlings were collected for analysis after 24 h, 48 h, 1 week and 2 weeks. Number of individuals on the studied plants was determined, and all the aphids were discarded from plants. Enzyme activity was measured with use of spectrophotometric method.

Results: The grain aphid feeding during the first 24 h caused an increase in the arginase activity within susceptible Tornado cv. and decrease in less susceptible Witon cv. After 48 h and 1 week of the aphid feeding activity of the enzyme decreased within tissue of the both studied cultivars and was again induced during the second week. Importance of the arginase in the chemical interactions between winter triticale and *S. avenae* is discussed.

Conclusions: Arginase activity was altered under the grain aphid feeding, and the observed variations in its activity was dependent on plant genotype, aphid number and feeding duration.

POSTER PRESENTATION

Formulations of the entomopathogenic fungi *Beauveria bassiana*, an agricultural pest control organism

Irina Urtubia, Andrés France

INIA Quilamapu, Chillán, Chile

The use of entomopathogenic fungi (EPF) is an effective alternative for agriculture pest control and development of sustainable agriculture, preserving natural resources and environment. However it is necessary to count on formulations allowing decrease viability loss and increase permanence on soil.

In this study, granule formulations were elaborated as pellets based on sodium alginate of conidia of EPF *Beauveria bassiana* strain B-323 belonging to the collection of Technological Center of Biological Control, which controlling Fuller's rose weevil (*Asynonychus cervinus*) y South American fruit tree weevil (*Naupactus xanthographus*), using two substrates: Kaolin (aluminum silicate) and plant residues (fiber and nutrients), plus an specific additive. Formulations were evaluated according to viability (expressed as germination index, GI) and incubation time at different temperatures (15, 20, 25, 30 and 35 ºC).

Formulations elaborated with plant residues showed the highest GI, 62.1 vs. 9.17 for kaolin. This value increase to 696 with additive. With respect to stability on time and GI, the best temperatures were 25, 20 and 15 ºC.

Formulates containing fiber and nutrients increase EPF survival and allow its development at different temperatures, allowing a higher success of soil applications and therefore a higher pest control level.

POSTER PRESENTATION

Mating success and mate choice in relation to sex ratio and mating experience in *Nysius huttoni* White (Heteroptera: Lygaeidae)

Qiao Wang, Linghuan Yang

Massey University, Palmerston North, New Zealand

Introduction: In polygamous mating systems males tend to minimize the probability of sperm competition while females encourage it. Theoretically, in the male-biased sex ratio male-male competition is expected to increase resulting in lower mating success while in the female-biased one male mating success should be higher. Here we investigated mating success and mate choice in relation to sex ratio and mating experience in a polygamous seed bug, *Nysius huttoni* White.

Methods: Petri dishes were used experimental arenas. Mating success and mate choice were recorded. Each Patri dish was considered a replicate.

Results: Mean mating success under even sex ratio was significantly lower than under the biased sex ratios. If a mated male had a chance to choose between a female that had mated with him 24 h ago and a female that had mated with another male 24 h ago, the male significantly preferred the female he had mated before to the female that had mated with another male. However, there was no clear preference by the mated female for mating between the male with which she had mated before and the male which had mated with another partner.

Conclusions: Biased sex ratios increase mating success rate in this species. Males can remember their partners for at least 24 h, and to minimize sperm competition they prefer their previous partners to other mated females. For females genetic diversity and fitness appear to be more important and thus do not have preference between their previous partners and other mated males.

POSTER PRESENTATION

Molecular, biochemical and histochemical characterization of two acetylcholinesterases from the German cockroach *Blattella germanica*

Min Kwon, Chan Sik Jung, Young Ho Koh, Si Hyeock Lee

[1]National Institute of Highland Agriculture, RDA, Pyeongchang, Korea, Republic of, [2]Korea Forest Research Institute, Seoul; [3]Ilsong Institute of Life Science, Hallym University, Anyang; [4]Seoul National University, Seoul, Republic of Korea

Introduction: *Blattella germanica*, is one of the major medically important species in most parts of the world and known to have well-characterized nervous system. Therefore, *B. germanica* is a good model insect to study the putative roles of two insect AChEs from evolutionary points of view and to predict fundamental functions of extra or surplus AChE.

Methods: Various methods such as cloning, real-time PCR, native PAGE, fluorescence *in situ* hybridization etc.

Results: Full length cDNAs encoding two AChEs; *Bgace1* and *Bgace2* were cloned and characterized. Ganglia produced distinct two major and two minor AChE bands in native PAGE, indicative of the presence of at least two active AChEs. *B. germanica* AChEs appeared to be mainly localized in the central nervous system as demonstrated by histochemical activity staining along with quantitative analysis of *Bgace* transcripts. Fluorescence *in situ* hybridization of the 1st thoracic ganglion confirmed that *Bgace1* is predominantly transcribed, and further showed that its transcript is found in almost entire region of inter- or motor neurons including the cell bodies and axonal/dendritic branches but *Bgace2* transcript is found only in the subset of neurons, particularly in cell body. In addition, certain neurons were observed to express *Bgace1* alone.

Conclusions: Two *ace* genes were identified from *B. germanica*,

POSTER PRESENTATION

Targeted cue-lure trapping, bait-spray, sanitation, sterile-male and parasitoid releases in an area wide integrated melon fly (Diptera: Tephritidae) control program in Hawaii

Eric B. Jang[1], Grant T. McQuate[1], Donald O. McInnis[1], Renato Bautista[1], Roger I. Vargas[1], Ronald F. L. Mau[2], Lyle Wong[3]

[1]USDA Agric. Research Service, Hilo, HI, United States, [2]Univ. of Hawaii, Honolulu, HI, United States, [3]Hawaii Dept. of Agric., Honolulu, HI, United States

Introduction: An area wide IPM approach to melon fly *Bactrocera cucurbitae* (Diptera:Tephritidae) suppression was undertaken as part of a Hawaii state-wide program funded by USDA-ARS Area Wide Initiative.

Methods: A grid of 1 cuelure trap/ km^2 over 40 km^2 was established in Kamuela, HI to pinpoint areas of infestation. A targeted male trapping array was applied based on the distribution of host plants (mapped using GIS). Monitoring existing traps led to increasing trap density where catch was highest to achieve male annihilation. Sanitation, bait spray, Sterile Insect Technique (SIT), and augmentation of *Psyttalia fletcheri* parasitoids were also applied.

Results: Pre-treatment trapping in the farming area indicated a melon fly population peak of 11.94±9.90 flies/trap/day (f/t/d) in October 2000. By 2003, mean grid trap catch over 16 weeks was 0.016±0.005 f/t/d /km^2, i.e. a 99.87% reduction. During 2000-2001 mean infestation was 50.6± 4.9% in sampled fruit. In 2002, with all suppression activities fully implemented, the infestation rate averaged 8.5±4.8% that is an 83.2% reduction. Between Aug. 2002 and Aug. 2003, infestation in all observed fruits over 40 km^2 averaged 14.3±2.9% after some suppression activities had been suspended. Uncultivated, wild hosts showed 87.5% mean decline in flies per gram of fruit.

Conclusions: A 3-component suppression strategy of sanitation, male annihilation and bait spray effectively suppresses melon fly.

POSTER PRESENTATION

Extension of the use of augmentoria for sanitation in a cropping system susceptible to the alien tephritid fruit flies (Diptera: Tephritidae) in Hawaii

Eric B. Jang, Lester M. Klungness, Grant T. McQuate

USDA-ARS, Hilo HI, United States

Introduction: This study reports efforts to demonstrate to growers of fruiting crops a technique to sequester emerging adult flies while conserving their parasitoid natural enemies. Sequestering infested fruit to prevent progeny survival is often overlooked.

Methods: Demonstration trials were conducted in 4 phases to determine whether growers on the Island of Hawaii would use a tent-like structure (augmentorium) to sequester fruit-fly infested, culled fruit.

Results: In phase one it was shown that 1127 *Bactrocera cucurbitae* (Coquillett) were recovered from cull fruit removed from the augmentorium, and that sanitation in combination with bait spray, and male lure trapping could reduce the level of infestation. Subsequently, phase two confirmed that the three techniques disrupted the breeding cycle and 2 farmers were convinced to use these techniques. In phase three, further expansion to 12 farms, whose 15 augmentoria were monitored, indicated that over 80% of the growers used the tents (22,217 adult flies recovered from the tents over 1260 days). In phase four, success of phases 1 to 3 convinced 30 farms to request 40 augmentoria and an opinion survey of those growers is reported.

Conclusions: The successful introduction of the augmentorium has implications for use of augmentoria to sequester the progeny of other insect pests and release their natural enemies.

POSTER PRESENTATION

Isolation and characterization of the novel antibacterial peptide Coprisin from a dung beetle, *Copris tripartitus*

Jae-Sam Hwang, Yeon-Ju Kim, Hea-Son Bang, Eun-Youn Yun, Seong-Ryul Kim, Kwan-Ho Park

NIAST, Suwon, Republic of Korea

Introduction: *Copris tripartitus* spends a lot of time in dung, which contains an abundance of pathogens. The larvae feed on dispose of fungi, decaying organic matter, dung and other organic materials in dung ball. It can be supposed that *C. tripartitus* must have antimicrobial activity against invading pathogen. Therefore, our purpose of the present study was to isolate and identify immune related genes in dung beetle, *C. tripartitus.*

Methods: Larvae were kept for 24h. cDNA Library from larvae of *C. tripartitus* immunized with *E. coli* was constructed by using a modification of Maruyama and Sugano's method (Maruyama and Sugano, 1994). Antibacterial activities of peptides were tested against *S. aureus,* MRSA, *E. faecalis, E. coli* ML-35*, P. aeruginosa,* MDRPA in a broth microdilution assay.

Results: Thirteen individual cDNA transcripts were expressed differentially in a total 1,862 random cDNA clones. One of up-regulated genes is a novel member of the insect defensin-like peptide(coprisin), a family of antibacterial peptide. Northern blot analysis showed that coprisin was up-regulated at 4hrs and reached the highest point level at 16h after injection of *E.coli*. The deduced amino acid sequence of coprisin was composed of 80 amino acids with predicted molecular weight of 8.6 kDa and PI of 8.72. Comparison of the deduced amino acid mature portion of coprisin with defensin-like peptide of other insect indicated that it has 79.1% and 67.4% identity with *Anomala cuprea* and *Allomyrina dichotoma*, respectively. In order to antibacterial peptides to the development of therapeutic agents, we looked for the active region of coprisin peptide and modified 9-mer peptide, LRCIALRKK-NH2, by changing amino acid sequences.

Conclusions: We isolated a new member of the insect defensin(coprisin) from the beetle, *Copris tripartitus.* Mature *C. tripartitus* defensin consisted of 43 amino acids and 6 cystein residues and showed 79.1% and 67.4% identity with *Anomala cuprea* defensin and *Allomyrina dichotoma* defensin, respectively. We modified oligopeptide and synthesized four 9-mer peptide. Modified 9-mer peptide, LLCIALRKK-NH2, is stronger antibacterial activity than LCAAHCLAIGRR-NH2 (*A.d.*-12De) and LHCIALRKK-NH2 (CopN5(22-30)) peptide against gram-negative and gram-positive bacteria. This peptide showed no haemolytic activity and quite stable at 100□ for several hours of incubation and in a wide pH range.

POSTER PRESENTATION

Identification of cry1-type genes and characterization of a novel cry1-type gene from *Bacillus thuringiensis* subsp. *alesti* strain LY-99

Xu Feng Qi, Ming Shun Li, Jae Young Choi, Ji Zhen Song, Yong Wang, Byung Rae Jin, Yeon Ho Je, Jian Hong Li

Huazhong Agricultural University, Wuhan, China

Bacillus thuringiensis strain LY-99 belonging to subsp. *alesti* (H3a3c), was isolated from Chinese tobacco warehouse and showed significantly high toxicity to *Plutella xylostella*. For the identification of the *cry1*-type genes from *B. thuringiensis* LY-99, an extended multiplex PCR-restriction fragment length polymorphism (PCR-RFLP) method was established by using two pairs of universal primers based on the conserved regions of the *cry1*-type genes to amplify around 2.4 kb *cry1*-type gene fragments. Then the DNA fragment was cloned into pGEM-T Easy vector and digested with *Eco*RI and *Eco*RV enzymes. Through this method, a known *cry1*-type gene was successfully identified from the reference strain, *B. thuringiensis* subsp. *alesti*. In addition, the RFLP patterns revealed that *B. thuringiensis* LY-99 included a novel *cry1A*-type gene in addition to *cry1Aa*, *cry1Ac*, *cry1Be* and *cry1Ea* genes. The novel *cry1A*-type gene was designated *cry1Ah2*(GenBank accession number: DQ269474). An inverse PCR method was used to amplify the flank regions of *cry1Ah2* gene. Finally, 3143 bp *Hin*dIII fragment from *B. thuringiensis* LY-99 plasmid DNA including 5' region and partial ORF was amplified, and sequence analysis revealed that *cry1Ah2* gene from LY-99 showed 89.31% of maximum sequence similarity with *cry1Ac1* crystal protein gene. In addition, the deduced amino acid sequence of Cry1Ah2 protein shared 87.80% of maximum identity with that of Cry1Ac2. This protein therefore belongs to a new class of *B. thuringiensis* crystal proteins.

POSTER PRESENTATION

Field efficacy of insecticides against jassid (*Amrasca biguttula biguttula* Ishida.) on *Abelmoschus esculentus* L. under sub-himalayan region of N-E India

Sunil Ghosh, Koushik Das

Uttar Banga Krishi Viswavidyalaya (University), Coochbehar, West Bengal/Northern, India

Introduction: Lady's finger (*Abelmoschus esculentus* L.) is an annual crop belongs to the family Malvaceae and one of the most important vegetable crops grown in tropical and sub-tropical areas. The crop is very much susceptible to various insect pests of which jassid (*Amrasca biguttula biguttula* Ishida.) is found to cause heavy damage. It is very difficult to control the pest as the fruits are plucked at frequent interval and consumed after little cooking and there is every possibility to retain toxic substances in the fruits which cause health hazards.

Methods: Studies were made to evaluate new insecticides against jassid of lady's finger under field conditions of sub-himalayan region of N-E India during post-kharif season. Nine insecticides including one phytopesticide neem oil(*Azadiracta indica*) were sprayed twice at 15 days interval. Total jassid population per 3 leaves were taken into account at 3,8and14 days after treatment. The data thus obtained were computed on the per cent of insect population suppressed and analyzed statistically.

Results: Variation in relative efficacy of different insecticides and their persistency at different days after treatment (DAT) on suppression of jassid population was significant. From the overall observation it was revealed that all the insecticides gave a satisfactory jassid control, having more than 65% mortality. Chlothianidine was found most effective insecticide to control jassid population. Imidachloprid was found to record best at 3 DAT closely followed by dimethoate. A rapid degradation of persistency was observed in imidachloprid than chlothianidine and dimethoate after 14 DAT. Neem oil also provide a satisfactory results at 3 DAT.

Conclusions: Imidachloprid, having lower persistency, is suitable for jassid control. Phytopesticide neem oil is of biological origin having less hazardous effect on health and so can be incorporated in the IPM programme of pest control in vegetable cultivation.

POSTER PRESENTATION

Parasitism of diamondback moth, *Plutella xylostella* L. by an endo-parasitoid braconid wasp, *Cotesia glomerata* L. at Highland

Min Kwon, Juil Kim, Seunghwan Lee

National Institute of Highland Agriculture, RDA, Pyeongchang, Gangwon; Seoul National University, Seoul, Korea, Republic of Korea

Introduction: *Cotesia glomerata* is well known for attacking larvae of imported cabbageworm (*Artogeia rapae*) in the field, but little information on attacking diamondback moth (DBM, *Plutella xylostella*) has reported. This study aimed to identify if *C. glomerata* can parasitize DBM larvae, and to investigate some biological characteristics of wasps.

Methods: The cocoons of *C. glomerata* collected in cabbage fields at Daegwallyeong area in Korea, asl 800 meter, were placed into acryl cylinder to emerge. Newly-emerged adults were allowed to mate for 2 days before fresh cabbage leaf with 200 second instar larvae was introduced into cylinder. After exposing for 48 h, cabbage leaf with parasitized larvae was removed from cylinder and placed on fresh 6-week-old cabbage.

Results: Parasitism rate of *C. glomerata* to imported cabbageworm was over 15% on average, and over 70% of cocoons emerged into adults. We identified that *C. glomerata* can attack DBM larvae and parasitize them successfully and efficiently. The parasitoids showed solitary type for DBM, not gregarious type. Parasitism rates were at the field sites werevery low, but up to 90% in cages.

Conclusions: As *C. glomerata* is not available commercially at this time, but this parasitoid could be promising to use as bio-control agent of DBM.

POSTER PRESENTATION

Cloning, expression, and sequence analysis of the major structural protein genes of the porcine reproductive and respiratory syndrome virus isolated in Korea

Hyun-Na Koo[1], Jeong-Mi Oh[1], Jae-Kyung Lee[1], Yeon-Ho Je[2], Byung-Rae Jin[3], Soo-Dong Woo[1]

[1]Department of Agricultural Biology, Chungbuk National University, Cheongju, Chungbuk, [2]Department of Agricultural Biotechnology, Seoul National University, Seoul, [3]College of Natural Resources and Life Science, Dong-A University, Busan, Republic of Korea

Introduction: Porcine reproductive and respiratory syndrome (PRRS) is an economically significant viral disease of swine. Each gene of the six major structural proteins (ORF2, ORF3, ORF4, ORF5, ORF6 and ORF7) of PRRSV isolated in Korea was cloned, sequenced, and expressed.

Methods: Each gene was amplified using degenerated PCR primers and cloned into PCR vector. After sequence analysis, each gene was cloned into baculovirus expression vector and expressed in insect cells. Expression of each protein was analyzed by SDS-PAGE and Western blot.

Results: The each gene analysis showed that Korean isolate is an American strain and the homology of amino acid sequence was from 91% to 100% when compared previous reports. ORFs 2 to 7 were inserted into recombinant baculoviruses downstream of the polyhedrin promoter. Insect cells infected with the respective recombinant baculovirus produced each protein. Expression of each protein was identified by RT-PCR and immunoblot with PRRSV-specific antibody, indicating that they were similar to the native proteins.

Conclusions: The ability to produce each protein in the baculovirus system indicate that these could be major candidates for the development of a vaccine against PRRSV.

POSTER PRESENTATION

Characterization of nucleopolyhedrovirus isolated from *Mamestra brassicae* (Lepidoptera: Noctuidae) in Korea

Jae Kyung Lee[1], Jeong-Mi Oh[1], Hyun-Na Koo[1], Yeon-Ho Je[2], Byung-Rae Jin[3], Soo-Dong Woo[1]

[1]Department of Agricultural Biology, Chungbuk National University, Cheongj, [2]Department of Agricultural Biotechnology, Seoul National University, Seoul; [3]College of Natural Resources and Life Science, Dong-A University, Busan, Republic of Korea

Introduction: The cabbage armyworm, *Mamestra brassicae*, is an important insect pest of vegetables and ornamental plants in Asia and Europe. Several nucleopolyhedroviruses (NPVs) have been isolated from *M. brassicae* and considered useful biological-control agents for *M. brassicae*. However, Korean strain of *M. brassicae* NPV (MbNPV) is poorly characterized. For the practical use of NPV as a control agent of noctuid pests, it is necessary to identify and characterize the virus strain in advance. The objective of our study was the pathogenic, morphologic and genetic characterization of a MbNPV isolate (MbNPV-K1) derived from a diseased larva of *M. brassicae* found in Korea.

Methods: The morphology of polyhedra was observed using SEM and TEM. The lethal dose and time were determined using *M. brassicae* larvae by droplet-feeding bioassay. The polyhedrin gene was amplified by PCR and sequenced. All results were compared with those of the previous commercialized MbNPV as a control.

Results: The morphology of polyhedra and the structure of polyhedrin gene did not show any significant difference between two viruses. But the size of polyhedra of MbNPV-K1 was slightly bigger than the control. The value of lethal concentration (LC_{50}) of MbNPV-K1 against 3rd instar larvae of *M. brassicae* was 15 times higher than the control. The lethal time was also shorter than the control.

Conclusions: The higher pathogenicity of MbNPV-K1 provides the possibility of the development of effective viral insecticide using this for the control of *M. brassicae*.

POSTER PRESENTATION

The mason bee *Osmia orientalis* uses the presence of visitors on the flower as resource assessment

Tomoyuki Yokoi, Kenji Fujisaki

Laboratory of Insect Ecology, Graduate School of Agriculture, Kyoto University, Kyoto, Japan

Introduction: If many bees visit the same flower patch, the probability that they meet on the same flower would increase with resource depletion. However, several social bees preferentially visit the flowers on which conspecifics are feeding. It would be beneficial for them to reduce the time spent on detecting rewarding flowers because floral resources are unpredictable. Field experiments were conducted to test whether the mason bee *Osmia orientalis* visits the flower of wild strawberry *Rubus hirsutus* on which heterospecifics are already feeding as a cue for resource assessment.

Methods: The frequency of encounter with other visitors on the same flower was recorded in three bees; *O. orientalis*, *Apis mellifera* and *Micrandrena* spp. We recorded visitation rate to flowers on which the different dead bees were artificially set.

Results: *O. orientalis* was one of the dominant visitors and always acquired the flower where other visitors were feeding. The visitation rate of *O. orientalis* was highest on flower where *Micrandrena* spp. was artificially set. *A. mellifera* and *Micrandrena* spp. rejected the flowers on which dead bees were set.

Conclusion: *O. orientalis* may recognize the presence of *Micrandrena* spp. on the flower as a cue for resource assessment. The visit to these flowers would be profitable because of the low cost to acquire the resources through the competition.

POSTER PRESENTATION

The value of public involvement in an entomological survey: a model from the UK

Peter M.J. Brown[1], Helen E. Roy[1], David B. Roy[1], Michael E.N. Majerus[2]

[1]NERC Centre for Ecology and Hydrology, Monks Wood, United Kingdom, [2]University of Cambridge, Cambridge, United Kingdom

The arrival in England of *Harmonia axyridis* Pallas (Coleoptera: Coccinellidae) represented something of a turning point in species recording in the UK. *Harmonia axyridis* is regarded as an alien invasive species in Europe. Concern by some entomologists that the species would have a seriously detrimental impact on native insects led to major national publicity following the insect's arrival. After verification of over 100 records of *H. axyridis* in 2004, the year of arrival, a project was funded for detailed monitoring of the spread of the species in the UK. A key element of the project was the development of a web-based recording system accessible by members of the general public. Increasingly high levels of access to the internet and digital photography made this project possible. Here we outline the recording system and infrastructure used to support the monitoring scheme, and highlight the importance of public involvement. In some respects the scheme is labour intensive, involving the verification of individual specimens by either photograph or specimen. However, there are several wider benefits of the scheme; firstly the model (in terms of the technology and systems used, as well as the biological spread model) is potentially transferable to other taxa, particularly other invasive species; secondly the engagement of the public in wildlife monitoring; thirdly the rejuvenation of a recording scheme for a whole family of insects (the Coccinellidae) alongside a high profile non-native species. We also reflect on the importance of publicity in making such a monitoring scheme effective, and explore the potential for further automation.

POSTER PRESENTATION

Mitochondrial genetic diversity and phylogeography of the Iberian populations of *Mioscirtus wagneri* (Orthoptera: Acrididae), a specialized grasshopper inhabiting highly fragmented hypersaline environments

Joaquin Ortego, Raul Bonal, Jose Miguel Aparicio, Pedro J Cordero

Instituto de Investigación en Recursos Cinegeticos-IREC, Ciudad Real, Spain

Introduction: Mediterranean inland hypersaline areas are globally threatened habitats harbouring many specialized organisms often endemic or constituting relict populations which frequently show disjunct distributions. Contraction of wider original habitats after historical climate changes/geological events and, more recently, human induced habitat loss have led these species to be distributed forming highly fragmented and isolated populations in small-sized patches of favourable habitats. Here, we analyze mitochondrial genetic diversity and phylogeography of *Mioscirtus wagneri*, a specialist orthoptera inhabiting hipersaline low grounds with patches of *Suaeda vera*, a plant on which it depends for food.

Methods: We used a 260 bp of the cytochrome oxidase subunit II and 486 bp of the 16S rRNA genes to study the genetic diversity and phylogeographic structure of *Mioscirtus wagneri* over the entire species distribution range in the Iberian Peninsula. For this purpose, we sampled a total of 227 individuals from 26 Iberian populations.

Results: After combining sequence information from the two mitochondrial genes we determined the presence of 12 unique haplotypes (COII: 9 haplotypes; 16S rRNA: 5 haplotypes) across the 227 specimens examined. Phylogenetic analyses revealed three mitochondrial DNA clades corresponding with northeast, central-southeast, and southwest populations. Populations from these three different geographic areas never shared any haplotype, indicating that gene flow between them is absent.

Conclusions: We conclude that the three *Mioscirtus wagneri* clades correspond with distinct evolutionary entities and such differences should be considered in future conservation programmes of Iberian hypersaline environments.

POSTER PRESENTATION

When umbrellas kill: the case of small reserves in sensitive habitats

Pedro J. Cordero, Joaquín Ortego, Raúl Bonal, Gustau Calabuig, Elena García-Vigón, José M Aparicio

Instituto Investigación en Recursos Cinegéticos (IREC)(UCLM, CSIC, JCCM), Ciudad Real, Castilla-La Mancha, Spain

Inland hyper-saline lagoons are singular and sensitive habitats of Mediterranean arid land often surrounded by dry crops and plugged land. They present a high amount of rare, specialised or endemic species of plants and invertebrates, insects included. Some are typical of saline environments and others from arid lands taking refuge in the vegetation rings around these lagoons. This fauna is poorly known, may present localised distributions, a low ability of dispersal and are submitted to a high risk of local/total extinction. In turn, several emblematic bird species with preferences in arid land or aquatic environments may gather at high densities and often are determinant of the importance given to these micro-reserves for conservationist agents, constitute an essential cultural value for visitors and are considered umbrella species in management decisions. However, local action plans for bird management and conservation or, simply, the increasing of natural populations of some species put at risk the persistence of these habitats and some of its invertebrate species. An over-population of medium/large-sized-omnivorous/insectivorous-birds may reduce prey because of high foraging pressure on insect rarities (i.e. orthopteroids), or because of habitat changes in the soil or vegetation where these endangered insects live. Two action plans are proposed: firstly cultural, by investing more on the knowledge and divulgation of invertebrate species values. Secondly of management, by increasing the area of vegetation ring preserved around these lagoons and by creating new patches in the surroundings. Both actions could ameliorate the harmful effects of birds on rare insects and would reduce the conservation conflict in these particular and sensitive habitats.

POSTER PRESENTATION

The evolutionary ecology of body size in seed parasites: the case of the acorn feeding Curculio

Raul Bonal[1], Tabitha Pearman[2], Josep Maria Espelta[3], Alberto Muñoz[4], Jose Miguel Aparicio[1], Joaquin Ortego[1], Pedro J. Cordero[1], Alfried Vogler[2]

[1]IREC (CSIC-UCLM-JCCM), Ciudad Real, Spain, [2]THE NATURAL HISTORY MUSEUM, London, United Kingdom, [3]CREAF-UAB, Barcelona, Spain, [4]IRN-CCMA-CSIC, Madrid, Spain

Introduction: The larvae of many granivorous insects, like the acorn feeding Curculio, are parasites which complete their development inside a single seed. Comparative interspecific analyses have shown that body size is correlated with the size of the seeds exploited. This suggests that larval growth could be constrained by seed size so that shifts to larger seeds would trigger body size increase due to its fitness benefits (e. g. higher survival). We studied whether seed size may constrain larval growth in *Curculio elephas*. In addition, we carried out an extensive sampling and assessed whether the adaptation to seed size may start at the intraspecific level.

Methods: We collected infested acorns in different localities of the Iberian Peninsula, measured the emerging larvae and finally opened the seeds to find out whether the food (i. e. cotyledons) had been depleted. We sequenced a fragment of mitochondrial DNA cytochrome oxidase subunit I (826 bp long) to consider the effect of neutral gene-flow in the analyses between populations.

Results: Seeds can be depleted and constrain larval growth. There was a correlation between larval size and seed size across populations due to local adaptation; phenotypic effects of seed size were ruled out including only individuals which developed *ad libitum*, unconstrained by food availability. This correlation was independent of neutral gene-flow between populations.

Conclusion: Seed size can constrain larval growth and may be an important factor for species diversification. This process can start at the intraspecific level with different populations locally adapted to seed size.

POSTER PRESENTATION

The simultaneous measurement of juvenile hormones and ecdysteroids in the haemolymph of crickets *Gryllus bimaculatus* (Ensifera: Gryllidae) by liquid chromatography-mass spectrometry (LC-MS)

Klaus H. Hoffmann, Stephanie Westerlund

University of Bayreuth, Animal Ecology I, Bayreuth, Germany

Radioimmunoassays are frequently used for the quantification of ecdysteroids in the haemolymph of insects, whereas for juvenile hormone titers, physicochemical methods such as GC-MS have been considered the most accurate. Unfortunately, extensive sample preparation and organic solvent usage for GC-MS, and the need of radioactivity in radioimmunoassays, are a major disadvantage for routine analyses. Here we use a time- and chemical-saving LC-MS method for the simultaneous detection of juvenile hormone (JH) and free ecdysteroids in the haemolymph of last instar larvae and adult crickets with the same degree of accuracy and precision as can be afforded with GC-MS and radioimmuno-assay, respectively (Westerlund and Hoffmann, 2004: Analyt. Bioanalyt. Chem. 379, 540-543).

Juvenile hormone III was the only JH homology found in last instar larvae and adults of both sexes. Female and male last instar larvae exhibited a rather steady JH III titer (27 $\pm$ 5 pg/µL), whereas in adults a maximum in the JH III was observed on day 4 after ecdysis for females (94 $\pm$ 35 pg/µL) and on day 3 for males (111 $\pm$ 20 pg/µL).

Ecdysone (E) was present in last instar larvae of both sexes as well as in adult females and males, whereas 20-hydroxyecdysone (20E) was only found in the larvae, but not in the haemolymph of adult animals. In last instar larvae, the maximal concentration of 20E on day 5 corresponds to the moulting process, whereas in adult females the titers of ecdysone and JH III are in parallel with ovarian weight gain and egg maturation.

Supported by the Deutsche Forschungsgemeinschaft GK 678/2.

POSTER PRESENTATION

Determining insect pest impact within multi-cropping systems as part of a holistic approach to diverse cropping systems evaluation

William J Weeks, Philippus D R van Heerden

[1]*Southern District and Research, Potchefstroom, North-West Province, South Africa,* [2]*Sugarcane Research Institute, Mount Edgecombe, South Africa*

Introduction: Multi-cropping systems, characterized by an intimate spatial and maximal temporal overlap, rank among the most complex ecological systems. Studies evaluating multi-cropping system impacts on insect pests often do not consider plant density effects.

Aim: To illustrate how information on insect infestation intensity and plant stress along with land use efficiency calculations can be employed to evaluate multi-cropping systems.

Methods: A cabbage/ carrot companion planting field trial with a split-plot experimental design was established. Insecticide applications and no-spraying were whole-plots with five sub-plot treatments *viz.* cabbage monoculture, carrot monoculture, 1:1, 1:3 and 1:5 cropping ratios (cabbage: carrot), replicated five times. Cabbage insects were sampled fortnightly from sub-plots on no-spraying whole-plots over 3 sampling dates. Chlorophyll *a* fluorescence measurements were recorded from cabbage and carrot leaves on all plots. The performance index (PI_{ABS}) was calculated from these measurements as indicator of plant stress. Cabbage head mass and carrot root mass was determined from all plots. Data was subjected to analysis of variance. Treatment means were separated using Fishers' protected t-test at the 5% level of significance (LSD).

Results: Results indicate low insect infestations on cabbage with no significant differences ($P > 0.05$) between sub-plot treatments and PI_{ABS} values. Cabbage PI_{ABS} values on the sprayed whole-plots were significantly ($P \leq 0.05$) lower, indicating a degree of phytotoxicity induced by insecticide applications. This corresponds with a 14% cabbage yield reduction on sprayed plots. Chlorophyll *a* fluorescence appears to be sensitive as an indicator of insecticide phytotoxicity. Future development of this approach will be done under higher insect infestation levels. Use of the Land Equivalent Ratio to evaluate this multi-cropping system will also be explored.

POSTER PRESENTATION

Phylogeography of the temperate bark beetle *Tomicus piniperda* (Coleoptera, Scolytinae): new evidence of a complex past history

Agnes Horn[1], Christian Stauffer[2], François Lieutier[1], Carole Kerdelhué[3]

[1]Université d'Orléans, Laboratoire de Biologie des LBGC UPRES EA 1207, Orléans, France, [2]Boku, University of Natural Ressources and Applied Life Sciences, Vienna, Austria, [3]INRA, UMR BIOGECO 1202, Cestas, France

Introduction: European temperate species have been largely affected by past climatic oscillations, leading to a general genetic pattern of southern richness and northern purity. The temperate and cold-tolerant bark-beetle *Tomicus piniperda* is largely present all over Europe except the Mediterranean Basin, and develops on pine species. We studied the phylogeography of the species in Europe to test (i) if its phylogeographic pattern reflects those of its main hosts; (ii) if classical southern refugia could be identified in spite of the species' sensitivity to dry climates; and (iii) if northern refugia could be found for this cold-tolerant organism.

Methods: A 797 pb part of the Cytochrome Oxydase I and II genes were sequenced for 150 individuals sampled in 34 European populations.

Results: 36 haplotypes were identified and joined in a single haplotype network. One haplotype was dominant in Europe but Iberian Peninsula, while this last region was characterized by numerous endemic haplotypes.

Conclusion: *T. piniperda* showed a phylogeographic pattern similar to that of its main host *Pinus sylvestris*, with genetic richness in Iberian Peninsula and a predominant haplotype in the rest of Europe, reflecting a rapid recolonization of northern regions during warmer periods. In Iberian Peninsula, the species may have survived the interglacials in fragmented refugia localized in high altitude, leading to isolated populations which poorly contributed to postglacial expansions. In the rest of Europe, some glacial refugia were identified in both southern and northern regions. Yet, high dispersal ability led to a weak genetic structure in Europe.

POSTER PRESENTATION

Colonization history of the Neartic leafhopper *Scaphoideus titanus* in Europe based on microsatellite and mitochondrial DNA variability

Daciana Papura[1], Christian Burban[2], Xavier Giresse[1], Carole Kerdelhué[2], François Delmotte[1], Van Helden Martin[1]

[1]INRA-ENITA, UMR Santé Végétale 1065, Bordeaux, France, [2]INRA, UMR BIOGECO 1202, Cestas, France

Introduction: The Nearctic leafhopper *Scaphoideus titanus* was accidentally introduced in Europe during the 20th century and expanded almost throughout the continent in about 60 years. *S. titanus* is the vector of Flavescence dorée phytoplasma, the causal agent of the most important grapevine yellow disease in European vineyards.

Material and methods: Native American *S. titanus* populations were compared to European populations using seven polymorphic nuclear microsatellite loci and a fragment of 623 bp of the mitochondrial cytochrome oxidase II ($tRNA^{LEU}$-COII) gene.

Results and discussion: Consistent with their recent history, invasive European populations showed much lower levels of genetic diversity than American populations, indicative of recent bottlenecks. Population differentiation inferred from microsatellite data was generally lower but significant in European populations (pairwise mean F_{ST} = 0.030) than among American populations (pairwise mean F_{ST} = 0.042). A significant pattern of isolation by distance was detected among American but not among European populations. Concerning mitochondrial data, none of the European haplotypes was found in the American populations from which they are assumed to originate. Clustering analysis on microsatellite data suggest that most European populations have originated from a main invasion event, with one additional introduction into southern Switzerland, where endemic mitotypes were found. After the initial establishment of *S. titanus* populations, the commercial exchanges of grapevine canes and grafts carrying eggs could have played an important role in the insect dispersal across European vineyards.

POSTER PRESENTATION

Insects in southern African rock art

Jeremy Hollmann[1], Mike Mostovski[2]

[1]Natal Museum and School of Anthropology, Gender and Historical Studies, University of KwaZulu-Natal, Pietermaritzburg, South Africa, [2]Natal Museum and School of Biological & Conservation Sciences, University of KwaZulu-Natal, Pietermaritzburg, South Africa

Southern African hunter-gatherers, the ancestors of contemporary Bushman peoples, have a long tradition of making rock art. This art is predominated by depictions of anthropomorphs and a restricted number of antelope species and large herbivores such as giraffe, rhinoceros and elephant. However, images of insects are also an important, if less numerous component of the art. Paintings of termites and bees are the most prominent categories and occur in particular regions. Other images that have been identified as insects, such as moths and locusts, are far less common. Our current understanding of the art is that painted and engraved depictions are supernaturally charged images, not simply depictions of everyday activities and favoured menu items. Insects play an important role in hunter-gatherer economy and cosmology and therefore our interpretations of paintings and engravings of insects are based upon ethnographic sources and analogies in order to interpret depictions of these arthropods.

POSTER PRESENTATION

Correlates between butterfly species richness and landscape composition and structure: a multi-scale analysis

Jean-Pierre Rossi, Inge van Halder

INRA, UMR1202 Biodiversity Genes & Communities, F-33610 Cestas, France

Introduction: Species richness is strongly affected by habitat type and landscape features. Most butterfly species need complementary resources (host-plants for egg laying and larvae development, nectar plants for adults, roosting-, resting- and over wintering-sites) during their life cycle. Therefore, species richness may be favoured in diverse landscapes. The present study aimed at determining to which extent butterfly species richness could be related to landscape features and if yes, at which spatial scales.

Methods: Butterfly species richness was estimated at 83 sampling points distributed among 2 study sites in the Landes de Gascogne (Southwestern France), in pine stands, deciduous woodlands and firebreaks. Around each sampling location, landscape was described within circular areas (buffers) of increasing sizes using a GIS database. For each buffer size, various landscape metrics were calculated in order to quantify important features such as landscape heterogeneity, fragmentation and composition.

Results and discussion: A total of 2750 individuals belonging to 44 species were recorded in the 83 plots. Partial Least Square Regression (PLS) showed the presence of a significant relationships between landscape metrics and species richness ($p=0.002$). Interestingly the strength of the relationship between landscape metrics and butterfly species richness changed dramatically according to the spatial scale (size of the buffer) and the variable considered. This work illustrates the multiscale nature of the relationships between butterflies and landscape and how adequate statistical tools (PLS) can be useful in unravelling such complex patterns. As a consequence, selection of landscape-based biodiversity indicators should be based on multi-scale approaches.

POSTER PRESENTATION

Post-storm study of the spatial distribution of the bark beetle *Ips sexedentatus* in a pine plantation forest (Landes de Gascogne, Southwestern France)

Jean-Pierre Rossi[1], Jean-Charles Samalens[1], Dominique Guyon[2], Inge van Halder[1], Hervé Jactel[1], Pierre Menassieu[1], Dominique Piou[3]

[1]INRA, UMR1202 Biodiversity Genes & Communities, F-33610 Cestas, France, [2]INRA, UR1263 EPHYSE, F-33140, Villenave d'Ornon, France, [3]DSF, Impasse R. Lavigne, F-33150 Cenon, France

Introduction: The bark beetle *Ips sexdentatus* (Boern) (Coleoptera, Scolytidae) is a serious pest of planted and natural pine forests causing important damages during outbreak phases. Outbreaks are triggered or facilitated by climatic events like windstorms that lead to increased amount of breeding material through felled timbers. In December 1999, Southwestern France was struck by a windstorm that felled more that 27 million m^3 of timber. In a forest of 1500 ha, we surveyed the spatial pattern of attacked trees and its relationship with the spatial location of the pine logs that were temporally stored in piles along stand edges during the post-storm process of fallen tree removal.

Methods: A GIS database was developed on the basis of a complete inventory of attacked trees and log piles. A total of 2393 and 3142 attacked trees were identified and mapped in 2001 and 2002. Patches of attacked trees were defined using kernel estimation coupled with Monte Carlo tests. Patches spatial distribution and their relationship with log piles were assessed using a new method designed to account for object shape in point pattern analysis [Wiegand *et al*, 2006, *J. Ecol*. 94, 825-837].

Results: There was a significant relationship between patches of trees attacked during the both years of the study and log piles. These results indicate that *I. sexdentatus* outbreaks exhibited large-scale spatial structure partly explained by forest management (log pile position) and landscape configuration (network of forest tracks). This suggests that log pile spatial distribution should be taken into account to optimize sampling schemes in forest health monitoring programmes.

POSTER PRESENTATION

Geostatistical analysis of pine processionary moth (*Thaumetopoea pityocampa*) spatial distribution at the landscape scale (Landes de Gascogne, Southwestern France)

Jean-Pierre Rossi[1], Jean-Charles Samalens[1], Hervé Jactel[1], Dominique Piou[2]

[1]INRA, UMR1202 Biodiversity Genes & Communities, F-33610 Cestas, France, [2]DSF, Impasse R. Lavigne, F-33150 Cenon, France

Introduction: The pine processionary moth (PPM) (*Thaumetopoea pityocampa* Denis & Schiffermüller: Lepidoptera Notodontidae) is the most important defoliator of pines in Southern Europe. It produces spectacular outbreaks and often displays non random spatial distributions which determinants remain to be fully understood. This survey aimed at describing the population spatial pattern and its variability through time and its relationship with landscape composition and structure.

Methods: We studied the dynamics of the PPM in pine plantations in the Landes de Gascogne (Southwestern France). Population density was estimated on 145 sites scattered on a 16 x 16 km grid with mesh of 2 Km. Data were collected during 3 consecutive years (2005-2007). Geostatistics were used to assess the presence of autocorrelation and to describe the population pattern by kriging. Data collected on different sampling dates were compared by means of Mantel tests.

Results and discussion: The population exhibited a strongly autocorrelated distribution in 2005 with patches of several kilometers. A very high local variability was superimposed on this long-range spatial structure that is likely due to the effects of local landscape features. Data collected in 2006 and 2007 showed no structure and very low population densities. These dates corresponded to the very end of the decline phase or the beginning of the non-outbreak phase. Sampling will be repeated for 4 additional years so as to determine if the spatial structure observed during the beginning and the outbreak phase is stable through time and to gain a better knowledge on how landscape affects population dynamics.

POSTER PRESENTATION

Effect of fire on arthopods in central semi-arid Argentina

F. Rodrigo Tizón[1], Daniel V. peláez[2], Omar Elía[3], Mirta Mayor[4]

[1]CERZOS, CIC, Departamento de Biología. Universidad Nacional del Sur., Bahía Blanca, Buenos Aires, Argentina, [2]CERZOS, CIC, Departamento de Agronomía. Universidad Nacional del Sur., Bahía Blanca, Buenos Aires, Argentina, [3]CERZOS, Departamento de Agronomía. Universidad Nacional del Sur., Bahía Blanca, Buenos Aires, Argentina, [4]Bahía Blanca, Buenos Aires, Argentina

Introduction: Fire plays a vital role in maintaining the communities of the region central semi-arid Argentina. The grasslands are subjected to burns to manage vegetation. Some of the desirable consequences of this practice are the increase of coverage of grass and the decrease of shrub species. However, the consequences of the animal communities are highly variable.

Methods: We studied the effect of the history of controlled fire at different frequencies, 3 (T_1, 2 replicates) y 6 (T_2, 2 replicates) years, and the short-term effects of fire on the epigean arthropods. Sampling was conducted in SE of the province of La Pampa (38º45´S, 63º45´W) in plots burned and unburned ($T_u T_1, T_2$), since 1991. In the fall of 2007, 20 pitfall traps per treatment were activated for a week, and ending winter, after a controlled burn the traps were re-activate ($T_{up} T_{1p}, T_{2p}$). Shannon-Wiener index and confidence intervals (bootstrap) were calculated.

Results: Comparisons of richness, abundance and diversity of arthropods orders response did not show significant differences ($p>0.05$) between treatments ($T_u T_1, T_2$). On the other hand, the diversity decrease significantly ($p <0.05$) in samples collected after two months of controlled burning ($T_{up} T_{1p}, T_{2p}$). In post-fire treatments the total number of individuals decreased with fire frequency increment, but the total number of orders remained relatively stable. Orders more adversely affected by the fires were Acari, Collembola and Homoptera while Hymenoptera and Coleptera were favored.

Conclusions: In the future, would be desirable to incorporate other level *taxa* to improve comprehension of the effect of fire on arthropods assemblages.

POSTER PRESENTATION

How many species of *Stenobasipteron* (Diptera: Nemestrinidae) in South Africa

Musa Mlambo, David Barraclough, Rob Slotow

University of KwaZulu-Natal, Durban, South Africa

Stenobasipteron Lichtwardt is one of three long-proboscid genera of Nemestrinidae (Diptera), which are important in Southern African pollination biology. Numerous endemic plant species with elongate floral tubes are pollinated by these long-proboscid species. *Stenobasipteron* has received virtually no taxonomic attention for the last 80 years, which has resulted in taxonomic confusion, misidentifications and the failure to recognise species complexes. The genus is mainly distributed through the eastern provinces of South Africa, and into Swaziland and Zimbabwe. Currently the genus includes three described species -- two from Zimbabwe (*S. arnoldi* & *S. gracile*) and one from South Africa (*S. wiedemanni*). *S. wiedemanni* is known to be restricted to forest habitats in the south-eastern provinces of KwaZulu-Natal and the Eastern Cape. Extensive morphological examination of more than 250 specimens has revealed that, within South Africa, *Stenobasipteron* now includes six valid species, i.e. *S. wiedemanni* and five new species. All the new species are distributed in the northeastern provinces of Mpumulanga and Limpopo, and occur in a variety of habitats. The fauna of neighbouring Southern African countries also requires taxonomic revision.

POSTER PRESENTATION

Stink bug management for soybeans in the southern United States

Scott Stewart[1], Angus Catchot[2], Gus Lorenz[3]

[1]University of Tennessee, Jackson, TN, United States, [2]Mississippi State University, Mississippi State, MS, United States, [3]University of Arkansas, Fayetteville, AR, United States

Information will be presented on stink bug pests (Hemiptera: Pentatomidae) and their management for soybeans grown in the southern United States. Stink bugs are considered the primary pests of soybeans in most areas of the southern United States. The most common pest species include the green stink bug (*Acrosternum hilare*), brown stink bug (*Euschistus servus*) and the southern green stink bug (*Nezara viridula*). The damage potential for these pests will be addressed. Management considerations, including the impacts of planting date, selection of maturity groups and insecticide selection will also be included.

POSTER PRESENTATION

Identification of host-plant attractants for the cranberry weevil, *Anthonomus musculus* Say (Coleoptera: Curculionidae)

Zsofia Szendrei[1], Edi Malo[2], Cesar Rodriguez-Saona[1]

[1]*Rutgers, The State University of New Jersey, Chatsworth, New Jersey, United States,* [2]*Departamento de Entomologia, El Colegio de la Frontera Sur, Tapachula, Chiapas, Mexico*

Introduction: The cranberry weevil is an oligophagous flower bud feeder native to North America. It causes significant economic injury on cultivated highbush blueberry, *Vaccinium corymbosum* L. (Ericaceae), and on cranberry, *Vaccinium macrocarpon* Ait. (Ericacea). This project was conducted in New Jersey, where the weevil causes major crop losses to blueberry growers. As part of an integrated response to this problem, we investigated the role of plant volatiles as attractants for monitoring or trapping.

Methods: We analyzed volatile compounds from blueberry leaves, buds, and flowers. More than 30 compounds were identified using GC-mass spectrometry and subsequently tested in electro-antennograms (EAG). Y-tube olfactometer assays were conducted to assess the attractiveness of damaged and undamaged buds and flowers.

Results: Weevil antennae were highly responsive to hexyl acetate, cis-3-hexenyl acetate, cis-3-hexenyl butyrate, methyl salicylate, cinnamyl alcohol, linalool oxide, linalool, and α-humulene. Cis-3-hexenyl butyrate and cinnamyl alcohol were emitted only from blueberry flowers. Cinnamyl alcohol was the major blueberry flower volatile. In laboratory assays, flower buds and flowers were attractive to weevils, and damaged buds were more attractive than undamaged buds.

Conclusion: This project has identified several volatile compounds from blueberries that can serve as a potential attractant for the cranberry weevil. In the spring 2008, traps baited with cinnamyl alcohol will be investigated for weevil attraction in the field. Two trap designs will be compared: soil-cone traps and yellow sticky cards at the canopy level. In addition, both Y-tube and field experiments will test whether conspecifics produce behaviorally active compounds.

POSTER PRESENTATION

Yield benefits of Thiamethoxam and Imadacloprid used as insecticide seed treatments in soybean in the mid-south region of the United States

Angus Catchot[1], Gus Lorenz[2], Scott Stewart[3], Roger Leonard[4]

[1]Mississippi State University, Mississippi State, MS, United States, [2]University of Arkansas, Little Rock, AR, United States, [3]The University of Tennessee, Jackson, TN, United States, [4]Louisiana State University, Baton Rouge, LA, United States

From 2003-2007, researchers in the mid-south region of the Unites States have studied the use of thiamethoxam and imadacloprid as insecticide seed treatments in soybean for control of early season pests. Yield summary of 66 university trials with thiamethoxam compared to untreated plots resulted in an average yield increase of 3.5 bu/acre. Yield summary of 34 university trials with imadacloprid compared to untreated plots resulted in an average yield increase of 2.8 bu/acre. Early season incidence of bean leaf beetle, *Cerotoma trifurcata*, thrips, *thrips sp.*, threecornered alfalfa hopper, *Spissistilus festinus*, scarab grubs, and grape colaspis grubs, *Colaspis brunnea* were reduced compared to untreated check plots.

POSTER PRESENTATION

X-ray microCT enables high-resolution 3-D imaging of the internal anatomy of live locusts

Jenan Al-Harib[1], Vicky Hunt[1], Keith Charnley[1], David Heatley[2], Duncan Bell[1], Nick Corps[1]

[1]University of Bath, Bath, United Kingdom, [2]Disect Systems Ltd, Suffolk, United Kingdom, [3]e2v scientific instruments, Buckinghamshire, United Kingdom

Introduction: Micro-CT scanning is widely used, particularly in medicine, but has rarely been applied to insects. The technique has great potential for providing fine-resolution images of the internal organs of living specimens. We have established the technique in an entomological context using young adult male desert locusts, *Schistocerca gregaria*. We chose this insect because it is large, its anatomy is well described and we wish to apply the technique in an on-going investigation of the pathology of a specific Acridid fungal pathogen.

Methods: Ten day old live and dead adult male locusts were used. X-Ray micro-CT scans were performed using either the Skyscan 1174 or 1172 scanner (www.skyscan.be). Each scan generated between 4 and 5 thousand slices at an inter pixel size of 10.6 microns. Using a modified form of the 'disect' software we viewed 8 bit data at 250 X 250, 512 X 512 or 2000 X 2000 resolution allowing us to view 900, 300 or about 40 slices at a time.

Results: The combination of a high resolution X-ray micro-CT scanner and user friendly 3-D viewing software gave excellent 3-D reconstructions of the internal structures of locust and new insights in particular of the configuration of the tracheal system.

Conclusion: Having established parameters for the use of microCT with the locust we will now use the technique to study the impact of the fungal pathogen, *Metarhizium anisopliae*, on the cuticle during host penetration at an improved scan resolution of just 2 microns per voxel.

POSTER PRESENTATION

Behavioral evidence for a long range female produced sex pheromone in C*allisphyris apicicornis* Fairmaire & Germain (Coleoptera: Cerambycidae: Lepturinae)

Tomislav Curkovic, Catalina Ferrera, Javier Munoz

University of Chile, Crop Protection Dept., Santiago, RM, Chile

Callisphyris apicicornis is a widely distributed wood borer in central Chile, that damages several tree fruit (apple), forest (*Betula* spp.), and ornamental (*Cotoneaster franchetti*) species. Adults emerge in spring and lay eggs on the branches of mature trees. The larvae bore through the bottom of the egg directly into the bark, where they feed on the cambium for 1 to 2 years. During this process the larvae regularly cut off pieces of branches, severely affecting the tree's framework. The pupal stage is about 1 month. None of these pre-adult stages are exposed and feasible for conventional insecticide control, nor have any effective biological control agents been found so far. Because this species attacks living trees and can eventually kill them in severe infestations, we have initiated a study of *C. apicicornis* sexual behavior and chemical ecology, to determine whether a pheromone-based control strategy might be feasible to control adults. Studies conducted in 2006 and 2007 strongly suggest that females use a long-range sex pheromone to attract males for mating. If confirmed, this will be the first evidence reproductive behaviors being mediated by female-produced sex attractant pheromones within the Lepturinae subfamily, and only the third report of female-produced attractants for any cerambycid species. The behavioral sequences during the final approach of a male to a pheromone-producing female have been videotaped and characterized for males (n = 36) and females (n = 20) in order to have a behavioral baseline to evaluate responses from adults to synthetic pheromone sources in the future.

POSTER PRESENTATION

Impact and incidence of dectes stem borer, *Dectes texanus texanus* (Coleoptera: Cerambycidae) in soybean in the Southern United States

Gus Lorenz, Scott Stewart, Angus Catchot

University of Arkansas, Lonoke, Arkansas, United States

Dectes stem borer, *Dectes texanus texanus*, also known as the soybean stem borer, is a native species distributed throughout much of the southern half of the United States in soybean producing areas. While traditionally considered a minor pest, in recent years a marked increase in incidence has been observed throughout the midsouthern states. Dectes damages the plant through petiole and mainstem tunneling but the most damage occurs late in the season as the larva moves to the base of plant and girdle the inside of the plant just above the soil line. This often results in lodging of the plant which, if severe enough may result in loss of yield. Studies have been initiated to determine the impact of Dectes in soybean and determine an effective method of control.

POSTER PRESENTATION

Comparison of the leaf litter ant fauna between an Atlantic Forest area and a *Pinus elliottii* stand (Pinaceae) in Rio Claro, SP, Brazil

Daniel Solis[1], Maria Santina Morini[2], Eduardo Fox[1], Carlos Jesus[1], Eduardo Diniz[1], Itamar Reiss[1], Thiago Moretti[3], Odair Bueno[1]

[1]Centro de Estudos de Insetos Sociais, Departamento de Biologia, Instituto de Biociências, UNESP, Rio Claro, São Paulo, Brazil, [2]Laboratório de Mirmecologia, Universidade de Mogi das Cruzes, Mogi das Cruzes, São Paulo, Brazil, [3]Departamento de Parasitologia, Instituto de Biociências, UNESP, Botucatu, São Paulo, Brazil

Introduction: Insects, especially ants, have been successfully used as environmental bioindicators in other studies. Ants possess a set of traits that enable fast local evaluations and make them for use in management programs, like adequate diversity and abundance in practically all terrestrial habitats. The present study surveyed the leaf litter ant fauna present in two different areas: a remanant semideciduous Atlantic Forest and a 100-year-old stand of *Pinus elliottii*. The species found in both areas were compared in terms of richness and similarity. Such data could be useful in Forest Handling Plans.

Methods: Over the warm and rainy period between November and December of 2007, fifty $1m^2$ leaf litter soil samples were taken of each area with Winkler extractors. The collected ants were identified as morphospecies by comparison with the entomological collection of Universidade de Mogi das Cruzes, SP, Brazil.

Results: A total of 71 species of 26 genera from nine subfamilies were collected from the Atlantic Forest, while 40 species of 23 genera from five subfamilies were obtained from the *P. elliottii* stand. The predominant subfamily in both areas was Myrmicinae and *Pheidole* was the most frequently collected genus. The areas had 12 species in common. The obtained species accumulation curve approached the asymptote, thus proving that the sampling was sufficient for the areas.

Conclusions: Our results show that ant fauna is richer in the Atlantic Forest. Moreover, we think they illustrate the *Pinus* stand cannot be regarded as a recovered forest.

POSTER PRESENTATION

Preliminary data about *Fulvius* phylogeny (Heteroptera: Miridae: Cylapinae)

Izabella Sadowska-Woda[1], Frederic Cherot[2], Jacek Gorczyca[3]

[1]Department of Biochemistry and Cell Biology, University of Rzeszow, 35-959 Rzeszow, Poland, [2]Département de Biologie des Organismes, Free University of Brussels,, 1050 Brussels, Belgium, [3]Department of Zoology, Silesian University, 40-007 Katowice, Poland

Introduction: The genus *Fulvius* STÅL, 1862 belongs to the tribe Fulvinii from subfamily Cylapinae. It is the larger genus of its tribe with about 80 species widely spread in the tropical and subtropical areas of all continents. Among other representatives of the tribe Fulviini the *Fulvius* species can be easily distinguished by an elongated black and yellow body, hemelytra with almost parallel margins, only slightly wider than the length of posterior margin of pronotum, tarsi always two-segmented, and second segment usually divided. The phylogenetic relationships of *Fulvius* species and consequently their classification are still bad known. We provide for the first time a cladistic analysis of the genus to test its subdivision in three groups of species, as defined in literature.

Methods: The cladistic analyses were performed under NONA version 2 and WINCLADA version 1.00.08 for WINDOWS 95-2000 or NT (both available on www.cladistics.com) on a matrix including 29 *Fulvius* species representative of the three groups and 31 characters of external anatomy, male and female genital structures (all non additive and informative, several multistate). A Ratchet strategy (1000/5/8) was applied.

Results: The majority compromise tree (L = 115, ci = 40, ri = 71 with unsupported nodes collapsed) of 2213 equally most parsimonious trees (L = 104, ci = 44, ri = 76) is provided.

Conclusions: The monophyly of the genus *Fulvius* as well as its subdivision in three main clades are confirmed by our analysis.

POSTER PRESENTATION

Researches regarding biodiversity in apple orchard ecosystems in the south-western part of Romania

Rada Istrate, Ioan Rosca

University of Agricultural Sciences and Veterinary Medicine – Bucharest, Bucharest, Romania

Introduction: Apple orchards are considered stable ecosystems, with precise interrelations between different food chains in which natural factors play an essential role. The disequilibrium between different populations categories some considered pests, others deemed useful (usually called ”natural enemies of pests”) calls for a change in the pest control strategy, which focuses on maximising natural control factors, and on directing control measures to the less polluted methods.

Methods: The observations and the harvest of the biologically material have been done in the vegetation period of the trees. The collected material was carried to the laboratory, preserved in 70^0 ethylic alcohols and identified.

Results: The fauna captured in apple orchard in sticky traps, was rich and varied most abundant belonging to the classed *Insecta.* The fauna captured, was more numerous with many predator and parasite specimens. The most common predator species were species of *Coccinellidae* and parasites insect species were well represented belonging especially to the order *Hymenoptera*, superfamily *Chalcidoidea*.

POSTER PRESENTATION

Evaluation of some selective materials as larvicides against the cedar leaf moth, *Acleris undulana* Walsingham

Halil Saribasak, Fedai Erler, Huseyin Cetin, Ayhan Serttas

[1]Southwest Anatolia Forestry Research Inst. Forest Protection and Environment Department, Antalya, Turkey, [2]Akdeniz University, Faculty of Agriculture, Department of Plant Protection, Antalya, Turkey, [3]Akdeniz University, Faculty of Arts and Science, Department of Biology, Antalya, Turkey, [4]Southwest Anatolia Forestry Research Inst. Forest Protection and Environment Department, Antalya, Turkey

Introduction: The cedar leaf moth, *Acleris undulana* Walsingham (Lepidoptera: Tortricidae), has recently become an important pest in the cedar forests in Turkey. In this study, the larvicidal activity of four botanical materials (Neemazal-T/S® and Greeneem® oil, and *Origanum onites* L. and *Pimpinella anisum* L. extracts) and a microbial preparation, *Bacillus thuringiensis* subsp. *kurstaki* (Bioinsecticide WP®) were evaluated against the young and older larvae of the pest under laboratory conditions.

Methods: Larval-dip bioassays were conducted to determine the contact toxicity of the test materials to cedar leaf moth larvae and were performed using direct-dip method.

Result: The results showed that all test materials had larvicidal action against the pest. *Btk* and Neemazal were identified as the most active materials for the larvicidal action, causing 100% larval mortality at their highest tested concentration, 3 g/l and 5 ml/l water, respectively. The other two materials, hot water extract of *O. onites* and Greeneem oil, achieved 96% and 95% mortalities, respectively, at their highest tested concentration (50 ml/l and 5 ml/l water, respectively). *P. anisum* extract caused a mortality of 64% against the young instars larvae of the pest at a concentration of 50 ml/l water.

Conclusions: Our overall results suggest that all materials tested are promising as larvicides against *A. undulana*, and hot water extracts from *O. onites* and *P. anisum* could be useful in the search of newer, more selective, and biodegradable larvicidal natural compounds.

POSTER PRESENTATION

The ipmPIPE: Not just soybean rust

James VanKirk, Julie Golod, Scott Isard

[1]Southern Region IPM Center, Raleigh, NC, United States, [2]Pennsylvania State University, State College, PA, United States

Developed originally to address Asian soybean rust in the United States, the *ipm*PIPE represents an approach that will be useful for managing other pests in other systems. Many factors contribute to the utility and success to date of the system. Key stakeholders are included in all project phases including needs assessment, development, implementation, verification, project governance, and evaluation. Critical information of several different types is integrated to produce useful crop, pest and risk predictions. A voluntary and confidential good farming practices tool allows growers to substantiate best management practices. Useful information is arranged and displayed using a map and and calendar-based interface that is intuitive and easy to use. Crop and pest managers are the initial beneficiaries of this system but many others including research scientists, extension educators, agribusiness, insurers, and regulatory agencies clearly benefit.

POSTER PRESENTATION

Side effects of pesticides on *Anystis baccarum* (Anystidae)

Khalil Talebi[1], Farhad Safarpour[2]

[1]College of Agriculture, University of Tehran, Karaj, Tehran, [2]College of Agriculture, University of Tehran, Karaj, Tehran, Islamic Republic of Iran

Introduction: The beneficial mite *Anystis baccarum* is a voracious predator feeding on two-spotted mites, aphids, thrips, scales and other small arthropods. As a result of special behavior, rearing technique of this predator is not developed. This study reports the sublethal effects of recommended concentrations of fenpropathrin, azinphos methyl, phosalone, propargite and heptenophos.

Method: Adults of *Anystis baccarum* were collected from a field with no previously spray of the tested pesticides in Karaj, Iran. Experiments were conducted at 25±1°C, 75±5% RH and photoperiod of 16:8 (L:D). Application of pesticides was carried out using a Potter tower and experimental units were 9 cm Petri dishes.

Results: Fenpropathrin and azinphos methyl were found to be very toxic to the predator. Even 8-day-old residues of these insecticides caused 100% mortality. Heptenophos was considered to be harmless. The hazard class of propargite and phosalone was not assessed in laboratory and semi-field and field tests were found to be necessary for their classification. These results could be useful for pesticide selection and their use in integrated pest management in orchards.

Conclusion: Fenpropathrin and azinphos methyl were harmful to *Anystis baccarum but* heptenophos was harmless. Field and semi-field tests were necessary to find out the hazard class of propargite and phosalone.

POSTER PRESENTATION

Functional diversity in the insect biocenosis of German pine forests – using the example of pest, parasitoids and hosts

Ulrich Schulz[1], Frank Dreger[2], Curt Majunke[1]

[1]University of Applied Sciences Eberswalde, Eberswalde, Brandenburg, Germany, [2]Leibniz-Centre for Agricultural Landscape Research (ZALF), Müncheberg, Brandenburg, Germany

Introduction: Large areas of the Scots pine forests in Germany are regularly attacked by pine defoliating larvae of the pine beauty moth, *Panolis flammea*. Some areas have been turned into mixed forests (*Pinus sylvestris* with *Quercus petraea*) in order to reduce outbreaks of forest pests and to encourage biodiversity.

Methods: Insects were collected in all strata of pure and mixed Scots pine forests in Brandenburg (northern Germany) using different traps. The two-tailed test was used to assess abundance-differences.

Results: Over 400 species of coleoptera were encountered in each pine forest. The deciduous trees which have been introduced into the mixed pine forest attract a higher diversity of phytophagous insects (e.g. 72 Noctuoidea species compared with 56 in the pure stand). A highly successful parasite of *Panolis flammea,* the tachinid species *Panzeria rudis*, had significantly higher population densities in the mixed pine forest than in the pure stand ($\alpha < 0.0022$).

Conclusions: The parasitic fly *Panzeria rudis* appears to benefit from the increased diversity of Lepidoptera in the mixed forest since it is not an obligate monophage on the pine beauty moth, but - as is known from other investigations - also parasitises on other hosts such as *Orthosia stabilis*, *Xestia c-nigrum* and *Xylena vetusta*.

This example of functional diversity shows that the biodiversity of insects in a forest is important not only from the perspective of nature conservation but also from the perspective of forest health.

POSTER PRESENTATION

Host plant preferences in *Sitona* spp. (Coleoptera: Curculionidae) on lupins (*Lupinus* spp.)

Christine Struck[1], Jeannine Lutz[1], Jana Grassel[2], Wolfgang H. Kirchner[2]

[1]University of Rostock, Faculty of Agricultural and Environmental Sciences, Institute for Land Use - Crop Health, Rostock, Germany, [2]Ruhr-University Bochum, Department of Biology and Biotechnology, Bochum, Germany

Introduction: Adults and larvae of the weevil species *Sitona griseus* and *Sitona gressorius* feed on leafs and roots of lupins (*Lupinus* spp.) and cause severe damage not only due to the loss of biomass, but also through secondary infections by soil-borne pathogens. However, the damage reported seems to vary greatly. Aim of the present study was to investigate food preferences of these beetles in the field using a broad spectrum of lupin species and varieties.

Methods: Six varieties of the European Blue Lupin *Lupinus angustifolius* (Boruta, Borlu, Vitabor, Boregine, Probor and Azuro), the Yellow Lupin *Lupinus luteus* (var. Bornal) and the Dwarf Lupin *Lupinus nanus* (var. Bordüre) were planted in randomized plots in 2006 and 2007. Leaf and root damage and the number of adult beetles and larvae of each species were determined.

Results: The results show that *Lupinus luteus* and *Lupinus nanus* are much less affected by the weevils than the varieties of the Blue Lupin. Significant differences were found between *Lupinus angustifolius* varieties.

Conclusions: The results indicate that both, attractiveness and palatability of the lupins are highly dependent on the variety specific spectra of secondary plant metabolites. Ongoing laboratory experiments suggest that both, volatile attractants and alkaloid repellents, affect the food preferences of *Sitona* spp.

POSTER PRESENTATION

An attempt at differentiation of fossil Formicinae species (Hymenoptera: Formicidae) from their wings

Ksenia Perfilieva

Lomonosov Moscow State University, Biologycal Faculty, Moscow, Russian Federation

Introduction: Some fields of myrmecology use wing venation features. These are research in the phylogeny, evolution and paleontology of ants. Many remains of ant wings have been found in Tertiary fossils, such as in the Oligocene Bembridge Marls, UK. However, the variability of ants wing is poorly understood and differentiation of ant species on fossil wings is very difficult.

Methods: Investigations has been made on six recent ant species of Formicinae, and fossil ants of Oecophylla from the Bembridge Marls. Characters of wing venation of the Formicinae species were studied by standard statistic and geometric morphometrics methods.

Results: Intraspecific variability and variations of wing features were studied at recent species of Formicinae. The limits of variability of the wings length are shown. Variability has it's determine structure on intraspecific level. Female's wings are narrower than male ones in Formicinae. However, the local differences across species are identical for various samples (only females, only males, females + males). Thus, there are the species-specific characters of wing venation. The results of our investigations have been used for differentiation of fossil wings remains of Oecophylla. The wings of females and males of two species were identified. Diagnostic characters of wing venation were described for this two extinct species of Oecophylla.

Conclusions: Studies of variability of recent ant wings allow to detect the regularity of wing venation variability, which can be used for differentiation of fossil wings remains.

POSTER PRESENTATION

Long way round: Global dispersal patterns of the invasive psocids *Liposcelis decolor* (Pearman) and *L. bostrychophila* Badonnel (Psocoptera: Liposcelididae)

Katarina Mikac

University of Canberra, Bruce, ACT, Australia

Introduction: *Liposcelis decolor* and *L. bostrychophila* are invasive psocids that are major pests of stored grain and grain storage structures globally. Currently there is limited information on the dispersal patterns and capabilities of *L. decolor* and *L. bostrychophila* despite their pest status. In this paper molecular markers were used to estimate their genetic structure and gene flow to gain an understanding of their global dispersal patterns.

Methods: Microsatellites and randomly amplified polymorphic DNA (RAPDs) were used to investigate the genetic structure, gene flow and dispersal among 21 global populations of *L. bostrychophila* and 5 Australian *L. decolor* populations respectively.

Results: Microsatellites and RAPDs both revealed low to moderate significant genetic structure among pairwise population comparisons for *L. decolor* (F_{ST}= 0.05 - 0.23) and *L. bostrychophila* (G_{ST}= 0.04 –0.54) respectively. Gene flow (N*m*) was mostly low for all pairwise populations comparisons for *L. bostrychophila* (N*m*= 1.13 - 1.57) and moderate for *L. decolor* (N*m*= 0.8 - 4.7). No pattern of isolation by distance was found among global populations of *L. decolor* and *L. bostrychophila*.

Conclusions: Although they are apterous and small in size both *L. bostrychophila* and *L. decolor* are capable of unrestricted geographic dispersal in excess of 15,000 kilometres probably through human facilitated global transport.

POSTER PRESENTATION

The effect of rotation crops, trash retention, weed control and prophylactic sprays on arthropod abundance in canola crops in south Western Australia

Svetlana Micic, Geoff Strickland, Tony Dore

Department of Agriculture and Food, Perth, WA, Australia

Canola (*Brassica napus* L.) is very susceptible to arthropod attack during the crop establishment phase. The earth mite complex, particularly the redlegged earth mite *Halotydeus destructor* (Tucker), is extremely damaging and can cause almost complete crop loss by killing seedlings. Other soil dwelling pests include weevils and beetles that chew on establishing crops. It is likely that the rapid adoption of minimum tillage farming systems has changed the soil environment to increase the abundance of these pests.

In response to increased arthropod abundance in the field, many farmers have resorted to the routine use of prophylactic sprays with synthetic pyrethroids to protect seedlings. Although cost effective and efficacious, the use of several consecutive synthetic pyrethroid sprays may increase the risk of insecticide resistance development in pests and be highly disruptive to beneficial species that could assist in the control of other pests later in the season.

Anecdotal evidence suggests that management practices such as weed control, trash retention and crop rotations may also influence the abundance of pests and beneficial species. These factors were investigated in replicated trials at two sites over two seasons. Our research showed that protecting canola from high populations of redlegged earth mites was essential to preserve yield. However, in low pest density situations the use of prophylactic sprays provided little or no benefit and adversely affected the populations of some beneficial species. These findings are discussed; including their relevance to recently reported high levels of resistance to synthetic pyrethroids in two redlegged mite populations in southern Western Australia.

POSTER PRESENTATION

High elevation emerging geometrid insect pests in the southwestern United States

Bobbe Fitzgibbon, Terry Rogers, Ann Lynch

USDA Forest Service, Flagstaff, Arizona, United States

Introduction: Since 1996, native geometrids have been responsible for 3 separate outbreaks at high elevations in the southwestern United States. Historically these insects were not known to cause damage. Speculation that climate change may be a factor in these outbreaks has led to the current study. Specimens taken at two of the outbreaks have both been identified as *Nepytia janetae;* the third geometrid has been identified as *Enypia griseata.* Adults of *N. janetae* were described in 1967 from collections made in Arizona and New Mexico. The larvae of the two insects identified as *Nepytia janetae* have been observed to have different feeding patterns, different elevational ranges and different host ranges in addition to physical differences. The third outbreak by a geometrid was found in a 2007 in Arizona. Significant tree mortality has been associated with heavy defoliation by the geometrids alone or in conjunction with secondary agents such as bark beetles and other defoliators.

Methods: Permanent plots have been set up at the sites of the first two outbreaks. Temperatures at the locations of outbreaks are being monitored and compared with historical data. Genetic testing will be necessary to determine if the insects identified as *N janetae* are indeed the same species.

Preliminary results: Mortality from the geometrid outbreak 1996-1999 varied by mountain range from 18 to 85%. Mortality due to the New Mexico *Nepytia janetae* outbreak 2005-2007 was already at 15% in the spring. Site factors do not appear to influence host susceptibility.

POSTER PRESENTATION

Biology and distribution of *Reduvius personatus* in two worlds

M. Javahery

McGill, Ste.Anne de Bellevue, Quebec, Canada

This work is a study of the biology of predatory *Reduvius personatus* (L.) from 1997-2008 in southeastern Canada. The distribution of this species was also studied from specimens in numerous collections from the "Old" and "New" worlds. Adults and nymphs were collected indoors and near light fixtures outdoors, in the southwest of Montreal. Breeding and rearing were carried out under variable temperatures from -10ºC in the winter to a maximum of 42ºC in the summer for ten years. Adults and nymphs were provided with flies and other soft-bodied insects or larvae. Nymphs did not feed during the winter and were resistance to cold temperatures. They lived for several weeks without food. The life cycle was completed after two winters of dormancy. Females appear from May to October, and lay 35 -138 eggs. Each egg has about 55 minuet micropilar processes. Embryonic development takes 2-3 weeks and over 90% of eggs hatch in July and August. Most of the first instars molt to second instars in 2-3 weeks in the summer. Cannibalistic behavior was observed in this species both during larval and adult stages. This *Reduvid* is not usually a harmful species towards humans. A comparison of data from biological studies made in Canada and the USA, versus those done in Europe indicates many similarities between populations of the Nearctic and Palearctic environments. Its distribution expands from 35º-55º in latitude north from west Europe to the east of the Caspian sea in the Palearctic, and 30º-50º north in the Nearctic regions.

POSTER PRESENTATION

Post-commercialization monitoring of Asian corn borer, O*strinia furnacalis* (Guenee), (Lepidoptera: Pyralidae)

Bonifacio Cayabyab[1], Edwin Alcantara[2], Augusto Sumalde[1], Wilma Cuaterno[3], Blair Siegried[4], Charisma Malenab[1], Jaynor Dangan[1], Josemari Belen[1]

[1]National Crop Protection Center - Crop Protection Cluster, Up Los Baños, Los Baños, Laguna, Philippines, [2]Institute of Molecular and Biotechnology, Los Baños, Laguna, Philippines, [3]Bureau of Plant Industry, Malate, Manila, Philippines, [4]Institute of Agriculture and Natural Resources, Department of Entomology University of Nebraska, Lincoln, Nebraska, United States

Since its approval for commercial use in 2002, farmer adoption of Bt-corn (Mon 810) had increased. About 300,000 hectares of total corn production area is planted to Bt-corn. Thus the Philippine is now ranked as #10 among 13 Biotech Mega-countries (James 2007). Post-commercialization monitoring of the performance of Bt-corn is required to detect the development of Asian Corn Borer (ACB), *Ostrinia furnacalis* (Guenee) resistance at the earliest possible time. This study attempted to estimate the frequency of Cry1Ab resistance alleles in the ACB using the F_2 screen described by Andow *et al*. (1998).

A total of two thousand twenty four (2,024) field-collected females of ACB were used to establish isofemale lines. Out of the surviving three hundred fifty three (353) isolines, twenty five thousand one hundred ninety seven (25,197) F_2 larvae were produced and found to be susceptible to Cry1Ab protein. Mortality rate for all of the isolines is at its peak during the first seven days of exposure to the toxin. A total of 800 isolines are expected to be tested in the duration of this study.

POSTER PRESENTATION

A SEM study of *Bovicola pelea*, a louse common to the Vaal Rhebuck (*Pelea capreolus*)

Martin Turner

University of Limpopo, Northern Province, South Africa

Introduction: Good morphological scanning electron microscopic (SEM) studies of lice are rare. This study provides new information as regards the micro-morphology of *Bovicola pelea*, a louse found on the Vaal Rhebuck, *Bovicola pelea*.

Methods: Live lice (9 males and 17 females) were collected and processed for electron microscopic viewing. Micromorphological features investigated included aspects of the head, thorax and abdomen and the appendages found on these three major body parts.

Results: A total average length of 1.1 mm was recorded for males and 1.25 for females. In both sexes, the forehead was markedly emarginated. The mandibles were notched and serrated. The medial groove was especially well developed. The antenna showed two large conical setae on a toothed distal segment. The antennal sensillae consisted of 12 apical pegs, 2 tuft organs protruding from 2 pore organs. The distal pore organ plate showed 2 radiate plate organs whilst the proximal plate showed 1. The mandibles were notched on the cutting edges and well serrated on the oral surfaces. Each leg bore an extended claw that closed toward a fixed appositional but shorter claw. Abdominal segments showed 6 pairs of spiracles, tergites and sternites with transverse rows of short setae. The gonopods covering the genital opening of the female displayed mitten-shaped claspers, slightly different to previously described light microscope images. Two large thoracic spiracles with hexagonal type of filtering apparatus were present.

Conclusions: This investigation should facilitate future identifications and morphological comparisons of this louse, by biologists, entomologists and veterinarians.

POSTER PRESENTATION

Identification of diapause-associated genes in the queen bumblebee, *Bombus terrestris*

Kyeong-Yeoll Lee[1], Dong-Woo Kim[1], Baek-Guen Kim[1], Mi-Sun Gong[1], Tae-Young Kwon[2], Yong-Jung Kwon[1]

[1]Kyungpook National University, Daegu, [2]Gyeongbuk Provincial Agricultural Technology Administration, Daegu, Republic of Korea

Introduction: *Bombus terrestris* is an economically important pollinator for greenhouse crops. To determine the mechanism of diapause regulation in adult queens of bumblebee we identified genes that associated with diapause and demonstrated whether those genes are regulated in relation to diapause process.

Methods: Diapause-associated genes were selected in the brains of queens using suppressive subtractive hybridization. In addition, genes that synthesize three heat shock proteins (*shsp, hsc70 and hsp90*) and vitellogenin were identified from queen's ovary and the fat bodies, respectively. Using Northern hybridization expression patterns of those genes were compared from six different stages in relation to diapause; pre-diapause, diapause initiation, chilling for 1, 2 and 3 months, and post-diapause.

Results: At the queen's brain the levels of three genes (*glucocerebrosidase*, *actin* and *glucose oxidase*) were high at pre- and post-diapause stages but downregulated during diapause. Particularly, the expression of both glucocerebrosidase and glucose oxidase were brain-specific when it compared with other tissues. At the queen's ovary both *hsc70* and *hsp90* levels downregulated whereas the *shsp* level was upregulated during diapause, especially chilling period. At the queen's fat bodies the vitellogenin gene was shut down at diapause initiation and upregulated after the completion of diapause.

Conclusions: Our results indicated that queens suppressed biochemical processes regarding metabolism and reproduction in relation to diapause. However, queens activated a unique process in the ovary, such as stress resistance, during diapause. Our results provide information that can be used for the control of diapause mechanism of important pollinator insect.

POSTER PRESENTATION

Fluctuation and population density of *Bemisia tabaci* (Genn.) on different host plants

Muhammad Arshad, Muhammad Shuaib, Yasir Ahmad, Abdul Ghani Lanjar

[1]Agriculture University Tando Jam, Sindh, Pakistan, [2]Community IPM Project, Punjab, Pakistan

Introduction: The population density of *Bemisia tabaci* (Genn.) was studied on different host plants during spring to summer season 2005

Methods: Seeds of sunflower (HO-1 variety), okra (Subz pari variety) and cotton (Hari dost, Reshmi and Niab-78 varieties) were sown. Weekly observations on the occurrences of whitefly were taken after germination till crop harvesting. Pest population was recorded from entire plant of each host plant those were randomly selected from field.

Results: The results indicate that *B. tabaci* appeared on sunflower from 15th March to May. Two peaks in population (5.60 ± 1.02) and (3.80 ± 0.89) per leaf were recorded in 3rd week of March and 1st week of May respectively. On okra highest population (9.04 ± 1.85) and (5.04 ± 1.28) was recorded in 3rd week of April and 4th week of May respectively. NIAB-78 variety of cotton harbored maximum population (9.32 ± 1.45), (7.44 ± 142) and (6.32 ± 1.23) in 2nd week of May, June and July, respectively. The peaks in *B. tabaci* population on Hari dost and Rashmi were also recorded in the same weeks. The population 7.04 ± 1.02, 5.36 ± 1.01 and 4.80 ± 0.86 on Hari dost and 5.68 ± 0.96, 4.52 ± 0.68 and 3.60 ± 0.74 on Rashmi was recorded, respectively.

Conclusions: The analysis of variance showed that there was non-significant difference between crops. However, LSD test showed non-significant difference in population of whitefly appeared on okra, sunflower and cotton variety Hari dost only. No impact of weather conditions was observed on population fluctuation of whitefly except crop stage.

POSTER PRESENTATION

Laboratory test on the response of acorn weevil, *Curculio glandium* (Coleoptera: Curculionidae) last instar larvae against entomopathogenic nematodes *Steinernema bicornutum* and *Heterorbabditis bacteriophora*

Mostafa Nikdel[1], Golamreza Niknam[2], Mahmood Shojaee[1], Hassan Askari[3], S.Abulghasem Mohammadi[2]

[1]Agriculture and Natural Resources Research Center of East-Azarbaijan province, Tabriz, [2]Faculty of Agriculture, University of Tabriz, Tabriz [3]Iranian Research Institute of Plant Protection, Tehran, Islamic Republic of Iran

Introduction: The acorn weevil, *Curculio glandium* Marsham is an important forest pest of oak trees in most of countries as well as Iran. The pest disturbs regeneration of host trees by feeding on their acorn. Need to control the pest and due to the limitations which are imposed by chemical pesticides application in natural resources, indigenous EPNs, *Heterorhabditis bacteriophora* and *Steinernema bicornutum* were tested against fifth instar larvae of acorn weevil of Arasbaran forest under laboratory conditions.

Methods: In the first experiment, penetration assay test was conducted using a suspension of 4000 IJs of the EPNs per 1 ml distilled water in multi–well plates. The plates were incubated for 12 h. at 25ºC and dead larvae dissected. In the second experiment, *H. bacteriophora* and *S. bicornutum* were applied at different concentrations (0, 150, 250, 500, 1000 and 2000 IJs per 1ml of distilled water) to test their ability to parasitize *C. glandium* fifth instar larvae in the 9 cm petri plates lined with filter papers. The experiments were conducted at two temperature ranges (21-24ºC and 25-28ºC).

Results: Penetration percentage was %1.6 and %0.55 for *H. bacteriophora* and *S. bicornutum*, respectively. Maximum mortality caused by *H. bacteriophora* and *S. bicornutum* were %58.3, %25 (at 21-24ºC) and %63.5, %30.5 (at25-28ºC), respectively. Analysis of variance revealed significant nematode specie and concentration as well as temperature effects on larva mortality. With increased concentration of nematode and temperature, larva mortality was increased. Based on probit analysis, LC50 of *H. bacteriophora* under two temperature ranges of 21-24ºC and 25 -28ºC were determined 1331 and 1037 IJs/ml, respectively. Regression analysis showed significant relationship between concentrations and larval mortality in the both of nematodes under two temperature ranges.

Conclusions: The highest penetration in larva and the highest mortality of fifth instar larvae of *C. glandium* was observed for *H. bacteriophora* under the both temperature ranges.

POSTER PRESENTATION

Distribution of Natal fruit fly, *Ceratitis rosa* Karsch (Diptera: Tephritidae), and false codling moth, *Thaumatotibia leucotreta* (Meyrick) (Lepidoptera: Tortricidae), two pests of citrus, in South Africa

Marelize de Villiers[1], Vaughan Hattingh[2]

[1]Department of Conservation Ecology & Entomology, Faculty of AgriSciences, Stellenbosch University, Private Bag X1, Matieland 7602, Stellenbosch, South Africa, [2]Citrus Research International, P.O. Box 2201, Matieland 7602, Stellenbosch, South Africa

Introduction: Natal fruit fly, *Ceratitis rosa* Karsch, and false codling moth, *Thaumatotibia leucotreta* (Meyrick), are pests of some South African fruit. Due to phytosanitary concern, these pests hinder international fruit trade. Knowing their current distribution, their potential global distribution can be modelled and the relevance of associated phytosanitary regulations evaluated.

Methods: Bucket traps baited with three-component BioLure®, and delta traps baited with pheromone, were placed in different South African climatic regions to trap *C. rosa* and *T. leucotreta* respectively. Three traps, serviced monthly, were used per monitoring area. Relative abundance, as a percentage of maximum monthly counts, was determined for months with highest and lowest abundance.

Results: Generally *C. rosa* was absent or had low abundance in regions with hot, dry summers. *Thaumatotibia leucotreta* occurred across all climatic regions, with localised occurrence of both highest abundance and apparent absence within the same climatic regions. Abundance was moderate but consistent across time and space in the south and east coastal regions, and the north-eastern part of the country, with warm or hot, rainy summers but varying winters.

Conclusions: This abundance distribution of *C. rosa* seemingly corresponded with climatic differences, suggesting it is a good candidate for modelling its potential global distribution based on climate. *Thaumatotibia leucotreta* did not show an abundance distribution pattern corresponding with climatic regions, suggesting that relative abundance is probably more sensitive to factors like host availability than to restrictions imposed by the climatic range covered during the study.

POSTER PRESENTATION

Pathogenicity and protease production relationship between three isolates of *Metarhizium anisopliae* Metch. on *Eurygaster integriceps* Puton (Hemiptera: Scutelleridae)

Mehdi Tork, Ali R. Bandani, Marjan Seyedi

Plant Protection Department, Faculty of Agriculture, University of Tehran, Karaj, Islamic Republic of Iran

Introduction: Sunn pest *Eurygaster integriceps* (Hem: Scutelleridae) is the major pest which causes serious damage to wheat and barley in the Middle East and some other countries. To control the pest, each year hectares of crops sprayed with pesticides. Entomopathogenic fungi can be used in the pest management procedures in order to reduce pesticide use. *Metarhizium anisopliae* Metch. is one of the most important fungi which are used in biological control of insect pests. So, the aim of the current study is to investigate virulence and enzyme production of three isolates including 4556, 3297 and M189 of *M.* anisopliae on Sunn pest.

Materials and Methods: Fungi were cultured on SDAY medial culture and maintained at 25 ± 2 ^{o}C and photoperiod of 16: 8 (L:D). After two weeks that sporulation occurred spores were taken and used for dipping bioassays. After determination of pathogenicity, logarithmic doses including 1×10^{4}, 1×10^{5}, 1×10^{6}, 1×10^{7} and 1×10^{8} spore/ml were prepared.

To study enzyme production, spores of these isolates were separately cultured in minimum media with 1% insect cuticle and left in shaker (130 rpm) for 10 days at 25 ± 2 ^{o}C. Protease activity was measured using Suc – Ala –Ala – Pro – Phe – pNA as substrate.

Results: The results showed that LC_{50} of 4556, 3297 and M 189 was 3.38×10^{5}, 5.60×10^{5} and 7.70×10^{5}, respectively. As can be seen 4556 isolate was most virulence than the two other isolates. Enzyme assays showed that enzyme production in 4556 isolate was more than the other two isolates (3297 and M198 isolates).

Conclusions: So, it was shown that there is a relative relationship between enzyme production and pathogen virulence.

POSTER PRESENTATION

Detection of two new species of the genus *Torymus* (Hymenoptera: Torymidae) parasitizing *Celticecis japonica* (Diptera: Cecidomyiidae) in Japan

Kazunori Matsuo

Kyushu University, Fukuoka, Japan

Introduction: Three parasitoid species, *Eupelmus urozonus* (Hymenoptera: Eupelmidae), *Torymus* sp. (Hymenoptera: Torymidae), and an unidentified endoparasitoid, have been known to attack larvae of *Celticecis japonica* Yukawa and Tsuda (Diptera: Cecidomyiidae) that induces galls on leaves and twigs of *Celtis sinensis* var. *japonica* and *C. jessoensis* (Ulmaceae) in Japan. Recently, I reared *Torymus* spp. from the galls induced by *C. japonica* and tried to identify these species.

Methods: I examined specimens obtained from galls of *C. japonica* in Japan by referring to the original descriptions of *T. diabolus* Moser and *T. huberi* (Hoffmeyer) that have been known to attack *Celticecis spiniformis* and an unidentified gall midge inducing galls on *Celtis* sp. in the Nearctic Region. I also compared the *Torymus* spp. from *Celtis* in Japan with 12 known species of *Torymus* attacking hosts other than *C. japonica* in Japan.

Results: I recognized three species of *Torymus* among the specimens reared from the galls of *C. japonica*. Two of them are distinguishable from *T. diabolus*, *T. huberi* and the 12 Japanese species of *Torymus*. The remaining species is not treated in this presentation because of the insufficient number of specimens.

Conclusions: The two species of *Torymus* seem to be new to science. One of them belongs to the *T. ercarum* species group, which was defined by Graham and Gijswijt (1998) and is known to parasitize Cynipidae inducing galls on *Quercus* spp. (Fagaceae) in the Palaearctic Region. The other new species does not belong to any species group in the Palaearctic Region.

POSTER PRESENTATION

Study on spider mites of plum and cherry orchard and biology of brown mite, *Bryobia rubrioculus* (Sheuten) (Acari: Tetranychidae) in Hamedan, Iran

Mohammad Khanjani, Amir Hosein Eghbalian

Bu Ali Sina University, Hamedan, Islamic Republic of Iran

Spider mites are important pests on plum and cherry trees. Study on spider mites associated with plum and cherry trees was carried out during 2005-2006 in west (Hamedan) of Iran。 In this study were collected four pider mites in phytophous role, their scientific names as follow: *Bryobia rurioculus* (Scheuten), *Eutetranychus orientalis* (Klein,, *Tetranychus turkestani* (Ugarov & Nikolski)) and *T. urticae* Koch Amongst them, brown mite was high level of population. At present this pest is one of the most important pests of cherry, plum and cherry trees in west of Iran. This pest was found bluntly on plum and cherry trees It causes considerable damage in some orchards of this area. So, its biology was studied during 2005-2006. The result showed that, this pest over wintered as egg on fruit trees shoots. The larvae of first generation appear early in April; at temperature 10.58 ℃. This pest creates 4-5 generations per year. Its high population was occurred in September in Hamedan orchards.

POSTER PRESENTATION

New observations on temperature increase due to maggot mass effect

Damien Charabidze[1], Didier Gosset[1], Benoit Bourel[2]

[1]Université Lille 2, Lille, France, [2]Faculté Libre des Sciences et Technologies, Lille, France

Introduction: The estimation of *post-mortem* interval in forensic entomology is related to the temperature of the environment in which maggots develop. Nevertheless, the activity of a maggot mass on a body can lead to a local increase in temperature. Difference between ambient and mass temperature range from 10°C to 15°C and temperature up to 45°C inside the maggot mass have been already observed in field experiments. Nevertheless, this complex phenomenon is not easy to characterise and little experimental data under controlled conditions has been documented so far.

Temperature increase seems to be linked to the local maggot density and the mass volume. Some studies indicate that the so-called maggot-mass effect usually begins when the larvae reach the end of the second instar, and continues until the post-feeding stage. Infrared thermometry has shown that larvae can store or generate heat, following a relationship proportional with the number of individuals; however the exact cause and its dynamics are still unknown.

Methods: Our measurements on *Protophormia terraenovae* maggot masses were performed using constant external temperatures and fixed number of larvae.

Results: Results show an important increase of temperature (up to 10°C), also for first second larvae less than 5 mm length, and a strong dependence to external temperature. Furthermore, heat generation increase linearly with the number of larvae, and rapidly extinguished in absence of food. Together, these results suggest that the heat is generated due to metabolic digestive process instead of friction between larvae.

Conclusion: The understanding of this phenomenon is determinant for forensic entomologists. The relationships between external temperature, number of maggots end heat production are used in the laboratory for modelling the development of maggots. The aim of the global project is the creation of a support decision system (SDS) applied in forensic entomology.

POSTER PRESENTATION

The main biotic limiting factors of gypsy moth (*Lymantria dispar* L.) populations in oak stands in southern Romania

Irinel Constantineanu, Raoul Constantineanu, Camil Stefan Lungu-Constantineanu, Romica Tomescu

[1]Biological Research Institute, Iasi, Romania, [2]Forest Research and Management Institute, Bucharest, Romania

Introduction: Researches were proceeded in 37 oak stands in Southern Romania affected by gypsy moth attack, where the authors recorded parasitoids and predators of immature stages of this defoliator and only one case of adult predation. Observations concerning those biotic mortality factors were achieved both in nontreated stands and in stands with integrated and microbiological treatements.

Methods: All observations and collects of immature stages (egg clusters, caterpillars and pupae) were made in the same plots. Each ones was isolated and kept in a climatological chamber. The parasitoid hatching was watched daily. For predators, the authors did field observations and watching the efficiency on their prey.

Results: The analyzed *Lymantria dispar* populations were limited by a complex of 34 primary parasitoids (33 parasitoid insect species and 1 nematod species – *Hexamermis albicans* Sieb.) and by 7 predator insect species and 1 avian species – *Coleus monedula* L. The most efficient parasitoids were *Exorista larvarum* L. and *Compsilura concinnata* Meig. (Diptera), the first one especially for pupae and the second one for larvae, while Hymenoptera species have had a less important role. *Dermestes erichsonii* Gnglb. (oophagous) and *Calosoma sycophanta* L. (for all stages) were the most efficient predators. Researches showed that the parasitization degree on *L. dispar* populations had varied between 16,5 % and 78,6 %, the highest pasitization degrees were achieved in nontreated stands and in those with microbiological treatments. We consider that in the studied oak stands, entomofagi were ones of the main limiting factors of *L. dispar* populations.

POSTER PRESENTATION

Head-shape convergences in lauxaniid flies (Diptera: Acalyptratae: Lauxaniidae): New light from an undescribed southern African taxon of trigonometopine flies?

Gregory Davies[1], Raymond Miller[2]

[1]Department of Natural Sciences, Natal Museum, Pietermaritzburg, KwaZulu-Natal, South Africa, [2]School of Biological and Conservation Sciences, University of KwaZulu-Natal, Pietermaritzburg, KwaZulu-Natal, South Africa

Lauxaniid flies (Diptera: Acalyptratae: Lauxaniidae) are renowned for their morphological diversity relative to other acalyptrate fly families. J.F. McAlpine commented in the landmark *Manual of Nearctic Diptera* on the "extraordinary morphological plasticity" shown by lauxaniids (McAlpine 1989: 1445). One long-standing problem in lauxaniid morphology is the occurrence of what can be termed the "trigonometopine syndrome". This body form is classically shown by the genus *Trigonometopus* Macquart, and comprises a sub-triangular head with elongated postfrons and generally receding prefrons, and to a lesser extent, a narrow thorax and abdomen, and elongated wings. Wheeler (1956) suggested all these flies represented a monophylum, which he even elevated to family status (Trigonometopidae). Future lauxaniid researchers have unanimously rejected such a proposal, suggesting that the similarity is due to convergence, possibly as the result of living amongst upright grass stems (Stuckenberg 1971: 516).

In this poster we highlight an undescribed genus of lauxaniid found in *Protea*-rich montane grassland and fynbos in South Africa that adds another example to the "trigonometopine syndrome". The genus consists of six species, all undescribed, which fall into two distinct clades. Our observations suggest that this genus is not closely related to other "trigonometopine syndrome" genera, adding evidence to multiple derivation of this morphology (i.e. convergence). Interestingly, the new genus includes species that have an unmodified head-shape, potentially throwing light on how a trigonometopine head-form evolves.

POSTER PRESENTATION

Chitinase inhibitors to manage aphids

Philippe Giordanengo, Julien Saguez, Charles Vincent

[1]Université de Picardie Jules Verne, Amiens, France, [2]Agriculture and Agri-Food Canada, Québec, Canada, [3]Agriculture and Agri-Food Canada, Québec, Canada

Introduction: Chitin is the main component of exoskeletton, trachea and peritrophic matrix of insects. Thus chitin metabolism appears an interesting target to manage insect pests. During post-embryonic development, the molting process involves chitinase activities to hydrolyze chitin and degrade the old cuticle. While chitin synthase has been widely used as target by numerous pesticides, chitinase has received much less attention. However, chitinase inhibitors have been reported for their toxic effects against bacteria, fungi and also insects. We investigate the relevance of different chitinase inhibitors in controlling the potato aphids *Myzus persicae* Sulzer and *Macrosiphum euphorbiae* Thomas which are among the main vectors of viruses on potato crop.

Methods: Two cyclic dipeptides, cyclo-(Proline-Tyrosine) and cyclo-(Histidine-Proline), the pseudotrisaccharide allosamidin and psammaplin A, a brominated tyrosine-derived compound, were selected owing to their different structure and mode of action on chitinases.

To evaluate their effects, the 4 chitinase inhibitors were delivered to aphids *M. persicae* and *M. euphorbiae* via a artificial diet. Nymphal survival, prereproductive period ,adult emergence and reproduction were recorded daily. These parameters were used to calculate the intrinsic rate of natural increase of the aphids populations.

Results: Cyclic dipeptides induced no or slight effects on aphids survival and performance. Aphids fed with allosamidin showed significantly reduced nymp survival and daily fecundity. Finally, psammaplin A used as food intake led to the complete death of the nymphs.

Conclusions: The present results demonstrated for the first time differential aphicidal effects of chitinase inhibitors of different nature on the polyphagous aphids *M. persicae* and *M. euphorbiae.* On the basis of observed developmental alterations, a hypothesis of the mode of action of these compounds is proposed. In the context of crop protection, our results highlight the interest of such strategy that has been shown relevant against bacteria and phytopathogenic fungi to control insect populations.

POSTER PRESENTATION

Does insecticide application in oilseed rape affect root fly damage of radish?

Nur Ahmed, Inger Åhman, Mats Lieberg, Eva Johansson

[1]Swedish University of Agricultural Sciences, Department of Agriculture-Farming System, Technology and Product Quality, Box No. 104 Alnarp, SE-230 53, Sweden, [2]Swedish University of Agricultural Sciences, Department of Agriculture-Farming System, Technology and Product Quality, Box No. 104 Alnarp,SE-230 53, Sweden, [3]Swedish University of Agricultural Sciences, Department of Agriculture-Farming System, Technology and Product Quality, Box No. 104 Alnarp, SE-230 53, Sweden, [4]Swedish University of Agricultural Sciences, Department of Landscape Architecture, Box No. 58 Alnarp, SE-230 53, Sweden.

Introduction: A chemical based strategy is most commonly used for pest control in agriculture, contributing to a high agricultural production and productivity. Insecticide side effects have been investigated in several studies. Investigations about influences of insecticide applications in fields on pests in neighbouring crops are more limited, especially so in near-by garden crops. Gardens and neighbouring farmers' fields may exchange pests via migration. The aim of the present investigation was to study influences and interchanges of pests between farmers' fields, sprayed and unsprayed, and neighbouring garden crops.

Methodology: Oilseed rape (*Brassica napus*) was established as a farmers' field crop and radish (*Raphanus sativus*) as a neighbouring garden crop. The field trial was carried out in Southern Sweden. In the corners of a rapeseed field (100 X 150m), three radish plots (2 x 1.5 m; 3.6 m apart) were sown in each direction; with new plots of radishes sown repeatedly during the season. Half of the oilseed rape area (100 X 77.5m) was treated with insecticides against flea beetles (*Phyllotreta* spp.) and pollen beetles (*Meligethes* spp.) according to recommendations by the Swedish Board of Agriculture. Root damage by root flies (*Delia* spp.) was recorded in the radish crop.

Results: In the urban fringe, private gardens are often situated adjacent to farmers' fields. This opens up for opinions on farming activities such as pesticide use. Also, chemical pest control in farmers' fields might affect the pest situation in private gardens. The preliminary results from this study indicate that radish plots closest to the oilseed rape have more root fly damage compared to plots further away from the field. No significant differences between plots nearby the treated versus the untreated side of the field were found.

POSTER PRESENTATION

Resitance of wild *Solanum* species against potato aphids

Vincent Le Roux, Charles Vincent, Sébastien Dugravot, Erick Campan, Philippe Giordanengo

[1]Université de Picardie Jules Verne, Amiens, France, [2]Agriculture and Agri-Food Canada, Québec, Canada, [3]INRA Agrocampus Rennes, Rennes, France, [4]UMR CNRS 5172, Toulouse, France, [5]Université de Picardie Jules Verne, Amiens, France

Introduction: Wild *Solanum* species related to the cultivated potato present a high genetic diversity. These materials are used by breeders to improve potato crop for resistance or tolerance characteristics such as resistance to insect pests. In this context we have determined the nature of resistance of 8 wild *Solanum* accessions (5 species) against aphids, vector of viruses.

Methods: We used three complementary experiments (physiology, olfactometry and electropenetrography) to determine the antixenosis or antibiosis resistance of wild *Solanum* and localization of resistance factors within plant tissues.

Results: None of the wild *Solanum* species had repulsive effects on aphids that precluded involvement of wild *Solanum* volatiles in resistance. We report for the first time at once antibiosis and antixenosis resistance of wild *Solanum* species against *M. euphorbiae*. At the opposite, resistance exhibited by all wild *Solanum* accessions was antixenosis against *M. persicae*.

Conclusions: Antixenosis against *M. persicae* seems to be widespread in the *Solanum* species when comparing our results with published works. However important variability in localization of antixenosis factors within plant tissues was determined between wild *Solanum* species and even between accessions of the same species, suggesting involvement of several resistance mechanisms. For a given wild *Solanum* accession resistance variability was also observed according to the two aphid species. To explain antixenosis or antibiosis, possible resistance mechanisms are discussed. Determining the nature of resistance of wild *Solanum* is essential to potato breeders to introduce resistant traits in the cultivated potato allowing creation of new resistant cultivars.

POSTER PRESENTATION

Effects of plant age and development on the *Mi-1.2*- mediated resistance of tomato against whitefly *Bemisia tabaci*

Clara I. Rodríguez, Mariano Muñiz, Gloria Nombela

Institute for Agricultural Sciences - Consejo Superior de Investigaciones Científicas (CSIC), Madrid, Spain

The sweetpotato whitefly *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) is an important pest of horticultural crops worldwide. This insect causes damage directly through phloem feeding or indirectly by transmission of plant viruses such as Tomato Yellow Leaf Curl Diseases (TYLCDs). The tomato gene *Mi-1.2* is responsible for resistance against the B and Q biotypes of *B. tabaci,* in addition to three species of root-knot nematodes (*Meloidogyne* spp.) and the potato aphid (*Macrosiphum euphorbiae*). It is known that tomato plants carrying *Mi-1.2* are resistant to root-knot nematodes early in development: seedlings inoculated at 24 hours after germination are resistant to nematode infection. In contrast, the *Mi-1.2*-mediated resistance against potato aphid is developmentally regulated, with fully expanded leaves becoming resistant only when plants are 4 to 5 weeks of age. We have observed *Mi-1.2*-regulated resistance to *B. tabaci* in 8-week old tomato plants but not in other experiments with younger plants. However, a definitive study lacked to investigate whether *Mi-1.2*-mediated resistance against *B. tabaci* is developmentally regulated. Two sets of assays have been carried out in the present study, with tomato plants cv. Motelle (with *Mi-1.2*) and Moneymaker (lacking *Mi-1.2*) under free-choice and no-choice conditions, to determine if plant age or development could have any effect on whitefly resistance. In the first set of assays, 3-, 5- and 8-week old plants were compared. In the second set of assays, two groups of 8-week old plants were compared, which had been grown under different temperatures (24 or 19ºC) to obtain different plant developments.

POSTER PRESENTATION

Leaf beetle fauna of the Mecsek Hills (southern Hungary) (Coleoptera: Chrysomelidae)

Károly Vig

Savaria Museum, Szombathely, Hungary

Introduction: The aim of this study was to obtain data on the leaf beetle fauna of the Mecsek Hills (Baranya County, southern Hungary).

Methods: The present account is based on the material preserved mainly in Janus Pannonius Museum (Pécs) and Hungarian Natural History Museum (Budapest) as well as on literature sources.

Results: A total of 352 leaf beetle species are listed from Mecsek Hills. In spite of the fact that Mecsek is one of the most diverse mountainous areas in Hungary, the overwhelming majority of the species is common and widely distributed in the forest steppes and forested hilly and lower mountainous districts of the country. It should be also pointed out, that a considerable number of locality data are very old and sometimes unreliable. From faunistical point of view the most remarkable species are *Oulema rufocyanea, Cheilotoma musciformis, Smaragdina flavicollis, Eupales ulema, Luperus rugifrons, Phyllotreta christinae, Aphthona herbigrada, Longitarsus lateripunctatus personatus, Neocrepidodera nigritula, Apteropeda orbiculata*. Two species (*Smaragdina graeca, Cryptocephalus bameuli*) are new to Hungarian fauna. The presence of *Cryptocephalus bicolor, Chrysolina fimbrialis, C. purpurascens rufocuprea, Chrysomela tremula, Longitarsus curtus, Longitarsus junicola, Longitarsus nanus, Neocrepidodera femorata, Dibolia cynoglossi, Psylliodes cupreatus* needs further confirmation. The occurrence of twenty-four species (i. e. *Pachybrachis hippophaes, P. pallidulus suturalis, Cryptocephalus rufipes, Timarcha corinthia, Chrysolina geminata, Sclerophaedon orbicularis, Longitarsus aeruginosus, L. ferrugineus, L. nigerrimus, L. suturatus, Neocrepidodera impressa, Podagrica fuscipes, Psylliodes marcidus, Hypocassida meridionalis*) is inconceivable in the territory, The identity of *Smaragdina tibialis hungarica* needs further examination.

POSTER PRESENTATION

Biocide effect of essentials oils extracted from *Capsicum annuum* (Solanaceae), *Zingiber officinale* (Zingiberaceae) and *Piper nigrum* (Piperaceae) on *Anopheles gambiae* Giles 1902 Diptera: Culicidae), a vector of malaria

Foko Daji Gisele Aurelie

University of Yaounde I, Yaounde, Cameroon

Malaria remains one of the major causes of morbidity and mortality worldwide. Integration of disease treatment with vector control is considered as the most effective means of disease control. The use of native plants with insecticidal properties is a new approach in the fight against malaria vectors. Volatile oils extracted by hydrodistillation from tree plants species obtained from the Agronomic Research Institute for Development (Yaounde-Cameroun), *Capsicum annuum* (*Solanaceae*) yellow and red varieties, *Zingiber officinale* (*Zingiberaceae*) and *Piper nigrum* (*Piperaceae)* were evaluate toxicity on adults of *Anopheles gambiae* under laboratory conditions using WHO cones covered with volatile oils treated nets. Oils dissolved in acetone, were tested at 7.8 %, 3.9 %, 2 %, 1 % and 0.3 % (w/v). The results showed that: the knockdown effect 3min after contact, with the adults of *An. gambiae* is superior to 95% for the oils extracted from *C. annuum* and *Z. officinale* at concentrations 7.8% and 3.9% this effect is of 70% with the *P. nigrum* oil at concentration 7.8% and 3.9%. 60min after the knockdown effect is superior to 90% for oils extracted from *C. annuum* and *Z. officinale* at concentration 7.8% this effect is of 63% with the *P. nigrum* oil. 60min after the knockdown effect is superior to 80% for oils extracted from *C. annuum* and *Z. officinale* at concentration 3.9% this effect is of 46% with the *P. nigrum* oil. 24 hours after, for the concentrations 7.8% and 3.9%, the mortality rate of adults is in average 90% for the oils extracted from *C. annuum* and *Z. officinale*. This rate is in average 45% with *P. nigrum* oil. *C. annuum* and *Z. officinale* seem this to be very useful for the control of adults of *An. gambiae*. Field trails should be carried out, particularly to evaluate the operational feasibility and dermal toxicity over a long period, especially to infants and children. It is important to determine whether widespread use of one of these biocides would produce an overall reduction of vector biting in a community.

POSTER PRESENTATION

Optimization of carbon:nitrogen ratio for *Beauveria bassiana* and *Metarhizium anisopliae* conidia production for bioassays against larvae of *Anopheles arabiensis*, a major African malaria vector

Luisa Nardini, Vince Gray

University of the Witwatersrand, Johannesburg, Gauteng, South Africa

Introduction: Mycelium and spores of the entomopathogenic Hyphomycetes, *Beauveria bassiana* and *Metarhizium anisopliae*, were produced using a diphasic fermentation process. Conidia produced from optimized diphasic culture were harvested and their pathogenicity tested against *Anopheles arabiensis* larvae. Infection was confirmed by electron microscopy.

Methods: The first phase of the diphasic fermentation involved liquid culture where the influence of different concentrations of sucrose, maltose, glucose and yeast extract, and different ratios of these nutrient sources, on mycelial growth was investigated. The second phase of fermentation (solid substrate) was initiated using fungi that had been cultured in broth solutions that produced optimum conidial yields in sporulation studies. The dried spores were harvested and tested against *An. arabiensis* larvae. For comparative purposes, a commercial preparation of *B. bassiana* was also tested.

Results: High spore yields were obtained for both *B. bassiana* and *M. anisopliae* indicating that liquid phase culture optimization was successful. All preparations were found to be pathogenic to the mosquito larvae and produced acceptable LT_{50} values, where at a spore concentration of 10^7 conidia.cm^{-2} high levels of mortality occurred and LT_{50} values of 43, 89 and 41 hours for *M. anisopliae, B. bassiana* and *B. bassiana* (commercial preparation) respectively, were obtained.

Conclusions: Diphasic fermentation proved to be a successful means for producing infectious spores of *B. bassiana* and *M. anisopliae*. The spores were able to cause infection in *An. arabiensis* larvae, as confirmed by electron microscopy. Furthermore, the spores that we produced by biphasic fermentation produced similar LT_{50} values to that obtained from a commercial preparation of *B. bassiana*.

POSTER PRESENTATION

Dose-dependent effects of Gal4 affects the development of *Drosophila melanogaster*

Fernanda Humann, Klaus Hartfelder, Maria Luisa Paçó-Larson

Universidade de São Paulo, Ribeirão Preto, São Paulo, Brazil

Introduction: The Gal4-upstream activating sequences (UAS) system is the most widely used strategy for achieving spatially restricted gene expression in *Drosophila*. Since UAS sequences are not found in the *D. melanogaster* genome, it is assumed that Gal4 drives the expression of UAS targeted genes without affecting neighboring tissues. We demonstrate here that this assumption has to be viewed with a *caveat* and that the expression of Gal4 may affect viability in ad dose-dependent manner.

Methods: We evaluated the viability of three *Drosophila* lines expressing Gal4. Two of these express Gal4 specifically in the ring gland and oenocytes: the one developed by us carries a 67 bp activator (RG67bp) from a DNA puff gene as a driver, the second is an enhancer-trap (PO206), and in the third line, the driver is an enhancer of an actin gene (Bloomington #3954). As control we used the parental line *yw.*

Results: The RG67bp line was not viable when grown at 25^0C and could only survive at 18^0C, a condition where Gal4 activity levels in *Drosophila* are diminished. In contrast, the PO206 line, which expresses Gal4 in the same tissues as RG67bp, could be maintained at 25^0C, albeit at a much reduced viability (38%) compared to the control. The actin-enhancer line, which ubiquitously expresses Gal4, also showed reduced viability (58%).

Conclusion: Gal4 can have adverse effects on *D. melanogaster* development, especially when expressed at high levels. This should be considered when interpreting results obtained from Gal4 constructs.

Financial Support: FAPESP

POSTER PRESENTATION

A phylogenetic analysis of armoured scale insects, based upon nuclear, mitochondrial, and endosymbiont gene sequences

Jeremy C. Andersen, Jin Wu, Matthew E. Gruwell, Geoffrey E. Morse, Sharlene Santana, Natalie Feliciano, Rodger Gwiazdowski, Benjamin B. Normark

University of Massachusetts Amherst, Amherst, Massachusetts, United States

Armoured scale insects (Diaspididae) are the most species-rich family of scale insects and one of the most economically important. They are promising subjects for the evolutionary study of physiology (no complete gut), genetics (chimerism, paternal genome elimination, frequent parthenogenesis) and coevolution (with host plants, parasitoids, *Septobasidium* fungi, endosymbiotic bacteria). Here we present an expanded molecular-phylogenetic analysis of relationships within this family. Our data matrix consists of fragments of two nuclear genes (elongation factor 1-alpha and the large subunit of ribosomal DNA), a mitochondrial region (cytochrome oxidase I-II), and a gene from the vertically transmitted primary endosymbiont *Uzinura diaspidicola* (small ribosomal subunit), with a combined total of 3523 base pairs. The terminal taxonomic units in the matrix are 256 individuals, representing over 123 species in 6 tribes. We find evidence for no more than two origins of paternal genome elimination.

POSTER PRESENTATION

Eye size in aphids

Thomas Döring[1], Johannes Spaethe[2]

[1]Imperial College London, Ascot, United Kingdom, [2]University of Vienna, Vienna, Austria

Introduction: Aphids lead a risky life when it comes to finding new host plants. Since vision plays a major role in finding suitable hosts, the animal's visual capabilities largely determine the success of locating food sources.

Methods: We measured several eye parameters, including vertical eye length (EL), and diameter of ommatidial lenses in the centre of the eye, as well as other morphological parameters, including total thorax length (TTL), in winged females of 24 aphid species. The animals, mainly from the sub-families Aphidinae and Calaphidinae, were collected from various field sites in the UK and Germany and from laboratory cultures. All measurements were done electronically (on-screen) on live pictures produced by a digital camera connected to a microscope and a PC. Five animals were measured per species on both the left and right eye. In some samples, the number of ommatidia per compound eye could be directly counted.

Results: The largest aphid was *Lachnus roboris* (TTL=1.52±0.03mm, mean±s.e.), the smallest was *Tuberculatus querceus* (TTL=0.51±0.01). Generally, eye size scaled positively with body size (EL vs. TTL: r^2=0.73, n=24). The ommatidial diameter (mean 0.010 mm) ranged from 0.008 mm (in the relatively small *Tinocallis takachihoensis*) to 0.016 mm (in the large *Tuberolachnus salignus*). The number of ommatidia per eye ranged from 127 (in *Rhopalosiphum padi*) to 268 (*Euceraphis betulae*). The mean divergence angle of ommatidia over all species was 7.6 degrees.

Conclusions: Our morphological measurements show that aphids, with their relatively few ommatidia and large interommatidial angles, have presumably a low spatial resolution.

POSTER PRESENTATION

Diversity and distribution of Collembola of Brazil: Relationships between systematics and the biodiversity crisis

Mark Culik

Instituto Capixaba de Pesquisa, Assistência Técnica e Extensão Rural – INCAPER, Vitória, Espírito Santo, Brazil

Collembola, common in soils throughout the world, are little known but important organisms because of their influences on soil fertility. This study provides an update on diversity and distribution of Collembola of Brazil based on a review of the literature and discusses this information and related observations with respect to systematics and the biodiversity crisis. There has been a noticeable increase in research on collembolans in Brazil recently with the number of articles published on Collembola of Brazil increasing from ~2/year prior to 2003 to >3 publications/year during the past 5 years (2003-2008). However, collembolan research in Brazil continues to remain restricted to limited areas, and with few exceptions remains limited to description of new species with studies of communities in specific environments almost nonexistent. The results demonstrate that descriptions of new species alone provide an incomplete knowledge of biodiversity and indicate the importance of faunistic and zoogeographic studies for providing a more accurate understanding of the biodiversity of specific areas. There is a great need for recognition of the importance of, and support for interdisciplinary, taxonomy-based surveys of insect communities, and actual publication of results of such research (such as species lists), i.e. a truly global approach to arthropod systematics, especially for biologically diverse but little known areas such as Brazil, not only to provide information essential for systematics (zoogeographical information etc.) but also to support development of integrated pest management and sustainable development, as well as (and as essential parts of) efforts to address the biodiversity crisis.

POSTER PRESENTATION

Responses of pollen beetles to petal colour: towards habitat management via manipulation of visual signals used in host-plant location

Samantha M. Cook, Matthew P. Skeller, John A. Pickett

Rothamsted Research, Harpenden/Herts, United Kingdom

Habitat manipulation as a means for control of herbivorous insects relies upon a thorough understanding of the host-plant location process. The crop habitat in push-pull strategies is manipulated so that the main crop is made to be as unattractive as possible (push) and pests are diverted to highly attractive traps or trap crops nearby (pull). Many pests use a combination of visual and olfactory cues in host-plant location, but manipulation of visual cues in push-pull strategies has been little explored. It is well known that the pollen beetle (*Meligethes aeneus*), a major pest of oilseed rape (*Brassica napus*) inflorescences, is attracted to the yellow colour of the petals. We investigated the responses of pollen beetles to flowers of a white-petalled oilseed rape cultivar that had been dyed different colours. Red and blue flowers were significantly less attractive than those dyed yellow, and the untreated white flowers. These results suggest that a main crop of oilseed rape with a petal colour other than yellow in combination with a yellow-petalled trap crop could act as an efficient push-pull tactic in the control of this pest.

POSTER PRESENTATION

Computational comparative analysis of insect genomes

Robert Waterhouse

Imperial College, London, United Kingdom

One of the major public health concerns of the new millennium centres on diseases transmitted to humans by blood-feeding insects. Sequencing of the *Anopheles gambiae* genome (Holt *et al*, 2002) drove an unprecedented acceleration in malaria research, particularly in the field of insect innate immunity, together with a growing appreciation of the importance of mosquito-parasite interactions. The second mosquito genome, *Aedes aegypti* (Nene *et al*, 2007), has enabled a comparative phylogenomic analysis of the insect immune repertoire among these two mosquitoes and the fruitfly *Drosophila melanogaster*. Analysis of immune signalling pathways and response modules revealed both conservative and rapidly evolving features associated with different functional gene categories and particular aspects of immune reactions (Waterhouse *et al*, 2007). These dynamics reflect in part the continuous readjustment between accommodation and rejection of pathogens and suggest how innate immunity may have evolved. The sequencing of additional genomes of insects of medical or agricultural importance such as the honeybee (*Apis mellifera*), the silkmoth (*Bombyx mori*), and the red flour beetle (*Tribolium castaneum*), enables informative comparative analyses across insect orders with the integration of data sources, and the employment of a range of methodologies to investigate the patterns of gene ancestry which can reflect the underlying biology.

POSTER PRESENTATION

Effects of kaolin on pear psylla oviposition

Haim Reuveny, Zehev Farkash, Amiram Levi-Shaked, Orna Akunis, Rieke Kedoshim

Migal Northern R&D, IPMC, Kiryat Shmona, Israel

Introduction: Control of pear psylla, *Cacopsylla bidens* (Sulc), in Israel is commonly based on use of Amitraz (in blossom time) and Abamectin (in summer). In a previous study we found that kaolin (Surround, WP) reduced the population level on blossoms when used before "green-tip" (GT). In this study the exact effects of kaolin and of application timing on the winter form of psylla were tested.

Methods: Two experiments were done, one started two months before GT (January) and the second one month before GT (February). In both experiments kaolin (at 3% concentration) was used three times (to reduce rain rinse-off) at one-day intervals. The numbers of eggs on spurs and the percentage of flower clusters bearing psylla nymphs were recorded.

Results: The number of eggs laid on spurs by winter-form females was significantly lower in the kaolin treatment than in the control.

Conclusions: These data explain the results of the previous study, which showed the effect of kaolin on 1st-generation psylla development. The winter form females were prevented from laying eggs on trees that were covered with kaolin. Use of kaolin on dormant trees can replace the use of Amitraz In blossom time and help to delay development of resistance in psylla, and to promote the presence of natural enemies and pollinators in pear orchards.

POSTER PRESENTATION

Rapid recovery of an insect-plant interaction following habitat loss and experimental wetland restoration

Corinne Watts

Landcare Research, Hamilton, New Zealand

Introduction: Restiad peat bogs are threatened ecosystems in northern New Zealand, yet several areas of bogs are still being mined commercially. This study examined whether wetland habitat loss and isolation can alter an insect-plant interaction, and how rapidly the interaction recovers following restoration.

Methods: We compared the damage done by an undescribed stem-mining moth on experimentally placed potted *Sporadanthus ferrugineus* (Restionaceae) plants at various distances (up to 800 m) from an intact habitat (the source population) over 18 weeks. Subsequently, to test the rate of recovery of the interaction we surveyed the damage on naturally regenerated *S. ferrugineus* plants on experimentally restored 'islands'.

Results: The proportion of stems damaged by 'Fred the Thread' (the stem-mining Lepidoptera; referred to in Robert Hoare's presentation, this conference), number of eggs and larvae and average larval size per metre of *S. ferrugineus* stem significantly decreased on the potted plants with increasing distance from the intact habitat. Loss of wetland habitat caused an almost complete 'collapse' of the specialist insect-plant functional interaction on isolated *Sporadanthus* plants at distances of between 400 and 800 m from the undisturbed wetland. However, recovery of the interaction following experimental habitat restoration was rapid. Three years after restoration, there was no significant difference in the frequency of oviposition on host plants at differing distances of isolation from the peatland and after six years restoration, the degree of herbivory damage had returned to pre-habitat loss levels.

POSTER PRESENTATION

Tick infestation rate of sheep and temporal distribution of ticks in Bahar, Hamadan Province, Iran, 2006-2007

Zakkyeh Telmadarraiy[1], Alireza Moradi[2]

[1]School of Public Health, Tehran University of Medical Sciences, P.O.Box6446-14155, Tehran; [2]Hamadan University of Medical Science, Hamadan, Islamic Republic of Iran

Introduction: The ticks are one of the main important ectoparasites of the livestock which cause economic losses, reduce animal products and transmission of pathogens to human and animals. Hamadan province including Bahar city is one of the most important husbandry centers in Iran.This study was conducted to determine tick infestation rate of sheep in Bahar.

Materials and methods: Sampling was performed seasonaly in 33 villages through one year during summer 2006- spring 2007. From each village two animal husbandries and from each animal husbandry 3 sheep were selected and tested for tick infestation. Ticks were identified using valid identification keys.

Findings: Tick infestation was detected in 85 (9.37%) out of 907 sheep. The spatial infestation rate was 20%, 6.9%, 4.3%, and 8.4% in spring, summer, autumn, and winter respectively. The highest infestation rate was seen in 2 year-old sheep and the lowest rate observed in sheep with more than four year-old. infestation rate was 10.20% in male and 8.41% in female sheep.

Totally 424 ticks were collected on the sheep which were classified into two families of Ixodidae(66.7%) and Argasidae(33.2%). They belong to four genera *Rhipicephalus* (45.2%), *Hyalomma* (19.3%), *Ornithodoros*(33.2%), and *Haemaphysalis*(2.1%), and to 11 species of *Rh.bursa*(33.9%), *O.lahorensis*(33.2%), *Rh.sanguineus* (11.3%), *Hy.dromedarii*(8.4%) ,*Hy.marginatum*(6.1%), *Hy.anatolicum*(2.5%), *Hy.detritum*(2.1%), *H.concinna*(0.94%), *H.punctata*(0.7%), *H. sulcata*(0.47%) and *Rh.turanicus*(0.23%). The highest tick seasonal activity was 46.9% in spring.

Conclusion: This study showed that there are a great number of tick species in this region including some important vectors pathogens. These data plus information about spatial and temporal distribution of ticks could help farmers and health authorities to monitor the population dynamic of ticks and to make good strategy for tick control.

POSTER PRESENTATION

Description of the immature stages of *Monomorium floricola* (Jerdon, 1851) (Hymenoptera: Formicidae)

Daniel Solis[1], Luciane Kato[2], Eduardo Fox[1], Carlos Jesus[1], Antonio Yabuki[1], Ana Eugênia Campos-Farinha[2], Odair Bueno[1]

[1]Departamento de Biologia, Instituto de Biociências, UNESP, Rio Claro, São Paulo, Brazil, [2]Laboratório de Sanidade Vegetal, Centro de Sanidade Vegetal, Instituto Biológico, São Paulo, São Paulo, Brazil

Introduction: Wheeler & Wheeler described over 700 larvae of different ant species and emphasized the relevance of certain characters to the systematics of this group. However, their descriptions occasionally ended up incomplete or were based on few specimens. This happened with the species *Monomorium floricola*. The present study aimed at determining the number of larval instars of *M. floricola* along with their growth rates and detailed descriptions of each immature stages were carried out.

Methods: Larval instars were determined by measuring head capsules (n=1785). Immatures of *M. floricola* were collected from laboratory colonies, measured and described through optical and scanning electronic microscopy. All measures are given as mean ± SD.

Results: Eggs (n=159) are ovoid and about 0.29 ± 0.01 x 0.18 ± 0.02 mm. There are three larval instars, with mean growth rate of 1.2276. In all instars, head capsule was subpentagonal and body pheidoloid in shape. Types and distribution of the body setae of the 1st larval instar is different from that of 2nd and 3rd ones. Larvae (n=150 each) of 1st, 2nd and 3rd instar were respectively 0.39 ± 0.05, 0.51 ± 0.06 and 0.86 ± 0.19 mm long, and 0.15 ± 0.01, 0.18 ± 0.02 and 0.35 ± 0.09 mm wide. Pupae (n=50) presented no cocoons and were 1.42 ± 0.07 mm-long.

Conclusions: Our results illustrated some traits of *M. floricola* that had been overlooked, such as details about the body setae, besides registering the number of larval instars and their dimensions.

POSTER PRESENTATION

Effects of *Cleome viscosa* L. (Capparidacae) extract on toxicity and the activity of carboxylesterase and glutathione-s-transferase in *Spodoptera litura* (Lepidoptera: Noctuidae)

Supojjanee Buatippawan[1], Vasakorn Bullangpoti[1], Suraphon Visetson[1], John Milne[2], Manthana Milne[3]

[1]Kasetsart University, Bangkok, Thailand; [2]Mahidol University, Bangkok, Thailand; [3]Department of Agriculture, Bangkok, Thailand

The senescent leaf *Cleome viscosa*, L. (Capparidacae) was investigated extract on second instars *Spodoptera litura* (Lepidoptera: Noctuidae) under the laboratory no-choice assay. The toxicity in terms of LC50 values ca. 34 mg ml^{-1} (r^2 = 0.95) at 24 after exposure by the dipping method. Also, in *in vitro* detoxification enzyme analysis, survival treated instars *S. litura* treated showed a inhibit respond to carboxylesterase and glutathione-s-transferase activities. Results indicate that these botanical pesticides have the potential to be as the alternative control program for *Spodoptera litura*.

POSTER PRESENTATION

Acute toxicity of *Jatropha gossypifolia* L. (Euphorbiaceae) extract to guppies (*Poecilia reticulata*)

Sudatip Siriarcharungroj[1], Vasakorn Bullangpoti[1], Chaiwud Sudthongkong[2]

[1]Kasetsart University, Bangkok, Thailand; [2]Samutsakron Coastal Research Center, Samutsakron, Thailand

Jatropha gossypifolia L. shows the insecticidal activity to control many insect pests in agricultural situations. Adult guppy fish (*Poecilia reticulata* standard test species) were selected for the bioassay experiments. The experiments were performed in four series and the 24-h LC_{50} value was determined for guppies. The acute toxicity experiments were carried out by static method and behavioral changes in guppies were determined for each *Jatropha gossypifolia* L. concentration extract which extracted by Soxhlet's extraction method with ethanol as solvent. Data obtained from the extract investigation were evaluated by the use of probit analysis statistical method and the 24-h LC_{50} value for guppy was estimated as *ca.* 3100 ppm (r^2 = 0.95). However, in this concentration, no mortality was observed at higher concentration for 30 second.

POSTER PRESENTATION

Investigation of acute toxicity of *Cleome viscosa* L. (Capparidacae) extract on guppies *Poecilia reticulata*

Varithron Chuaysuwan[1], Vasakorn Bullangpoti[1], Chaiwud Sudthongkong[2]

[1]Kasetsart University, Bangkok, Thailand; [2]Samutsakron Coastal Research Center, Samutsakron, Thailand

Cleome viscosa, L. (Capparidacae), Thai-plant species, have phytocidal chemical components and responsible for controlling and repelling insects from the host plants. To avoid potential toxic pollutant contaminating aquatic ecosystems, this present study was investigated for acute toxicity. Guppy fish (*Poecilia reticulata*) were selected for the bioassay experiments. The experiments were repeated 3 times and the 24-h LC_{50} was determined for the guppies. The static test method of acute toxicity test was used. Water temperature was regulated at 20 ± 1 ℃. In addition, behavioral changes at each concentration were observed for the individual fish. Data obtained from the acute toxicity tests were evaluated using the probit analysis statistical method. The 24-h LC_{50} value for guppy was estimated as *ca.* 5300 ppm (r^2 = 0.96). However, in this concentration, no mortality was observed at higher concentration for 30 second.

POSTER PRESENTATION

Qualitative analysis of the effect of oxycodone (opioid analgesic) on the development rate of *Chrysomya megacephala* (Diptera: Calliphoridae) and its importance for estimating of the post-mortem interval in Brazil

Maicon Diego Grella[1], Patricia Jacqueline Thyssen[2]

[1]UNICAMP, Campinas, SP, Brazil, [2]UNESP, Botucatu, SP, Brazil

Introduction: Recent research has demonstrated that the presence of drugs in decomposing tissues may alter the insect development rate when they using such tissues as food, thus potentially altering estimates of the post-mortem interval (PMI). The oxycodone, opioid semi-synthetic similar to the morphine, is a drug subject to abuse, resulting in respiratory depression and death. In this study, we investigated the effect of the oxycodone on the development rate of *Chrysomya megacephala* (Diptera: Calliphoridae) immatures.

Methods: Groups of larvae were placed in artificial diet containing Oxycodone in 3 different concentrations: 0.5 x LD (lethal dose), 1 x DL and 2 x DL. The control group was reared on the diet containing no drug. Weights were recorded for groups of 10 larvae at 12 h intervals up to the end of the larval stage.

Results: There was not a significant effect of the drug concentration on larval development as measured by weight ($F = 0.06$; $p = 0.97$). Immatures from all groups reached the developmental total time (egg-adult) at 225 h. The emergence rate was 92%, 94.2%, 90.6% and 95.1%, respectively, for control, 0.5 x LD, 1 x LD and 2 x LD groups.

Conclusion: Studies done with different drugs in several species of Calliphoridae suggest that larval development respond differently to the presence of each drug. Although our results show that oxycodone not cause interference in maggots, the register of this knowledge is important, especially when there is a need to determine the PMI using entomological means

POSTER PRESENTATION

Effects of imidacroprid and fipronil insecticide application on the larvae and adults of *Sympetrum frequens* (Libellulidae: Odonata)

Hiroshi Jinguji, Tetsuyuki Ueda

[1]Miyagi University, Sendai, Miyagi, Japan, [2]Ishikawa Prefectural college, Nonoshi, Ishikawa, Japan

Introduction: The insecticides fipronil and imidacloprid are effectively used against sucking insect pests of rice. Since these agents are absorbed by rice seedlings and stored in their tissues, they are usually applied to nursery boxes before planting. The effects of imidacroprid and fipronil on the life history of *Sympetrum frequens* larvae and adults were monitored using an experimental micro-paddy lysimeter for the duration of the cultivation period.

Methods: Groundwater was added to nine small micro-paddy lysimeters (350mm×500mm×300mm (H)) to a depth of approximately 3cm. Three lysimeters were treated with imidacroprid, three with fiproni, and the remaining three were left untreated and were used as controls. Three hundred eggs were laid on the soil surface of each of the nine lysimeters and the larval populations, larval development, and emergence patterns of *Sympetrum frequens* were observed in each lysimeter.

Results: The absence of *Sympetrum frequens* larvae from fipronil-treated-lysimeters was most remarkable and exuviae were not observed. Imidacroprid-treated-lysimeters had approximately 60% of the larvae observed in control lysimeters. In addition, larvae in the imidacloprid lysimeter had lower mean specific growth rates and the length of adult wings was decreased relative to those observed in the control lysimeter. Emergence in imidacloprid lysimeters was also significantly lower than it was in the control.

Conclusions: The application of fipronil and imidacroprid to seedling in the nursery box, and the subsequent transplanting of these into an experimental lysimeter, was associated with a decrease in the abundance of *Sympetrum frequens* larvae and adults.

POSTER PRESENTATION

Classification of the plant bugs from Korea (Hemitpera: Miridae)

Yong Jung Kwon[1], Kyeong-Yeoll Lee[1], Ohseok Kwon[1], Young Jae Cho[1], Sang Jae Suh[2], Tae Young Kwon[3]

[1]School of Applied Biology & Chemistry, Kyungpook National University, Daegu; [2]Department of Environmental Horticulture, Kyungpook National University, Daegu; [3]Division of Horticultural Research, Gyeongbuk Provincial Agricultural Technology Administration, Daegu Republic of Korea

The Miridae are the most species rich family-level grouping of true bugs, with approximately 10,200 described species recognized as now (Schuh, 1995). Plant bugs are widely distributed all over the zoogeographical regions of the world. Many mirid bugs are associated with herbaceous plants predominantly inhabiting grasslands, bushes of forests and sometimes cultivated areas, while many others are predacious to other insects and mites. Thus most of the species play a key role either in natural system or in agro-ecosystems constituting herbivores as primary consumers as well as predators as secondary ones.

The present work revises all the known species of the family Miridae from Korea. A total of 231 species belonging to 95 genera under 6 subfamilies are arranged herein, of which 1 genus with 2 species are new to science, and 12 species are first recorded in Korea. Keys are given for all the taxa respectively, host plants and distributional data are also provided for each species.

POSTER PRESENTATION

Staphylinini in Australia: phylogenetic and biogeographic review, with revision of some little-known and new taxa (Coleoptera: Staphylinidae)

Alexey Solodovnikov[1], Alfred Newton[2]

[1]Department of Entomology, Natural History Museum of Denmark/University of Copenhagen, Universitetsparken 15, 2100 Copenhagen, Denmark, [2]Zoology Department, Field Museum of Natural History, 1400 South Lake Shore Drive, Chicago, Illinois 60605, United States

Introduction: The Australian fauna of the mega-diverse rove beetle tribe Staphylinini (>210 genera and 5,400 species worldwide) appears depauperate compared to other regions, with only 158 species placed in 24 mostly widespread genera reported so far, but this reflects lack of attention more than reality. Our study, incorporating review of large recent collections, seeks to provide in preliminary fashion a phylogenetic framework and better understanding of the biogeographic origins of the Australian fauna, as background for more detailed studies including much descriptive taxonomic work that will be needed to fully unveil the fauna. The phylogenetic analysis (about 70 taxa and 70 adult morphological characters) extends an earlier analysis of Staphylinini by Solodovnikov by including an extensive sample of Australian taxa.

Results: Viewed in the context of what is known about the world fauna of the tribe, the Australian fauna includes three distinct elements: species of widespread genera that most likely arrived in Australia relatively recently, probably from the north; "ghosts of Gondwana", species of genera (including at least four new genera) that are restricted to southern temperate areas in Australia, New Zealand, southern South America and sometimes nearby areas; and several indigenous genera (including one new) that are phylogenetically isolated, with no known close relatives outside Australia. This last group is partially revised, with description of the new genus (two new species), and revision of Antimerus (five new species) and Lonia. One widespread genus (Tympanophorus) is also recorded from Australia for the first time, based on a new species.

POSTER PRESENTATION

Libnotes immaculipennis Senior-White (Diptera: Limoniidae), a pest of oyster mushroom *Pleurotus ostreatus*: a preliminary study in Bogor, Indonesia

Nina Maryana, Dewi Sartiami

Bogor Agricultural University, Faculty of Agriculture, Department of Plant Protection, Bogor, West Java, Indonesia

Introduction: *Libnotes immaculipennis* (Diptera: Limoniidae) is a pest of oyster mushroom *Pleurotus ostreatus*. It does not directly attack fruit-bodies, but causes loss of mushroom production by damaging bag-logs, substrates for fungus growth. We studied *L. immaculipennis* to obtain fundamental information on its biology.

Methods: Field surveys were performed in 2007 at three different localities in Bogor Regency, Indonesia. We investigated developmental stages in the laboratory of Bogor Agricultural University.

Results: Eggs were oval, 0.25 mm in long-axis and 0.17 mm in short-axis. Egg stage lasted for 3.30 ± 0.46 days. Larval body lengths were about 1.53, 2.76, 4.77, and 9.45 mm, in respective stadia. Larval stage lasted for 9.30 ± 0.57 days. Larvae were found in damped bag-logs. They decreased the density of mycelia and inhibited growth of mycelia on bag-logs. Pupal length was 8.55 ± 0.71 mm and pupal stage lasted for 2 days. Body length was about 0.78 in males and 0.67 cm in females. The longevity of males and females were 3.09 ± 2.08 and 3.64 ± 2.17 days, respectively. Each female laid 104.00 ± 81.20 eggs. The average number of larvae per bag-log varied with localities. Larval population density was lower in Cibuntu Batas than in Cikarawang or on Sukamaju I. Adult density was relatively high in Cibuntu Batas.

Conclusions: Total duration from egg to adult was about 14.6 days, and life cycle was 16.9 days. When the population density becomes high, *L. immaculipennis* would become a serious pest of oyster mushrooms.

POSTER PRESENTATION

Advances in Australian spider wasp systematics (Hymenoptera: Pompilidae)

Lars Krogmann, Michael C. Day, Andrew D. Austin, Steven J.B. Cooper

[1]Staatliches Museum für Naturkunde Stuttgart, Stuttgart, Germany, [2]National Museum Cardiff, Cardiff, United Kingdom, [3]Australian Centre for Evolutionary Biology and Biodiversity, School of Earth and Environmental Sciences, The University of Adelaide, Adelaide, Australia, [4]Evolutionary Biology Unit, South Australian Museum, Adelaide, Australia

Spider-hunting wasps (Hymenoptera, Pompilidae) are a diverse group of parasitic wasps that prey exclusively on spiders. Females search and hunt for spiders, which they paralyse and store in a previously constructed nest as food for their developing larvae. All pompilid species provide a single spider per nest cell on which they lay a single egg. The Australian pompilid fauna is huge with an estimate of 500+ species, about 60% of which are undescribed. The primary aim of the current project is to develop a synopsis of the Australian pompilid genera. Based on extensive morphological and molecular data we will also derive a robust phylogeny and reclassification of the Pompilidae to provide an evolutionary framework for ecological and behavioural research on the family.

POSTER PRESENTATION

Evaluation of farm lands located in urban area and industrial complex using insect diversity indices

Young-Cheol Choi, Jong-Gill Kim, Ji-Young Choi, Won-Tae Kim, Ha-Sik Shim, Beong-Do Park

National Institute of Agricultural Science and Technology, SUWON, Republic of Korea

Introduction: To evaluate environment of farm lands using indicator insects and evaluation indices, the insect abundance of which is one of the major criteria for the evaluation of agricultural environment of farm land in urban areas and industrial complex, three sites (Ansan, Daesan, Suncheon) were designated and monitored.

Methods: For the evaluation of agricultural environment of farm land in urban areas and industrial complex, the flora of agricultural land and the population of insects were surveyed, and the insect diversity indices of farm land were analyzed in three sites.

Results: The flora of agricultural land was more than urban areas and industrial complex of that in three sites. Soil, water and air pollution of urban areas and industrial complex were more serious than those of agricultural land in three sites. Overall population of insects were high from June to August in the surveyed three sites. Collected insects in agricultural land were 12 order, 106 family and 166 species, those in urban areas were 11 order, 102 family and 148 species, and in industrial complex were 11 order, 100 family and 152 species. Species and population belonging to Coleoptera was dominant in the surveyed sites. The insect diversity indices of farm land were 2.36 in agricultural land, 1.92 urban areas and industrial complex.

Conclusions: Agricultural environment of agricultural land was good, urban areas was common and industrial complex was poor. Based on the major criteria of evaluation items, the criteria were selected as diversity index over 2.1, insect indicator *Pheropsophus javanus* in agricultural land, diversity index 1.5-2.0, insect indicator *Nephotettix cincticeps* in urban areas, diversity index below 1.5, insect indicator *Pagria signata* in industrial complex.

POSTER PRESENTATION

Mechanisms of resistance to DNA damage in insect cell Sf9

I-Cheng Cheng, How-Jing Lee, Tsing-Cheng Wang

[1]Department of Entomology, National Taiwan University, Taipei, Taiwan, [2]Institute of Cellular and Organismic Biology, Academia Sinica, Taipei, Taiwan

Insect cells are known to be much more resistant to ionizing radiation (IR) and other DNA-damaged chemicals than mammalian cells in culture. This phenomenon seems to imply that insect cells might possess certain unique mechanisms responsible for resistance to DNA-damaged treatments. For further investigations, a lepidopteran cell line, Sf9, and several cell lines of human origin were included in this study. Insect cells were found to be more resistant to X-irradiation and hydrogen peroxide than human cell lines, and had less DNA damage induced due to the more efficient in DNA repair, which was confirmed by the single cell gel electrophoresis technique (Comet assay). Sf9 also exhibited the higher antioxidant ability to remove reactive oxygen species (ROS) induced by IR and hydrogen peroxide. Insect cells, on the other hand, were found to be equally sensitive to methylating agents as human cells. Methylating agents induce cell death by forming DNA adducts, which later on were cleaved by mismatch repair enzymes thereby generate fatal DNA strand breaks. Methylating agent-induced cytotoxicity consequently is not associated with the intracellular level of ROS. Therefore, the higher efficiency in removing ROS in Sf9 were unable to increase the resistance to methylating agents, as it did to IR, hydrogen peroxide, bleomycin, and streptonigrin in Sf9 cells.

POSTER PRESENTATION

Effect of Gamma Radiation on the Histology of the testis of red date palm weevils: *Rhynchophorus ferrugineus* (Olivier) (Coleoptera: Curculionidae)

Waleed Al-Waneen, Mohammed Al-Kalifah, Hassan Al-Ayedh

[1]Natural Resources and Environmental Research Institute, Riyadh, Saudi Arabia, [2]College of Science, King Saud University, Riyadh, Saudi Arabia

Histological changes in the testis of Red date palm weevils *Rhynchophorus ferrugineus* (Olivier) were investigated by irradiating male weevils with 15-Gy of Gamma radiation at Natural Resources and Environmental Research Institute, King Abdulaziz City for Science and Technology, Riyadh, Saudi Arabia.
Histological slides made with ordinary and electron microscope at various magnifications revealed damaged spermatic tubules, spermatogonia, spermatogonial cysts and a clear breakage at the junction of spermatic tube and vas efferens that disconnected the normal passage of sperm movement toward vas deferens via vas efferens.

POSTER PRESENTATION

Selection of non-target Lepidoptera species for ecological risk assessment of Bt maize in South Africa

Annemie Van Wyk, Johnnie Van den Berg, Huib Van Hamburg

[1]ARC - Grain Crops Institute, Potchefstroom, South Africa, [2]North-West University, Potchefstroom, South Africa

Introduction: It is essential to assess environmental risk that Bt maize may hold and to study its effect on species assemblages fulfilling a variety of ecosystem functions. Environmental risk assessment can be improved through the use of an ecological model. Local species can be classified functionally and prioritized to identify test species. Except for *Busseola fusca* and *Chilo partellus,* the target species of Bt maize in South Africa, other Lepidoptera species are also exposed to Bt toxin.

Methods: An ecological approach was followed for selection of non-target Lepidoptera, using data collected on the biodiversity of Lepidoptera species that are primary consumers of maize. Nine primary non-target lepidopterous consumers were identified. A selection matrix was developed in which species was ranked for its maximum potential exposure to maize. Non-target Lepidoptera most likely to be affected were identified and prioritized for future testing and inclusion in risk assessments. Several non-target species were prioritized for close association with maize, general occurrence in maize growing regions and potential for economic damage if they become secondary pests. In the selection matrix, knowledge gaps were identified for future research.

Results: Non-target species populations with the highest maximum potential exposure to Bt toxin are *Sesamia calamistis*, *Helicoverpa armigera* and *Acantholeucania loreyi*. *Eublemma gayneri* can be considered to be a "value unknown" species. Because of their sporadic occurrence *Agrotis segetum* and *Spodoptera exigua* are of lesser importance, but should be considered during pre- and post-release monitoring.

POSTER PRESENTATION

Detection of iAChE organophosphate resistance in *Bactrocera oleae* from Turkey

George Skavdis, Hanife Genc, John Vontas

[1]Democritus University of Thrace, Department of Molecular Biology and Genetics, Dimitras 19, 68100 Alexandroupolis, Greece, [2]Canakkale Onsekiz Mart University, Faculty of Agriculture, Department of Plant Protection, Terzioglu Campus, 17020 Canakkale, Turkey, [3]Laboratory of Pesticides Science, Agricultural University of Athens, Iera Odos 75, 11855 Athens, Greece

Introduction: The olive fruit fly *Bactrocera oleae* (Gmelin) (Diptera:Tephritidae) is the most important olive pest worldwide. Its control in S.E. Europe has been based on organophosphate insecticides for many decades. However their intensive use has lead to development of iAChE resistance, due to the selection of two resistance mutations (I199V and G488S). The frequency of these mutations in Turkey has not been investigated. Furthermore, a test previously developed to detect the G488S in field populations may not be as robust as originally thought, as revealed by more recent extensive sequencing data.

Methods: We designed a new PCR-RFLP diagnostic assay, for the unequivocal detection of the G488S mutation, based on primer induced mutagenesis, by introducing a point mismatch at the reverse primer, which resulted in the generation of an MbiI restriction site at the PCR product of the resistant allele. The test was applied to insects collected from olive orchards regularly treated with insecticides and no treated with insecticides in Canakkale province, Turkey.

Results: The novel PCR-RFLP allows the safe determination of the G488S resistance mutation. Although the frequency of the G488S resistance mutation was as expected higher in the sprayed areas, a significant percentage of flies from neighboring non sprayed areas also carried the resistance allele.

Conclusions: A novel molecular diagnostic assay able to reliably monitor the frequency of the iAChE G488S resistance mutation was developed. Its application in *B. oleae* populations from Turkey showed the high abundance of this mutation, especially in areas with intense organophosphate spray history.

POSTER PRESENTATION

Occurrence and seasonality of Aphididae and Coccinellidae species associated with lettuce cultivated under variable shade house conditions in the central Free State (South Africa)

Johan Pretorius, Schalk Louw, Pierre Venter

[1]Department of Agriculture, Central University of Technology, Bloemfontein, Free State, South Africa, [2]Department of Zoology and Entomology, University of the Free State, Bloemfontein, Free State, South Africa, [3]Unit for Applied Food Science and Biotechnology, Central University Technology, Bloemfontein, Free State, South Africa

Introduction: Consumer demands have resulted in the year-round production of lettuce in certain areas of Southern Africa. The sequential planting of this crop puts it at risk to attack by several aphid species throughout the year, complicating control strategies.

Methods: Lettuce was planted throughout a one-year period (December 2005 - November 2006) in two different shade house structures (one partially and one fully covered with shade netting) to determine the occurrence and seasonality of different aphid species and their associated coccinellid predatory guilds.

Results: A total of nine aphid species and five coccinellid species were observed. Both structures harboured similar aphid and coccinellid species, with minor exceptions. The aphid species *A. lactucae*, *M. euphorbiae* and *Aphis* sp. 1 showed no seasonality, being present throughout the trial period. By employing Sørensen's coefficient of similarity, it was determined that these species occurred during similar periods in both structures. The aphid, *N. ribisnigri*, also exhibited similar occurrence in both structures, but only during the warmer months of December – March. The coccinellids *H. variegata* and *Scymnus* sp. 1 were the two predatory coccinellid species which showed a significant similar association with *A. lactucae*, *M. euphorbiae* and *Aphis* sp. 1.

Conclusions: *A. lactucae*, *M. euphorbiae* and *Aphis* sp. 1 pose the greatest threat to lettuce producers in the central Free State, while *N. ribisnigri* is a potential threat during the warmer months, and *M. persicae* during the cooler months. *H. variegata* and *Scymnus* sp. 1 have potential as possible biological control agents.

POSTER PRESENTATION

The contribution of biological control to management of an invasive weed, *Acacia cyclops*, in South Africa

Fiona Impson[1], Carien Kleinjan[1], John Hoffmann[1], Judy Post[2], Cliff Moran[1]

[1]University of Cape Town, Rondebosch, South Africa, [2]Plant Protection Research Institute, Stellenbosch, South Africa

Acacia cyclops is a plant of Australian origin, which has become an invasive environmental weed in South Africa. Suitable climatic and edaphic factors combined with high annual seed-yields have contributed to the invasiveness of the plant. Since 1994, two insect biological control agents have been introduced successfully against this weed in South Africa. The first of these, a seed-feeding weevil, *Melanterius servulus*, despite slow dispersal, has made a large contribution towards reducing the annual seed output (and hence the aggressiveness and spread) of *A. cyclops*. The second and more recent introduction, the flower-galling midge, *Dasineura dielsi*, has spread rapidly and has the ability to curb pod production very dramatically. Unlike some of the gall-forming agents used in biological control programmes, the midge does not have any negative impacts on the vegetative growth of its host plant. This is an additional benefit due to the utilization of *A. cyclops* wood as a fuel source. Despite the combined contribution of these insects in limiting the annual seed-production, the success of these two agents in managing populations of *A. cyclops*, ultimately rests on what impacts, if any, they are having on the seed-banks of the host plant. Preliminary investigations demonstrate that due to the relatively short-lived nature of the seed bank, biological control can play an important role in the integrated management of *A. cyclops*.

POSTER PRESENTATION

Developing the sterile insect technique for *Thaumatotibia leucotreta* (Lepidoptera: Tortricidae): Radiation biology and inherited sterility

Stephanie Bloem, James E. Carpenter, J. Hendrik Hofmeyr

[1]USDA APHIS, Raleigh, North Carolina, United States, [2]USDA ARS, Tifton, Georgia, United States, [3]Citrus Research International, Citrusdal, Western Cape, South Africa

False codling moth, *Thaumatotibia leucotreta* (Meyrick), male and female mature pupae and newly emerged adults were treated with increasing doses of gamma radiation and then either inbred or out-crossed with fertile counterparts. For newly emerged adults, there was no significant relationship between dose of radiation and insect fecundity when untreated females were mated to treated males (N♀ by T♂). However, fecundity of treated females mated to either untreated (T♀ by N♂) or treated males (T♀ by T♂) declined as the dose of radiation increased. A similar trend was observed when mature pupae were treated. The dose at which 100% sterility was achieved in treated females mated to untreated males (T♀ by N♂) for both adults and pupae was 200 Gy. In contrast, newly emerged adult males treated with 350 Gy still had a residual fertility of 5.2% when mated to untreated females and newly emerged adult males that were treated as pupae had a residual fertility of 3.3%. Inherited effects resulting from irradiation of parental (P_1) males with selected doses of radiation were recorded for the F_1 generation. Decreased F_1 fecundity and fertility, increased F_1 mortality during development, and a significant shift in the F_1 sex ratio in favor of males was observed when increasing doses of radiation were applied to the P_1 males.

POSTER PRESENTATION

Developing the sterile insect technique for *Thaumatotibia leucotreta* (Lepidoptera: Tortricidae): influence of radiation dose and release ratio on fruit damage and population growth in field cages

J. Hendrik Hofmeyr, James E. Carpenter, Stephanie Bloem

[1]Citrus Research International, Citrusdal, Western Cape, South Africa, [2]USDA ARS, Tifton, Georgia, United States, [3]USDA APHIS, Raleigh, North Carolina, United States

The effect of radiation dose and different release ratios of treated (T) to untreated (U) false codling moth, *Thaumatotibia leucotreta* (Meyrick), on the incidence of fruit damage, the competitiveness of the treated males, and population growth was examined inside field-cages. Navel orange trees were individually enclosed in large nylon mesh cages. Newly emerged adult moths treated with either 150 or 200 Gy of gamma radiation were released into the cages at ratios of 5T:1U or 10T:1U. The fruit was collected after four weeks and the number of damaged fruit and larval entries per cage were recorded for each treatment. Infested fruit was maintained in the laboratory until all emerging F_1 progeny were collected and out-crossed to untreated moths of the opposite gender.

Treatment had a significant effect on the mean number of larval entries and on the number of undamaged fruit per cage. The number of larval entries as well as the number of F_1 progeny per cage decreased as the overflooding ratio increased. A significant reduction in egg hatch was observed in the progeny of crosses between F_1 females or F_1 males originating from the treatment cages when compared to crosses of F_1 moths originating from the control cages. The lowest mean number of fertile F_1 adult females and males was obtained from the 150 Gy and 10T:1U ratio treatment. This treatment also showed the lowest per generation rate of increase (<1 from the P_1 to the F_1 generation), suggesting that growth in the fertile population would have been prevented if releases of treated moths at this dose and ratio were maintained in the field.

POSTER PRESENTATION

Developing the sterile insect technique for *Thaumatotibia leucotreta* (Lepidoptera: Tortricidae): Pilot project and commercialization

J. Hendrik Hofmeyr, James E. Carpenter, Stephanie Bloem

[1]Citrus Research International, Citrusdal, Western Cape, South Africa, [2]USDA ARS, Tifton, Georgia, United States, [3]USDA APHIS, Raleigh, North Carolina, United States

A pilot experiment to determine the potential of the Sterile Insect Technique (SIT) to suppress false codling moth (FCM), *Thaumatotibia leucotreta*, in citrus orchards, was conducted in Citrusdal, Western Cape, South Africa. One thousand mixed gender FCM treated with 150 Gy gamma irradiation were released twice a week for 56 weeks in 35 ha of oranges. The releases were made by hand from an ATV quad bike at 40 m intervals between release rows. Distribution and longevity were monitored with sex pheromone in delta traps. The released moths distributed adequately and fully overlapped between release rows. The desired overflooding ratio of 10 released males to one wild male was exceeded by margins of up to 188:1 and a mean of 43:1 was maintained for the duration of the release period. Fruit drop surveys were conducted once a week in release and control orchards. Fruit drop due to FCM was reduced by 94,4% in the release area compared to an untreated control orchard.

An insectary for the mass rearing of 15 million FCM per week for release in 6000 ha of citrus trees in the Citrusdal region was consequently constructed. The building covers 2000 m^2 and consists of a diet preparation room, aseptic egg inoculation rooms, an egg laying room, 20 larval rearing and pupation rooms, a moth eclosion room, several cold rooms, a 20 kGy gamma irradiation facility and a general cleaning area.

The commercial project is being phased in over three years. Rearing of insects began in September 2007 and moth releases in 1500 ha of citrus commenced in November 2007. Moths were released twice a week from a gyrocopter and were supplemented by ATV releases when necessitated by factors such as orchard topography and adverse weather conditions. The SIT programme is currently a multidisciplinary operation to suppress FCM and consists of strict orchard sanitation to remove infested fruit, moth releases and the selective treatment of problem areas with an environmentally-friendly granulovirus spray product. Results are not yet available.

POSTER PRESENTATION

Diversity and abundance of spiders (Arachnida: Araneae) in the field and tree layers of Erfenis Dam Nature Reserve, Free State Province

René Fourie, Charles Haddad

University of the Free State, Bloemfontein, South Africa

Introduction: The Grassland Biome dominates the central area of South Africa and is dominated by a single layer of grass and an absence of trees, except in a few localised areas.

Methods: From November 2005 to August 2007, spiders (Arachnida: Araneae) were collected every three months from the Erfenis Dam Nature Reserve in the Free State Province, South Africa. Spiders were collected from three tree species (*Acacia karroo*, *Rhus lancea* and *Rhus ciliata*) and four different types of grasslands (uniform *Themeda triandra*, mixed, weedy and woodland grasslands). Beats were used to collect the tree-dwelling spiders and sweeps were used to collect the grass-dwelling spiders.

Results: During the period of two years a total of 496 tree-dwelling spiders were collected, representing 17 families and 54 species, while 1649 grass-dwelling spiders were collected, representing 15 families and 84 species. More spiders were found during the summer months, when the temperature and rainfall are higher, than during the winter months. A bottom-up effect from rainfall might be a reason why there are more spiders in the summer season. The higher rainfall leads to denser vegetation growth, which attracts more insects, providing more prey to spiders. More spider species, as well as individuals, were collected from the grasslands than from the tree layers, but the tree layers had a greater diversity of spider families.

Conclusion: It seems that vegetation complexity and structure, and season of flowering, determine the dominant spider families and species in grassland.

POSTER PRESENTATION

Influence of hemipteran pests on the grain quality of *Sorghum bicolor* (L.) Moenich

Anél Grobler[1], José Parau[2]

[1]University of the Free State, Bloemfontein, South Africa, [2]Chemtura (Pty) Ltd., Kempton Park, South Africa

Introduction: Panicle feeding bugs of the order Hemiptera reduce sorghum grain quality by sucking sap from developing sorghum grains, resulting in shrivelled grains with red-brown feeding punctures. These damaged grains are small, poorly developed and often infected by fungi. The study was aimed at quantifying seed germination and mass of different sorghum cultivars relative to this insect damage.

Methods: The germination rates and mass for 15 red and 15 white sorghum cultivar lines were determined. Damage to field sampled grains of these lines received from the Potchefstroom Grain Crops Institute was scored visually on a scale of 0 to 3.

Results: When mass and germination were compared, it was mostly found that grains with less damage had a higher mass and germination percentage. The red sorghum cultivar lines usually had a higher mass and germination percentage than the white cultivar lines. The white cultivar lines showed higher damage indices than the red cultivar lines.

Conclusions: Damaged sorghum grains have poor germination rates and are more susceptible to grain moulds. Red sorghum lines appear to be more resistant to mould and insect damage because of higher tannin content.

POSTER PRESENTATION

The use of blowfly larvae in entomotoxicology - the influence of gunshot residue on insect succession and the development of *Chrysomya chloropyga* (Diptera: Calliphoridae) larvae

Shaun Hoffman, Theuns van der Linde, Piet van der Merwe

University of the Free State, Bloemfontein, South Africa

Introduction: Entomotoxicology is a specialized field where insects are used as toxicological indicators on decomposing human bodies when poisoning, drug abuse or murder with a fire arm is expected. A number of substances can be detected in necrophilous blowfly larvae. Reliable results in forensic entomology is dependent on the correct calculation of the post-mortem interval (PMI). The development stage of the fly larvae is used to determine the PMI. A foreign substance being ingested by larvae can alter the developmental time as well as the growth rate of the larvae. The importance of the correct calculation of the PMI is vital in suicide, drug overdose and murder investigations.

Methods: Pigs were euthanased, shot and placed in the field to decompose. The hind legs of the pigs were cut off after being shot and used in the laboratory for further assays. Larvae were sampled every six hours from the hind legs in the laboratory. The larvae were measured and weighed.

Results: Preliminary results indicated that gunshot residue GSR had a suppressing effect on larval development. Larvae that fed on the hind legs containing GSR, fed directly in and around the bullet wound and were significantly smaller than the larvae feeding on the control.

The larvae that fed on the hind legs containing GSR, all contained significantly higher concentrations of Lead (Pb) and Barium (Ba) and Calcium (Ca) than the larvae feeding on the control.

Conclusions: This suggests that GSR may initially have a suppressing effect on the development rate of larvae.

POSTER PRESENTATION

Effect of honey and temperature on longevity and fecundity of *Dirhinus himalayanus* and *Spalangia endius*, the parasitoids of *Musca domestica*

Hamdan Ahmad[2], Idris Ghani[1], Ahmad Salleh[2]

[1]Universiti Kebangsaan Malaysia, Bangi, Selangor, Malaysia, [2]Department of Veterinary Services, Putrajaya, W.P., Malaysia

Introduction: Two species of parasitoid namely *Dirhinus himalayanus* and *Splangia endius* commonly found in poultry farms in Malaysia. The study was conducted to determine the optimum honey concentration and temperature for rearing these parasitoids.

Methods: The parasitoids were two experiments; (1) parasitoid treated with different honey concentrations (nothing, water only, 10% honey, 20 % honey, 30% honey, 40% honey, 60% honey, 80% honey and pure honey) at a constant temperature (28 ℃) and (2) parasitoid treated with different temperatures on the 10% honey solution (10% honey). Parasitoid's longevity and fecundity was recorded for 60 days.

Results: Mean longevity and fecundity *D. himalayanus* are significantly ($P<0.05$) higher than *S. endius*. Parasitoid without food, fed with water or honey live 6.1 ± 0.45 days, 10.3 ± 0.70 days and 24.0 ± 2.52 days respectively. Longevity and fecundity of *S. endius* and *D. himalayanus* was significantly ($P< 0.05$) higher when fed on 10 - 30% honey solutions than fed with honey solutions. Means longevity and fecundity parasitoids reared at 28 - 30^{o}C were significantly ($P<0.05$) higher than at other temperatures.

Conclusions: Results indicated that these parasitoids are potentially be used as biological agents of housefly as they could be produced commercially at 28 – 30^{o}C fed with 10 - 30% honey and can survive without food for several days.

POSTER PRESENTATION

Pest control system effects on the arthropod communities in Romanian apple orchards

Sonica Drosu[1], Grigore Margarit[1], Constantina Chireceanu[1], Maria Ciobanu[1], Ioan Rosca[2], Maria Neamtu[3]

[1]Research-development Institute for Plant Protection, Bucharest, Romania, [2]University of Agronomical Sciences and Veterinary Medicine, Bucharest, Romania, [3]Research and Development Station for Fruit Tree Growing, Baneasa, Bucharest, Romania

Introduction: The comparative study on the beneficial fauna and the pests under two treatment systems in apple orchards was carried out. These two variants (low polluting treatment system and conventional system) were observed in 2 orchards with different history of the treatment practice (one with the intensive treatments in the previous years and other with IPM practice) and different climate conditions.

Methods: Three sampling methods were used to catch the arthropods between April – September 2007: (i) beating branches of trees into entomological funnel with 0.5 m^2 opening; (ii) yellow sticky traps; (iii) pitfall trapping. Samples were taken to the laboratory for specimen identification; they were identified to family and to species as well as possible.

Results: Both beneficial fauna and pests registered a lower effective in the first type of orchard (with previous intensive treatment) than those with IPM practice. The beneficial and the pests had total individuals approximately equal in the 2 variants at beating method and at yellow sticky traps; pitfall traps registered higher number of beneficial fauna than pests. During the year the number of the beneficial fauna increased from April to September in the experimental variant (low polluting treatment system).

The beneficial fauna was represented mostly by Heteroptera (Fam. Miridae-*Deraeocoris lutescens* Sch.), Hymenoptera (Fam. Calcididae and Braconidae) and Coleoptera (Fam. Coccinellidae-*Coccinella 7 punctata, Adalia bipunctata* L., Fam. Carabidae-*Bembidion properans* L.). The main pests belong at following: Thysanoptera (Fam. Thripidae-*Thrips spp.*), Homoptera (Fam. Aphididae, Cicadelidae), Coleoptera (Fam. Carabidae-*Harpalus spp.*, Fam. Chrysomelidae-*Phylotreta spp.*). The pheromone traps and the visual observations showed high population of the codling moth (*Cydia pomonella* L.) and summer fruit tortrix moth (*Adoxophyes reticulana* Hb.).

Conclusions: This study shows that the main effect of farming practice is to influence the abundance and structure of the fauna in the apple orchards and the implications in keeping bioecological equilibrium.

POSTER PRESENTATION

Integrated control system of pests and diseases of winter cereals crops by seed treatment in Romania

Popov Constantin, Cana Lidia, Raranciuc Steluta

National Agricultural Research and Development Institute, Fundulea, Romania

Introduction: In Romania, production of winter cereals crops (wheat, rye, triticale and barley) is often conditioned by various pests and pathogens. In order to save production, use of various measures was necessary, sometimes inadequate, to control the harmful organisms.

Methods: Researches took into consideration insect pests, of which particular interest is shown by: *Zabrus tenebrioides*, *Agriotes spp.* and aphid species (*Macrosiphum avenae, Rhopalosiphum maidis, R. padi, Metopolophium dirhodum, Schizaphis graminum*), vectors for *BYD* and *WDV*, also diseases *Tilletia spp., Fusarium spp.* in wheat, rye, triticale and respectively *Ustilago nuda, Pyrenophora spp.* in barley and two-row barley.

Results: Thus, soil pest control was based for a long period, nearly exclusively, on organochoride insecticides, applied as dust, this particularly contributing to environment pollution and destroying beneficial fauna. Likewise, long-term use of ethyl-mercury chlorine for treating wheat seed against the wheat bunt led to onset of pathogen resistance to this chemical. It is worth mentioning as unsuitable the high share of monoculture of spiked cereals and ignorance of optimum seed-time, thus favourizing reproduction of some pests and pathogens. Due to these facts, in the last decades approaching of numerous investigations has been imposed, having to outline the real ecological factors to be considered in developing a system of integrated control of pests and diseases of winter wheat and barley crops.

Conclusions: In the present, for pest control are used insecticides or insect-fungicides for seed treatments: tiametoxam and imidacloprid are the main active ingredients, used on 1.5 mil. ha.

POSTER PRESENTATION

Morphological identification of Chalcidoidea wasps occurring on *Erythrina caffra* and *E. lysistemon* and the impact of nutrient availability and concentration on survival rates

Burgert Muller[1], Schalk Louw[1], Gerhard Prinsloo[2], Stefan Neser[3]

[1]Department of Zoology and Entomology, University of the Free State, Bloemfontein, Free State, South Africa, [2]ARC-PPRI (Biosystematics Division), Pretoria, South Africa, [3]ARC-PPRI (Weeds Research Division), Pretoria, South Africa

Introduction: *Erythrina* species are of cardinal importance in various ecosystems, as well as various social and ornamental viewpoints. Across the Pacific and Asiatic islands, an invasive eulophid wasp, *Quadrastichus erythrinae*, is causing havoc by inducing galls on various species of *Erythrina* trees, which can ultimately lead to mortality. African species of coral tree are also galled by various indigenous Eulophidae wasp species. There are also inquilines and parasitoids present, making the insect-plant interactions much more intricate than in other countries where the insects are invasive. The purpose of the present study is to unravel this *Erythrina* gall wasp complex.

Methods: A key to the sampled insects was compiled, together with illustrations for identification. The survival rates of the wasps were determined by the availability and concentration of different nutrients (sugar water and honey), with water as control.

Results: The wasps sampled to date were two species of *Quadrastichus* spp., two species of *Aprostocetus* spp. (Eulophidae), one species of *Bruchophagus* sp. (Eurytomidae), and currently two unidentified Chalcidoidea species. Nutrient availability greatly influenced and increased the wasps' survival, with concentration influencing feeding time.

Conclusion: The knowledge of which wasps occur in the complex is the first step to unravelling it. Nutrient concentration and availability help with the optimisation of host specificity trials.

POSTER PRESENTATION

IPM of sunn pest (*Eurygaster* spp. and *Aelia* spp.) in Romania

Popov Constantin, Rosca Ioan, Raranciuc Steluta

National Agricultural Research and Development Institute, Fundulea, Romania

Introduction: Sunn pest (*Eurygaster integriceps, E. austriaca, E. maura, E. testudinaria, Aelia acuminata* and *A. rostrata*) is one of the most important pests of wheat in Romania.

Methods: The insect effectives are estimated at the end of control campaign, before leaving crops towards forests and also the attack level is analysed, by establishing the percentage of stung kernels, this representing an early step in evaluation of insect effectives which will infest crops in the next year.

Results: The following elements have been examined: ratio between species and their distribution areas in Romania, size and space distribution of sunn pest populations, study of annual peculiarities of their life cycle, relationships between pest and oophagous parasites and establishing of the economic damage thresholds and the means for their control. Thus, the share of various elements has been established, and namely: prevalence of *Eurygaster integriceps* has been proved, covering a damaging area of account 1,000,000 ha of wheat crops in 24 districts; contribution of oophagous parasites and the economic damage thresholds, as differentially calculated in accordance with crop vegetation stage and harvest destination. Climate conditions and surfaces cropped with wheat and oak forests, differentiate damaging area in a very favourable zone (15 districts) and a less suitable area (9 districts).

Conclusions: Forecast and warning are permanent concerns in the whole country, and they are based on a methodology developed by NARDI Fundulea, and applied across the country by the Department Phytosanitary Quarantine. Chemical control of sunn pest in Romania is supported by Government.

POSTER PRESENTATION

IPM of *Tanymecus dilaticollis* Gyll. : The main pest of maize crops in Romania

Popov Constantin, Raranciuc Steluta, Cana Lidia

National Agricultural Research and Development Institute, Fundulea, Romania

Introduction: The maize is one of the most important crops in Romania, being cultivated on three million ha. Their crop technology involves complex protection measures vs. pests and pathogens.

Methods: The main pest of maize in Romania, which affects more than 1.0 mil. ha is *Tanymecus dilaticollis*. The seed treatment with neonicotinoidic insecticides have been developed by recent researches. In the same time seed treatment was included in an IPM system in which agrotehnic methods play an important role, taking into consideration treatments in vegetation for particular situations.

Results: The greatest damages are produced by *Tanymecus dilaticollis* attack even from the emergence. In order to avoid the damages or total crop compromising, the adoption of a complex measures system based on seed treating is necessary, as follows:

for areas where the preceding crop was a winter spike cereal, vetch-oats mixture, bean, soybean, pea or linseed, the chemical treatments are not indicated, because the density registers low values till 3 individuals/m^2;

if the preceding crop was maize, sunflower, sugar beet or sorghum, the maize seed treating is recommended with the following ingredient: carbofuran, thiamethoxam, imidachloprid, and bensultap;

in the case of favourable climatic conditions for pest appearance, after plant emergence,the application of one correction treatment during vegetation is recommended on seed areas treated with: thiamethoxam, thiachloprid, acetamiprid, fipronil, dimetoat+cipertrin or bensultap.

Conclusions: In the present, for pest control are used insecticides for seed treatments: tiametoxam and imidacloprid are the main active ingredients, used on 0.7 mil. ha.

POSTER PRESENTATION

Evaluation of the arthropod populations in vineyards under different management strategies

Constantina Chireceanu[1], Adrian Serdinescu[2], Loreta Dumitrascu[2], Silvia Cazacu[2], Sonica Drosu[1]

[1]Research-Development Institute for Plant Protection, Bucharest, Romania, [2]Research Institute for Viticulture and Enology, Valea Calugareasca Prahova, Saint Helena

Introduction: A comparative study was undertaken concerning the arthropod populations in vineyard under conventional, biological and integrated pest management strategies and permanent ground cover, herbicide treated and vegetation-free conditions.

The survey was carried out in vineyards of the Research Institute for Viticulture and Enology Valea Calugarească (south-east sub Carpathian region of Romania).

Methods: The beating of vine foliage technique and the pitfall trapping were used for collecting arthropods from May to September in 2006-2007. A specific Romanian pheromone trap was used for capturing the grape berry moths. The arthropods were taxonomically identified and separated into two categories, the pests and beneficial, those where analyzed separately.

Results: The structure and seasonal dynamic of pests and beneficial were appreciated for each experimental blocks. It was established that the pest arthropods were represented mainly by major pest of vineyard, grape berry moths and leaf- and plant-hopers. The useful arthropods were represented by spiders group and generalist predators in the families Coccinellidae, Chrysopidae, Nabidae, and Syrphidae. Arthropod populations were low in the spring and increased during the summer. The vine blocks managed by biological program exhibited a higher abundance of the two fauna categories than in integrated and conventional programmes. Similar trends were observed in ground cover blocks, showing that pest a useful fauna was influenced by presence of vegetation in vineyards.

Conclusions: Our studies showed that the densities of pests and associated natural enemies are influenced by the pest management strategies a ground cover practices in vineyard.

POSTER PRESENTATION

IPM of *Tetranychus urticae* Koch. : The main pest of soybean crops in Romania

Popov Constantin[1], Rosca Ioan[2], Raranciuc Steluta[1]

[1]National Agricultural Research and Development Institut, Fundulea, Romania, [2]University of Agricultural Sciences and Veterinary Medicine, Bucharest, Romania

Introduction: In Romania, soybean is considered an important crop, which currently occupies about 130,000 ha, on all over the country. One of limitative pest is *Tetranychus urticae*.

Methods: To establish the life-cycle and number of generations, the occurring of pest mobile stages, species bio-ecology under various conditions on different legumes (soybean, pea, and bean) the attack way and the level of damages, were followed. To perform the control technology, it was tested an assortment of chemicals.

Results: The researches showed that under conditions of Romania, *Tetranychus urticae* wintered as adult into soil, underground or vegetable debris and into tree bark cracks. During a year, it develops six generations. The average duration of a generation was of 27 days, at an air average temperature of 21.6^0C and 38 days at 11.8^0C. During summer, the development is faster than the first and last generations, developed at lower temperatures. For soybean crop, the third and fourth generations are economically important. The occurring and development of these generations coincide with the end of soybean growth and reproductive stage. The warning should be made at the occurring of mobile forms from third and fourth generations. A lot of commercial products with different active ingredient,(*amitraz, bromprop*ilat, *dicofol, dimetoat, fenbutatin oxide, fenpiroximat, propargit, spirodiclofe,* had result effective from trials.

Conclusions: The best results were obtained by the application of two chemical treatments. In this way, the mobile forms of third and fourth generations are controlled.

POSTER PRESENTATION

Storage pests and seed injury in farm storage facilities in Namibia

Vaclav Stejskal

Crop Research Institute, Prague, Czech Republic

Introduction: There is a controversy over the extent of weight loss potential caused by storage pests.

Methods: A survey of stored product pests, their natural enemies, grain storage and pest management approaches in northern Namibia was conducted.

Results and Conclusions: The survey revealed five types of crop commodities (pearl millet, sorghum, cowpea, maize, feed mixture) stored in four types of grain stores (baskets, bag stags-flat stores, concrete bin, metal containers). No synthetic pesticides or plastic sheeting was recorded. Wooden-ash natural pesticide is the only protectant used. Ten insect pest species were found affiliated to the orders of Coleoptera (*Attagenus fasciatus, Callosobruchus subinnotatus, Cryptolestes ferrugineus, Oryzaephilus surinamensis, Rhyzopertha dominica and Tribolium castaneum*), Lepidoptera (*Corcyra cephalonica, Sitotroga cerealella*), Psocoptera (*Liposcelis paeta*) and Blattodea (*Blattella germanica*). Out of these, seven species were recognized as new stored-products pests for Namibia. Although listed for southern Africa region, no storage pest-mites (Acari) and Sitophilus spp., Prostephanus sp. or Trogoderma sp. beetles were traced. We found four new species of natural enemies of storage pests recruiting from insects (*Habrobracon hebetor, Cephalonomia wattersoni, Brachymeria sp.*) and mites (*Blattisocius tarsalis*). There is a controversy over the extent of weight loss potential caused by storage pests. In this work we report unusually high pest related losses (i.e. losses >95%) to stored legumes (*Vigna unguicula, Arachis hypogea* - Leguminosae) in Namibia caused by combined infestation by pyralid moth (*C. cephalonica*) and bruchid beetles (*C. subinnotatus*). This study was supported by the by MZe (project Vyzkumny zamer 0002700603).

POSTER PRESENTATION

The effects of biological-control-agent herbivory on water hyacinth plants: Resource and nutrient allocation; herbivore-induced plant defenses; and photosynthetic mechanisms and outputs

Kate Lorentz, Martin Hill, Marcus Byrne, Bradley Ripley

[1]Rhodes University, Grahamstown, South Africa, [2]University of the Witwatersrand, Johannesburg, South Africa

Six biological control agents have been released since the initiation of the biological control programme against water hyacinth (*Eichhornia crassipes*) in South Africa in 1973. Those agents released are either plant material chewers or sap-suckers. Little is known about the effects of insect herbivory on plant physiology. This involves understanding herbivore stress induced disruptions to photosynthetic mechanisms and outputs; the translocation of nutrient and resources within plant material; and plant defense responses in the form of volatile organic compounds. Furthermore, the impacts of herbivore-induced changes in plant nutrient quality on the herbivore population are poorly understood. Shifts in resources and nutrients from one plant organ to another may make some parts of the plant more prone to attack by biological control agents. Stable isotope ratio analyses at natural abundance levels have been used to track the translocation of carbon and nitrogen from water media throughout plants, in both the presence and absence of agent herbivory. Chlorophyll fluorescence analysis has been used to measure altered potential photosynthetic output as a result of herbivory. Results of headspace sampling of water hyacinth plants exposed to herbivory have been analyzed for volatile compound elucidates (isoprenoids, phenylpropanoids/benzenoids and fatty acid derivatives) by using gas chromatography.

Preliminary results show that whilst low levels of herbivory have little effect on plant growth parameters, they do induce changes in plant physiology. However water hyacinth appears to be capable of compensating fairly high levels of herbivory from both guilds of agents released.

POSTER PRESENTATION

Pest thrips of Bulgaria

Gerald Moritz[1], Vladimir Krumov[2], Olia Karadjova[2]

[1]Martin-Luther University, Halle, Germany, [2]Plant Protection Institute, Kostinbrod, Bulgaria

Introduction: Thrips are among the most damaging insect pests on tomatoes, cucumbers, onions, tobacco, cereals and ornamentals, causing considerable economic losses in Bulgaria. Besides direct damage, caused by feeding, thrips also cause far more serious indirect damages through transmitting plant viruses – agents of diseases, against which there is currently no effective control. An early species determination is necessary to avoid yield losses.

Dichotomous identification keys require good systematic training. The lack of taxonomists brings the need of creation of user-friendly identification software that can be used by anyone – from quarantine workers and economic entomologists, to the virologists and ecologists concerned with crops.

Methods: For creation of the CD-ROM, Lucid 3 software was used. The molecular key is based on the amplification of ribosomal ITS1 and ITS2 regions and restriction fragment length polymorphism (ITS-RFLP). High-quality light microscope and SEM pictures were made.

Results: The interactive key of Pest thrips of Bulgaria was made combining molecular and morphological features for identification. Besides the identification part the CD-ROM includes useful information for the methods used, general information for thrips, their biology, distribution and host-plants. The software will be available in 3 languages – Bulgarian, English and Russian.

Conclusions: The Pest thrips of Bulgaria interactive key allows fast and reliable diagnostics of all stages that can be done even from non-specialist in thrips taxonomy.

POSTER PRESENTATION

Influence of morphological and anatomical characteristics of the leaves on the host selection by *Frankliniella occidentalis* (Pergande) (Thyasanoptera: Thripidae)

Maria Papadaki, Vili Harizanova, Andreas Bournazakis

[1]Technological Education Institute of Crete, Heraklion, Crete, Greece, [2]Agricultural University of Plovdiv, Plovdiv, Bulgaria, [3]University of Crete, Heraklion, Crete, Greece

Introduction: The thrips *Frankliniella occidentalis* is one of the most important insect pests in vegetable crops in greenhouses on the island of Crete (Greece). Leaves features such as trichome length, width as well as thickness of leaves cuticle and waxes can have a profound effect on the acceptability of a plant. We recently showed that the insect's preference for the leaves of several vegetables is variable, ranging from the highest levels for eggplants to a minimum ones for pepper.

Methods: The morphological and anatomical structure of the leaves of different crops – including number, length and shape (original microscope photos) of trichomes, number, length and width of stomata, leaf thickness, thickness of spongy and palisade parenchyma, thickness of upper and lower epidermis- were studied.

Results: Number of trichomes on the lower epidermis is moderately correlated and length of trichomes is significantly correlated (r) with the population density of *F. occidentalis*. Number of stomata is moderately negatively correlated and length of stomata is weakly negatively correlated. Width of stomata is significantly correlated with the preference of *F. occidentalis* to the different crops. Leaf thickness and spongy parenchyma is weakly negatively correlated. Thickness of upper, lower epidermis and palisade parenchyma is moderately negatively correlated.

Conclusions: The leaves of the most preferred crop (eggplant) are densely pubescent and those of the least preferred one (pepper) are glabrous. Morphological and anatomical characteristics play an important role for the preference of *F. occidentalis* for the crop species. Morphology of trichomes is connected to host selection.

POSTER PRESENTATION

Biodiversity of the insect pest fauna from rape crops in Romania

Popov Constantin[1], Rosca Ioan[2], Cana Lidia[1]

[1]National Agricultural Research and Development Institute, Fundulea, Romania, [2]University of Agricultural Sciences and Veterinary Medicine, Bucharest, Romania

Introduction: Rape crop for oil in Romania registered an important extension, in 2007 being cultivated on 250,000 ha. In this paper is presented biodiversity of crop's insect pests.

Methods: Researches referring biodiversity of insect fauna from rape were conducted in 5 representative localities, by insect collecting from 10 to 10 days in the whole vegetation period, through pitfall traps, pheromone traps, Yellow sticky traps, entomological net and plant analysis for presence of insects onto and into the stem or seeds.

Results: There were registered species of insects from the main insect orders (*Homoptera* – 3 species; *Heteroptera* – 4; *Coleoptera* – 25; *Lepidoptera* – 9; *Hymenoptera* – 1; *Diptera* - 6). Damage impact was present differentiated in function of plant development stage and pest life cycle in the attack moment. Important damages were registered in different periods of time from case to case. Thus, in autumn, soon after emergency, the plants were attacked by *Athalia colibri, Pieris brassicae, Phyllotreta atra*. In the spring, the attack was done by *Entomoscelis adonidis, Ceuthorrynchus picitarsis* and in late spring, before and after flowering, by *Brevicorynae brassicae, Meligetes aeneus*, *Athalia colibri, Agriotes* spp., *Loxostege stricticalis, Phytomyza rufipes*. During the ripening of pods and seeds maturation the attack is continued by *Eurydema ornata, Dolycoris baccarum, Contarinia nasturtii, Dasineura brassicae, Ceuthorrynchus napi, Lygus pratensis*.

Conclusions: Importance of attack of different species on rape in different plant growth stages impose application of a plant protection technology, which include seed treatment and 1-2 spraying with insecticides during vegetation time.

POSTER PRESENTATION

Fat body influence in the dynamics of the sunn pest (*Eurygaster integriceps* Put.) populations in Romania

Popov Constantin, Cana Lidia, Raranciuc Steluta

National Agricultural Research and Development Institute, Fundulea, Romania

Introduction: The fat body presents a significant role into the life-cycle of *Eurygaster integriceps*, constituting one of the most important factors of perpetuation and numerical blasting with invasion role.

Methods: The prolificacy of populations was studied under field and controlled conditions, by individualized couples, collected at the end of diapause, in spring. The fat analyses were performed on groups of 25 or 100 insects, separately on sexes and weight groups.

Results: The accumulation of reserve matter and the fat body level among this species present a great no uniformity, both individually and from one zone to another or from one generation to another, being the consequence of a complex of factors from which the climatic and agro technical ones are the most important. The mean value of the fat body is different between sexes too. The fat body level influences the mortality during diapause, the sterility and fertility, strongly influencing the bug population multiplication. The insects with low level of fat matter accumulations have a high mortality percentage during diapause as well as a very low fertility. The fat body is consumed in a proportion of 25% for maturation during diapause and 50% for oviposition. The main factor of the formation of a well developed fat body is the complete rearing of adults under the best conditions. This factor is the premise of an optimum development of bug population in a specific area determining an adequate multiplication.

Conclusions: The multiplication index, calculated by fat body, ranges between 0 and 56.47.

POSTER PRESENTATION

Fitness and fertility of interpopulation matings in *Pareuchaetes insulata* (Lepidoptera: Arctiidae): a biocontrol agent of *Chromolaena odorata* (Asteraceae) in South Africa.

Nontembeko Dube[1], Yoseph Assefa[2], Terence Olckers[3], Costas Zachariades[1]

[1]Agricultural Research Council-Plant Protection Research Institute, Hilton, South Africa, [2]North West University, Potchefstroom, South Africa, [3]University of KwaZulu-Natal, Pietermaritzburg, South Africa, [4]Agricultural Research Council-Plant Protection Research Institute, Hilton, South Africa

Introduction: *Pareuchaetes insulata* from Florida and Jamaica were released separately at several sites each in South Africa, but only one (Florida) site was definitely established. It is likely that insects from this established site interbred with insects from the Jamaican population released at nearby sites. The aims of this study were to test whether there were differences in biology between two populations and whether hybridization affected the fitness of either.

Methods: Trials comprising breeding of a Florida population from the only established site in South Africa (SAF) and a Jamaica (J) population from a laboratory culture, crossbreeding and two back-crossing were conducted. The fitness was determined by measuring fecundity, egg viability, longevity, larval development and survival rates. Genetic differences were analysed using mitochondrial DNA.

Results: The SAF population was superior to the J population in fecundity. Hybridization of these populations reduced the fitness of SAF population. It is unknown whether these differences in fitness reflect differences in their native regions, laboratory cultures or response to South African *C. odorata*. No genetic difference between the two populations was evident.

Conclusion: Different populations of the same agent species may have different levels of fitness, and hybridization may negatively affect the fitness of stronger populations. *Pareuchaetes insulata* has proved to be a difficult agent to establish in South African fields, for various possible reasons. The lower fitness of the J population may have reduced its likelihood of establishing successfully, and reduced the fitness of the established SAF population where it came into contact.

POSTER PRESENTATION

Molecular and functional characterization of serotonin receptors in the cockroach *Periplaneta americana*

Britta Troppmann[1], Arnd Baumann[2], Wolfgang Blenau[1]

[1]University of Potsdam, Institute of Biochemistry and Biology, Potsdam, Germany, [2]Research Centre Jülich, Institute of Neurosciences and Biophysics, Jülich, Germany

Biogenic amines are important messenger substances in the central nervous system as well as in the periphery. In invertebrates, the group of classical biogenic amines consists of five members: dopamine, tyramine, octopamine, histamine, and serotonin (5-HT). The indolamine 5-HT is known to function as a neurotransmitter, neuromodulator and neurohormone and affects behaviors as diverse as locomotion, circadian rhythms, and learning. 5-HT mediates these multifaceted effects predominantly by binding to members of the superfamily of G protein–coupled receptors. The identification and functional characterization of these receptors is decisive for the comprehension of the cellular pathways influenced by 5-HT. Here, we focus on our results concerning a serotonin receptor of *P. americana.*

Using a strategy based on PCR with degenerate primers and RACE PCR we achieved a cDNA sequence encoding a putative serotonin receptor. The full length cDNA (Pea*5-ht1*) comprises 2,564 base pairs and encodes a protein of 683 amino acids (Pea5-HT_1) that displays the characteristic heptahelical structure of G protein-coupled receptors. The tissue-specific expression pattern of the receptor mRNA has been investigated by RT-PCR and indicates high levels of expression in samples of brain, salivary glands and midgut. The distribution of the receptor protein was analyzed by immunohistochemistry with a specific affinity-purified antibody. In order to clarify the functional and pharmacological properties of the cloned receptor, we studied a HEK293 cell line, stably expressing the Pea5-HT_1 receptor protein. Stimulation with 5-HT induces a significant decrease in intracellular cAMP levels. This effect can be antagonized by the substances methiothepin and WAY100635.

POSTER PRESENTATION

Evolutionary analysis of *Anopheles minimus* species complex by the molecular markers of ribosomal and mitochondrial genes

CM Ho[1], YH Lin[2], HJ Teng[3], TY Zhao[4], T Toma[5]

[1]National University of Yang Ming University, Taipei, Taiwan, [2]Yuan Pei University, Shinchu, Taiwan, [3]Centre of Disease Control, Department of Health, Taipei, Taiwan, [4]Institute of Microbilology and Epidemiology, Bejing, China, [5]Faculty of Medicine University of Rykyus, Nishihara, Okinawa, Japan

Introduction: *An. minimus* is a primary vector of malaria in Southeast Asia. The taxon *An. minimus* has shown to consist of at least four sibling species. We describe here the sequence of the ribosomal DNA (rDNA) and mitochondrial genes of this species complex that distributed in Taiwan, Mainland china and Rykyu Achipelago, Japan.

Methods: Larvae or adults of *An. minimus* were collected from 12 locations at three counties in Taiwan, southwest parts of Mainland China, and Ishgaki Island, Rykyu Archipelago, Japan. Total DNA was extracted these specimens, and the target genes were amplified by polymerase chain reaction (PCR). Primers used for amplification were designed based on the published data base for *Anopheles*. The PCR products were cloned and sequenced. Finally, the evolutionary relationships of the *An. minimus* were analyzed with the sequences of nucleotide or deduced amino acid in data base using Neighbour-joining methods.

Results: Examining 12 populations of *An. minimus* in Taiwan, the ITS-2 and D region of the 28 S rDNA of *An. minimus* was 496 bp and 375 bp in length, respectively. 2-nucleotide divergence was found between populations, but no intraspecific variation in the D region of 28S. Identical sequence of the whole mitochondrial COII gene was shown in all populations. The similar results were also found in partial sequence of the mitochondrial ND5. The NJ trees derived from these fragments revealed that *An. minimus* in Taiwan was most closed to *An. minimus* species A of southwest parts of Main China. However, the population of *An. minimus* in Ishigaki Island, Rykyu Archipelago had the highest similarity to that of *An. minimus* species E based of the sequences of ITS-2, D-region of 28 S and mitochondrial COII gene.

Conclusion: Get together the molecular evidence of the ribosomal gene and mitochondrial genes suggests that the *An. minimus* A existing in Taiwan and the southwest parts of Mainland China was derived from the ancestor populations with closed lineage before the landscape separation 20,000 years ago. Since then, their progenies are expanded in the ecological environments similar to that of their ancestors. On the other hands, *An. minimus* E in Ishigaki Island appears to be an originally variant species.

POSTER PRESENTATION

Survey and seasonal activity of adult mosquitoes (Diptera: Culicidae) in Riyadh City, Saudi Arabia

Mohammed Al-Kheraiji[1], Azzam Alahmed[2], Salah Kheir[2]

[1]Natural Resources and Environmental Research Institute, King Abdulaziz City for Science & Technology (KACST), Riyadh, Saudi Arabia, [2]Plant Protection Dept., College of Food and Agric. Sciences, King Saud University, Riyadh, Saudi Arabia

A survey for adult mosquitoes (Diptera: Culicidae) in Riyadh City, Saudi Arabia, was undertaken during the period June 2003-July 2004 using light traps; .and the following 15 different species were collected*:*

Aedes. caspius (Pallas)*, Anopheles. stephensi* Liston *, An. coustani* Laveran*, An. dthali* Patton; *An. pretoriensis* (Theobald);*Culex laticinctus, Cx. perexguus* Theobald*, Cx. pipiens* L*; Cx. quinquefasciatus* Say*, Cx. simpsoni* Theobald*, Cx. sinaiticus* Kirkpatrick; *Cx. theileri* Theobald*; Cx. tritaeniorhynchus* Giles*, Cx. univittatus* Theobald and *Culiseta longiareolata* (Macquart)*.*

During the survey, 6646 adult mosquitoes, which represented 4 genera, were collected.. Out of these, 6446 were *Culex* (96.99%), 147 were *Aedes* (2.21%), 39 were *Anopheles* (0.59%) and 14 were *Culiseta* (0.21%). All these species were reported for the time in Riyadh City, except *Cx .molestus pipiens*, which has been reported earlier.

The seasonal activity of adult mosquitoes in Riyadh City was also investigated. The study showed that the adult mosquitoes were present throughout the year, but at different densities depending on the prevailing climatic conditions. The study showed two peaks for the seasonal activity of the adults; in December-January, and in April- May, where temperature and humidity were optimum.

POSTER PRESENTATION

The management of *Scyphophorus acupunctatus* Gyllenhal (Coleoptera: Curculionidae) on *Agave americana* L. (Agavaceae) in South Africa

Franciska Jordaan, Schalk Louw

[1]University of the Free State, Bloemfontein, Free State, South Africa, [2]University of the Free State, Bloemfontein, Free State, South Africa

Introduction: *Agave americana* L. is cultivated by Agava Distillers (Pty) Ltd at Graaf Reinet in the Eastern Cape and used to produce an alcoholic beverage referred to as Agava®. *Scyphophorus acupunctatus* Gyllenhal (Coleoptera: Curculionidae), the *Agave* weevil, is an important pest of *A. tequilana* Weber and *A. americana* L. It feeds on the core of both plants, dispersing through flight once a year.

Methods: Fungal isolates have been done from the cadavers of *S. acupunctatus* and an entomopathogen has been isolated and identified, the weevils were then exposed to the spores of the pathogen in a water suspension. Olfactory tests are also being conducted in the laboratory, using a Y-olfactometer and a variety of lures. These lures include fresh and fermented plant materials from various host species, and the pheromone of the banana weevil, *Cosmopolites sordidus* Germar. The aim is to attain an attractant.

Results: The pathogen was identified as a strain of *Beauveria bassiana* which targets the *Agave* weevil. It grows and feeds on the internal organs of the weevil, killing the weevil, and then growing out of the cadaver and producing spores. If the weevil dies inside the core of the plant, the spores can distribute and infect other weevils, subsequently killing them. A 100% mortality rate and a 50% fungal growth rate were recorded from weevils exposed to the pathogen.

Conclusion: The attractant and entomopathogen will be combined in “attract and infect” traps and deployed as a management tactic. Field application studies will ultimately be conducted.

POSTER PRESENTATION

In situ identification of powdery stinkbug egg package status as a management practice in pistachio orchards in South Africa.

Schalk Louw

University of the Free State, Bloemfontein, South Africa

Introduction: Pistachio, *Pistacia vera* (Anacardiaceae), is an important new nut crop to South Africa. Presently, large orchards of these trees are under cultivation at IDC-Green Valley Nuts (GVN) near Prieska in the Northern Cape Province. The powdery stinkbug, *Atelocera raptoria* (Hemiptera: Pentatomidae), is a primary pest on this crop, attacking nut clusters and causing severe tissue necrosis to individual nuts.

Method: Initially, identification of *A. raptoria* egg packages through visual scouting was cumbersome and problematic, largely due to the lack of bio-ecological data regarding the species. Subsequently, several studies were conducted on the life-cycle and general ecology of *A. raptoria* in the GVN orchards.

Results: As a result it was determined that an egg-parasitoid, *Trissolcus basalis* (Hymenoptera: Sceleonidae), successfully parasitizes a significant number of *A. raptoria* egg packages in the orchards, showing promise as a possible biological control agent. Furthermore, continuous scouting in the orchards revealed that the status of *A. raptoria* egg packages could be determined *in situ* and that a pictorial guide could be compiled that could be used as an efficient scouting tool.

Conclusion: The simplicity of this tactic is believed to encourage a continuation of scouting GVN management in the orchards. Continued orchard scouting is of crucial importance when considering pest management strategies towards the management of *A. raptoria* (and other stink bugs) on pistachio in South Africa.

POSTER PRESENTATION

Adult experiences influence foraging and oviposition behaviour of *Lysiphlebus fabarum* (Hymenoptera: Aphidiidae) females

Arash Rasekh[1], A. Kharazi Pakdel[1], J.P. Michaud[2], H. Allahyari[1]

[1]University of Tehran, Karaj, Tehran, Islamic Republic of Iran; [2]Kansas State University, Hays, Kansas, United States

In Iran, the black bean aphid (*Aphis fabae* Scop.) is heavily parasitized by the aphid parasitoid *Lysiphlebus fabarum*, both on agricultural crops and associated weeds. The influence of adult experience on foraging behavior was examined in *L. fabarum*. Three-Day-old females of a thelytokous population were each provided with two sequential host patches consisting of 20 2nd instar *A. fabae* that were either healthy or previously parasitized (24 h prior to the experiment), Each female was subsequently transferred to a patch containing 15 healthy 2nd instars. Another experiment, parasitoids were grown under three different daylength conditions; parasitized aphids were grown under short daylength (L10:D14) and subjected the adults to the same conditions, parasitized aphids were reared under long day conditions (L16:D8) and subjected the adults to short days, both parasitized aphids and adults were grown under long day conditions. Females exposed to previously parasitized aphids displayed longer residence times in the 2nd patch and encountered and attacked a larger of aphids before leaving, including aphids probed more than 25 seconds, the threshold time required for oviposition. More aphids were either killed or parasitized in the second patch when the first patch contained previously parasitized hosts, but there was no difference in the rate of superparasitism. Daylength results showed, parasitoids under short day's conditions displayed longer residence times and parasitized more aphids than two other treatments. Short days indicate the end of the aphid season and previously parasitized aphids indicate competition with other females for hosts. Thus exposure to short days and low value hosts raised the value of subsequently encountered host patches.

POSTER PRESENTATION

The species composition and bio-ecology of *Culicoides* spp. frequenting livestock in the Bloemfontein district

Julian Liebenberg[1], Theuns Van der Linde[1], Gert Venter[2], Anne-Marie Pretorius[1]

[1]University of the Free State, Bloemfontein, South Africa, [2]ARC-Onderstepoort Veterinary Institute, Pretoria, South Africa

Introduction: *Culicoides* midges are known to be some of the most important vectors of viral diseases of livestock, such as bluetongue (BT) disease of sheep, African horse sickness (AHS) and bovine ephemeral fever (BEF) in South Africa. Therefore a study on the *Culicoides* midges and vector potential is being undertaken to aid in the control of these diseases and minimize losses.

Methods: Midges were collected from February 2007 to date, using 220V and 12V down draught light traps set up at horse stables in order to determine the species composition, relative abundance and seasonality of the midges. The following surveys are also planned for the future namely, the host preference and abundance of the midge species at horses, sheep, cattle and pigs respectively. Potential breeding habitats of *Culicoides* midges will be explored, to identify possible control strategies. The optimal development temperature and optimal preferred relative humidity (RH) for *C. imicola* and *C. bolitinos* will be determined to aid in the development of an early warning system against periods of high risk for disease spread. Both biological and chemical control of the midges and midge breeding sites will be evaluated.

Results: Preliminary results have shown that *Culicoides* numbers have been very low during 2007 with more midges emerging early in 2008 due to favourable environmental conditions.

Conclusions: The obtained results following these experiments will hopefully lead to more efficient control of *Culicoides* borne disease in Southern Africa.

POSTER PRESENTATION

Insect transferrin functions as an antioxidant protein in a beetle larva

Bo Yeon Kim[1], Kwang Sik Lee[1], Young Moo Choo[1], Iksoo Kim[2], Yeon Ho Je[3], Soo Dong Woo[4], Sang Mong Lee[5], Hyun Cheol Park[5], Hung Dae Sohn[1], Byung Rae Jin[1]

[1]Dong-A University, Busan, Republic of Korea, [2]Chonnam National University, Chonnam, Republic of Korea, [3]Seoul National University, Seoul, Republic of Korea, [4]Chungbuk National University, Chunbbuk, Republic of Korea, [5]Pusan National University, Busan, Republic of Korea

Introduction: In insects transferrin is known as an iron transporter, an antibiotic agent, a vitellogenin, and a juvenile hormone regulated protein. Here, a novel functional role for insect transferrin as an antioxidant protein is demonstrated.

Results: Stressors, such as heat shock, fungal challenge, and H_2O_2 exposure, cause upregulation of the white-spotted flower chafer *Protaetia brevitarsis* (Coleoptera: Scarabaeidae) transferrin (*PbTf*) mRNA in the fat body and increases PbTf protein levels in the hemolymph. RNA interference (RNAi) treated *PbTf* reduction causes increased iron and H_2O_2 levels in the hemolymph and results in induction of apoptotic cell death in the fat body during exposure to stress. The observed effects of *PbTf* RNAi suggest that PbTf inhibits stress-induced apoptosis by diminishing the Fenton reaction via the binding of iron.

Conclusion: Based on these results, we concluded that insect transferrin may be part of the antioxidative defenses and is an antioxidant protein.

POSTER PRESENTATION

Diversity of herbivorous and predatory Hemiptera on sorghum panicles in South Africa

Marlene Kruger[1], Johnnie Van Den Berg[1], Hannelene Du Plessis[2]

[1]North-West University, Potchefstroom, South Africa, [2]ARC-Grain Crop Institute, Potchefstroom, South Africa

Introduction: During the past two decades, panicle-feeding Hemiptera became serious pests of sorghum in West and Central Africa. Prior to this study, no research had been done on these insects in South Africa. Objectives of this study were to determine the abundance and diversity of panicle-feeding Hemiptera on sorghum.
Methods: Collection was done using a plastic bag method and a D-Vac. A check list was compiled and the temporal distribution of different Hemiptera species determined during panicle development.
Results: The total number of adults and nymphs collected during this study was 23 798. Forty herbivorous Hemiptera species were collected. The most abundant family was the Miridae followed by the Lygaeidae which made up 41 % and 17 % respectively of the total number of individuals. *Eurystylus bellevoyi*, *Campylomma* sp., *Creontiades pallidus*, *Nysius natalensis*, *Nezara viridula* and *Sthenaridea suturalis* were the most abundant species and also occurred widely in the sorghum production area. Infestation levels of these species were generally low compared to that in other parts of Africa but comparatively high infestation levels were observed at some sites. There was no clear distinction between insect numbers during different panicle development. The general tendency was that nearly all species were present from the flowering stage onwards and that numbers declined when grain hardened. The predatory Hemiptera, *Orius* sp. and *Deraeocoris* sp., were recorded at all sampling sites.
Conclusion: Future research should be directed at establishing the relationship between the incidence of Hemiptera infestation and yield or quality loss of sorghum.

POSTER PRESENTATION

Water mite fauna in the Sakha Republic, Russia

Hiroshi Abe, Semenchenko Ksenia, Gennady Boeskorov

[1]Nihon University, Fujisawa, Kanagawa, Japan, [2]Institute of Biology and Soil Sciences, Vladivostok, Russian Federation, [3]Institute of Applied Ecology of the North Academy of Sciences of the Sakha Republic, Yakutsk, Russian Federation

A faunal survey of water mites was executed from 10 August 2006 to 27 August 2006 in Yakutsk and Tiksi, the north-eastern Siberia. During the survey four species (*Unionicola* (*Unionicola*) *gracilipalpis, Neumania* (*Neumania*) *vernalis, Arrenurus* (*Arrenurus*) *cf. cuspidifer, Midea orbiculata*) and three unidentified species (*Tiphys* sp., *Limnesia* sp., *Arrenurus* sp.) in Hydrachnellae and two species (*Porohalacarus alpinus*, *Porolohmannella violacea*) in Halacaridae were recorded from Yakutsk. Two species (*Tiphys* (*Tiphys*) *scaurus, Lebertia* (*Pilolebertia*) *porosa*) and two unidentified species (*Lebertia* sp*., Feltria* sp.) in Hydrachnellae were found in Tiksi. Among the water mites mentioned above, only one species, *Lebertia* (*Pilolebertia*) *porosa,* has been recorded from Yakutia, the other five species in Hydrachnellae and two species in Halacaridae were collected in Yakutia for the first time. All these species have a wide distribution in Eurasian continent and typical for the fauna in Europe.

POSTER PRESENTATION

The organosilicone, Break-Thru S240 and its effect on increased movement of a spray application into maize plant whorls and the efficacy of insecticides applied against stem borers in maize

Olivier Slabbert, Johnnie van den Berg, Dave Viljoen

North-West University, Potchefstroom, South Africa

Introduction: Chemical control of the maize stem borers *Busseola fusca* and *Chilo partellus* is often uneconomical or ineffective. Conventional insecticide applications often do not reach larvae inside whorl leaves. Thorough coverage of the target area is an important factor affecting the efficacy of insecticides. Organosilicones reduce the surface tension of water in spray solutions thus improving spreading of droplets on waxy, hydrophobic surfaces of the target plant's leaf surface. The aims of this study were to determine the effect of different dosages of the organosilicone, Break-Thru S240, on the depth of water movement into whorls of maize plants as well as the efficacy of different insecticides applied with the organosilicone Break-Thru S240.

Methods: In one experiment a colorant dye was added to indicate movement of the spray into plant whorls. In the other experiment insecticides were applied together with Break-Thru S240. All treatments were applied by using a CO_2-pressurised knapsack sprayer. Five plants of each replicate were sampled and dissected to determine the distance of movement of the spray application into plant whorls. The number of surviving larvae (*Chilo partellus*) on ten plants per replicate was counted to determine insecticide efficacy.

Results: The addition of Break-Thru S240 resulted in an increased distance of movement of water applications into plant whorls as well as an increase in insecticide efficacy.

Conclusion: This study provides information about the increased movement of organosilicones, water and insecticide applications on maize plants, which may lead to improved stem borer control measures.

POSTER PRESENTATION

Pr-lynx1, a modulator of nicotinic acetylcholine receptors in the insect

Young Moo Choo[1], Kwang Sik Lee[1], Bo Yeon Kim[1], Jianhong Li[2], Jong Gill Kim[3], Jae Heon Lee[1], Hung Dae Sohn[1], Byung Rae Jin[1]

[1]Dong-A University, Busan, Republic of Korea, [2]Huazhong Agricultural University, Wuhan, China, [3]National Institute of Agricultural Science and Technology, Suwon, Republic of Korea

Introduction: Insect nicotinic acetylcholine receptors (nAChRs) are targets for insecticides. Despite the importance of the nAChR as a major target for insecticide action, modulators of nAChRs in insects remain unidentified. Here we describe the cloning and identification of a nAChR modulator gene in an insect.

Results: A nAChR modulator gene was isolated by searching the firefly *Pyrocoelia rufa* cDNA library, and the gene itself encodes a protein 120 amino acids in length, named *Pr-lynx1*. *Pr-lynx1* shares all the features, including a cysteine-rich consensus motif and common gene structure, of the *Ly-6*/*neurotoxin* superfamily. The recombinant Pr-lynx1, which is expressed as a 12-kDa polypeptide in baculovirus-infected insect Sf9 cells, is normally present at the cell surface as a GPI-anchored protein. Northern and Western blot analyses revealed that Pr-lynx1 is expressed in various tissues, such as the ganglion, brain, mandibular muscle, proventriculus, leg muscle, and epidermis. This expression pattern is similar to the distribution of nAChRs as assayed by α3 nAChR immunoreactivity. Co-expression of Pr-lynx1 in *Xenopus* oocytes expressing α3β4 nAChRs results in an increase in acetylcholine-evoked macroscopic currents

Conclusion: Our results indicate a functional role of Pr-lynx1 as a protein modulator for nAChRs. This study on *Pr-lynx1* is the first report of a modulator of nAChRs in an insect species.

POSTER PRESENTATION

Biochemical characterization of venom from the endoparasitoid wasp *Pteromalus puparum* (Hymenoptera: Pteromalidae)

Jia-Ying Zhu, Gong-Yin Ye, Zhong Zhang, Cui Hu

Institute of Insect Sciences, College of Agriculture and Biotechnology, Zhejiang University, Hangzhou 310029, China

Introduction: *Pteromalus puparum* is a predominant pupal endoparasitoid of *Pieris rapae*, which has evolved a unique means to adapt to the hosts immune system, as there are no other parasitoid-associated factors other than venom are found in the female reproductive organ. The biochemical characters of its crude venom were preliminary investigated.

Methods: SDS-PAGE and two-dimensional (2-D) PAGE were used to explore the venom protein components. Cytotoxicity to hemocytes *in vitro* assay was performed to examine the effects of physical and chemical factors on the venom physiological functions. Different enzymatic methods were used for measuring the enzyme categories and its dynamic activity in the venom.

Results: SDS-PAGE profile revealed many bands of a broad of molecular weight range from 14.4 to higher than 116.0 kDa demonstrating the presence of numerous proteins in the venom. 2-D PAGE resulted in 56 evident protein spots with pI range from 4-7. With regard to the hemocytes cytotoxicity, the venom was sensitive to pH, temperature, host's larvae salivary secretion and mid-gut fluid incubation and some organic solution such as hexane, chloroform and methanol, while this was not the case for salt concentration (NaCl), proteinase K and the detergents such as SDS, Tween 20, Triton-X 100, NP 40 and CHAPS. Enzymatic assays indicated that acid phosphatase, alkaline phosphatase, phosphodiesterase, phospholipase, and esterase were present in the venom and their enzyme activities were time-course related to the parasitoid development.

POSTER PRESENTATION

Molecular cloning and characterization of a glycosyl hydrolase family 9 cellulase expressed throughout the digestive tract of the emma field cricket, Teleogryllus emma

Namjung Kim[2], Young Moo Choo[1], Kwang Sik Lee[1], Seong Jin Hong[2], Kwang Youl Seol[2], Yeon Ho Je[3], Hung Dae Sohn[1], Byung Rae Jin[1]

[1]Dong-A University, Busan, Republic of Korea, [2]National Institute of Agricultural Science and Technology, Suwon, Republic of Korea, [3]Seoul National University, Seoul, Republic of Korea

Introduction: A novel endogenous β-1,4-endoglucanase (EG) gene belonging to the glycosyl hydrolase family 9 (GHF 9) that is expressed throughout the digestive tract of the emma field cricket, *Teleogryllus emma*, was cloned and characterized.

Results: A novel EG gene, named *TeEG-I,* consists of eight exons encoding 453 amino acid residues and exists as a single copy in the *T. emma* genome. *TeEG-I* possesses all the features, including signature motifs and catalytic domains, of GHF 9 members, sharing high levels of identity with the termite, *Mastotermes darwiniensis* (64% protein sequence identity), and the cockroach, *Panesthia cribrata* (62%), GHF 9 cellulases. Recombinant TeEG-I, which is expressed as a 47-kDa polypeptide in baculovirus-infected insect Sf9 cells, showed an optimal pH and temperature of pH 5.0 and 40 ℃. The K_m and V_{max} values for digestion of carboxymethyl cellulose were 5.4 mg/ml and 3118.4 units/mg, respectively. Northern and Western blot analyses revealed that TeEG-I was expressed throughout the digestive tract, which correlated with the TeEG-I distribution and cellulase activity in the digestive tract as assayed by immunofluorescence staining and enzyme activity assay, respectively. These results indicate that TeEG-I is expressed throughout the entire digestive tract of *T. emma*, suggesting a functional role of endogenous TeEG-I in a sequential cellulose digestion process throughout the *T. emma* digestion tract.

Conclusion: Based on these results, we suggest that endogenous TeEG-I could be involved in sequential cellulose digestion throughout the *T. emma* digestive tract.

POSTER PRESENTATION

Selection of host plants for nest building by the Japanese foliage spider, *Cheiracanthium japonicum* (Araneae: Miturgidae)

Yutaka Hironaka, Hiroshi Abe

[1]Nihon University College of Bioresource Sciences, Fujisawa, Kanagawa, Japan, [2]Nihon University College of Bioresource Sciences, Fujisawa, Kanagawa, Japan

Introduction: The purpose of the present study is to elucidate the relationship between host plants and nest-types of *Cheiracanthium japonicum* in the developmental stages of the spider. The spider builds a nest mainly with a monocotyledonous plant leaf. Its nest forms vary not only according to the developmental stages of the spider but according to their use for molting, mating and breeding.

Materials and Methods: We examined the developmental stages of the spider and the plant species used to build a nest by the spider. The vegetation cover of the study area was fully investigated and the numbers of the nests and the host plant species were recorded. In addition, the leaf toughness and leaf width of each host plant were also recoded to examine physical factors relating to the spider's selection of host plant species.

Results and Discussion: As the developmental stages of the spider proceeded, the frequency of use of the two host plant species, *Miscanthus sinensis* and *Phragmites australis,* increased. Especially these two plants were typically used for breeding-nests. There was no significant relationship between the composition of the host plant species and that of the entire flora in the study area. Leaf toughness and leaf width of the host plants were correlated positively with the nest-type in the developmental stages. These results showed that *C. japonicum* recognizes the leaf toughness and leaf width and selects the preferable host plant according to the nest-types relating to the developmental stages.

POSTER PRESENTATION

Effect of the superparasitism and multiparasitism in the Biological Control of the "Pine Shoot Moth", Rhyacionia buoliana (Schiff.) (Lepidoptera: Tortricidae) in Chile.

Mar Ramos, Cecilia Ruiz, Dolly Lanfranco

Faculty of Forest Sciences, Universidad Austral de Chile, Valdivia, XIV region, Chile

Introduction: The superparasitism is a parasitoid strategy that supposes the presence of two or more larvae competing for the same host, resulting in the death of the less competitive larvae. This strategy takes place when the same host is attacked several times by the same female parasitoid species.

The multiparasitism or interespecífic superparasitism take place when the same host is attacked by two different species of female parasitoids.

Both strategies occur in the biological control of one of the pest species on the Chilean pine forest plantations, *Rhyacionia buoliana* (Schiff.) (Lepidoptera: Tortricidae).

The superparasitism produced by the introduced parasitoid *Orgilus obscurator* (Ness.) (Hymenoptera: Braconidae) and the multiparasitism given by a second parasitoid without specific determination yet, *Temelucha sp*. (Hymenoptera: Ichneumonidae), can be affecting the effectiveness of the biological control of this pest species.

Methods: A total of 268 larvae of *R. buoliana* were extracted of a field of the VIII region of South Chile and reared during four months under controlled conditions of laboratory. Every week, 10 larvae were dissected. The data obtained during the rearing were used in a model of population dynamics, to quantify the incidence of superparasitism and multiparasitism.

Results: The obtained results show a loss of effectiveness of the introduced parasitoid *O. obscurator* and a significant increase of larvae not parasitized, raising the population density of the pest species.

Conclusions: The competition resultant of the superparasitism and the multiparasitism between these two species is affecting the biological control of *R. buoliana* negatively.

POSTER PRESENTATION

Developing a predictive degree day model for field sand fly vector of visceral leishmaniasis in the Northwest of Iran

Mohammad Ali Oshaghi, Naseh Maleki, Ezat-aldin Javadian, Yavar Rassi, Zabiholah Zarei, Fatemeh Mohtarami

Tehran University of Medical Sciences, School of Public Health, Tehran, Islamic Republic of Iran

Introduction: Temperature plays a significant role in insect development where a rise in temperature accelerates the insect's metabolic rate, increases egg production and makes blood feeding more frequents. It also shortens and speeds up pathogen development within insects. Visceral leishmaniasis is one of the most important diseases which transmit by different sandfly species.

Methods: A phenological model was used to estimate number of generation, peak activity and temporal variability of the most important vector of VL, *Phlebotomus perfiliewi* in one of the main VL foci in northwest Iran. The development zero and the thermal requirements of *P.papatasi* were measured under laboratory conditions and were used as a model for *P.perfiliewi* under field condition.

Results: The complete life cycle (egg to egg) development of *P.papatasi* required 273 degree day (DD) and developmental zero (Dz) values were 12.99℃ for egg, 23.07℃ for larvae, and 21.23℃ for pupa. Field samplings of adult *P. perfiliewi* determined that the first adult population occurred in mid-to-end June. The highest population density was observed in early August, but that in early September the population density decreased rapidly, with the adult population disappearing completely in late September. Matching the population dynamics with the development data revealed that in Germi region, *P.perfiliewi* has only one generation per year.

Conclusion: This is the first phenological study about vectors of VL in Iran. The phenological data could be used in constructing effective control programs against the diseases and their vectors.

POSTER PRESENTATION

Life cycle traits of *Cheiracanthium lascivum* examined by a breeding experiment

Haruhiro Rokuta, Yutaka Hironaka, Hiroshi Abe

[1]Department of Animal Science and Resources, College of Bioresource Sciences, Nihon University, Fujisawa, Kanagawa, Japan, [2]Graduate School of Bioresouce Sciences, Nihon University, Fujisawa, Kanagawa, Japan, [3]Biological Laboratory, College of Bioresource Sciences, Nihon University, Fujisawa, Kanagawa, Japan

Up to date, detailed studies on the life cycle and the ecology of *Cheiracanthium lascivum* have been quite limited. The purpose of the present study is to elucidate the hatching period, disperse time, molting period, and mortality rate of the spiderlings, and to study the female's behavior from reproduction till death under the laboratory conditions. The reproduction occurred only once a year and the females' reproduction period was about a month long. The post-reproduction period was estimated to be less than a month long. The females didn't eat anything during their maternal care — like spiders of the family Salticidae, Antrodiaetidae, etc. Hatchings took place during about two weeks, and then the spiderlings molted into the second instar in the cocoon. The spiderlings dispersed seven days after their hatching. The intervals between instars correlated positively with the age development. The mortality rate was the highest in the second instar after dispersing.

POSTER PRESENTATION

Evaluation of some selective preparations for the control of the mushroom phorid fly, Megaselia halterata (Wood)

Fedai Erler[1], Ersin Polat[2], Halil Demir[2], Huseyin Cetin[3], Tugba Erdemir[1]

[1]Akdeniz University, Faculty of Agriculture, Department of Plant Protection, Antalya, Turkey,
[2]Akdeniz Universit, Faculty of Agriculture, Department of Horticulture, Antalya, Turkey,
[3]Akdeniz University, Faculty of Arts and Science, Department of Biology, Antalya, Turkey

Introduction: Over the last decade, cecidomyiid, sciarid and phorid flies have become one of most damaging pest groups of mushroom in the Antalya-Korkuteli district (southwestern Turkey) where about 45% of the total mushroom production and more than 50% of the total compost production of the country are produced.

Methods: Three commercial microbial preparations [a bacterial larvicide, *Bacillus thuringiensis* var. israelensis (*Bti* for short) - Gnatrol®; a granulavirus - Madex®; and an entomopathogenic nematode, *Steinernema feltiae* - Entonem®)] and a biologically derived insecticide, spinosad - Laser® were evaluated for the control of *Megaselia halterata* (Wood) (Diptera: Phoridae), the most common species in the district, by soil drench to sufficiently wet the top 10-cm soil surface layer where larvae are found. The effect of the test materials were evaluated by measuring larval damage (mean number of mushroom fruits damaged by the larvae per bag) and counting the emerging adults of the pest (mean number of emerging adults per bag) in each treatment.

Results: *Bti* and spinosad were found the most active materials, but had a short-term efficacy. Although *S. feltiae* was less active than *Bti* and spinosad, it had a long-lasting activity which lasted until the growing period was completed. The granulavirus (Madex) was found the least active preparation used in the study.

Conclusions: Our overall results suggest that *Bti*, spinosad and *S. feltiae* can be used as alternatives to conventional insecticides used in the control of mushroom phorid fly.

POSTER PRESENTATION

Spectral sensitivity in two winged forms of the black bean aphid

Thomas Döring, Sayako Arai, Jim Hardie

Imperial College London, Ascot, United Kingdom

Introduction: Although the visual sense is of considerable importance for host finding in herbivorous insects, only little is known about their colour vision. Therefore, electroretinogram measurements were conducted to measure spectral sensitivity of the compound eye in winged female gynoparae and virginoparae of *Aphis fabae*.

Methods: Light flashes (0.5 s), varied in wavelength (320 to 640 nm, 10 nm steps) and in light intensity were produced with a Xenon lamp and monochromatic and grey filters. The flashes were applied to the eye either after dark adaptation or after adaptation in yellow light, (5 animals per adaptation condition and per morph). The summed response from light sensitive cells was recorded with a tungsten electrode inserted into the eye, while an indifferent electrode rested in the abdomen. The amplified signal was displayed on a PC.
Results: The overall shape of the sensitivity curve was similar in gynoparae and virginoparae. Pooled data from both morphs revealed maximal spectral sensitivity at 550 nm after dark adaptation and at 530 nm after yellow adaptation. Sensitivity to blue light was significantly increased after yellow adaptation compared to dark adaptation. Sensitivity sharply decreased with increasing wavelengths >550 nm and was very low (<2.5%) in the red domain (640 nm).

Conclusions: The results suggest that *A. fabae* at least possesses a green receptor and possibly also a blue receptor, but that the presence of a red receptor is unlikely.

POSTER PRESENTATION

Life stage composition of growing cultures of the house dust mite, Dermatophagoides farinae

Swetha Poola, Larry Arlian, Marjorie Morgan

Wright State University, Dayton, OH, United States

Background: House dust mites are a major source of indoor allergens in homes worldwide. Commercially grown dust mites are used to make extracts for diagnostic testing and immunotherapy. The life stage composition and allergen content of mite populations in developing cultures used to make extracts is relatively undefined. The purpose of this study was to define the population growth rate, life stage profile and allergen content of growing cultures of *Dermatophagoides farinae*.

Methods: *Dermatophagoides farinae* was cultured and the mite and allergen characteristic of the culture determined at 2-week interval for up to 10 weeks.

Results: The mite population grew exponentially for the first 6 weeks and then remained relatively stable at 8 and 10 wks as the growth medium was depleted. Larvae were the most numerous developing life stage at all times but were particularly abundant during the early 4-6 week growth period. Among all life stages, adults (females and males) were the most abundant stages at all times and comprised the highest percentage of the population during weeks 8 and 10 when the population size had plateaued. Protonymphs were the least numerous life stage during the entire 10-week culture period and comprised <5% of all active life stages. Egg density in the cultures increased during weeks 2, 4, and 6 and peaked at week 8 and declined at week 10.

Conclusion: The life stage composition of a developing culture changes as the mite population increases in size and this may effect the allergen composition of the culture.

POSTER PRESENTATION

Field responses of *Halyomorpha halys* to methyl 2,4,6-decatrienoate

George Hamilton[1], Ashot Khrimian[2], Peter Shearer[3]

[1]Rutgers University, New Brunswick, NJ, United States, [2]USDA ARS, Beltville, MD, United States, [3]Rutgers University Agricultural Research and Extension Center, Bridgeton, NJ, United States

In the United States, *Halyomorpha halys* (Stål) (Hemiptera: Pentatomidae)is a polyphagous, introduced Asian pest that damages various trees, vegetables, and leguminous crops. In its native range, it is reported to be attracted to methyl (2*E*,4*E*,6*Z*)-decatrienoate, the aggregation pheromone of the brown-winged green bug, *Plautia stali*. In 2003 and 2004, we conducted studies to evaluate the attractiveness of this compound and its isomers, methyl (2*Z*,4*E*,6*Z*)-decatrienoate and methyl (2*E*,4*Z*,6*Z*)-decatrienoate, to late fall individuals. In 2005 and 2006, we conducted additional field trials in late fall to evaluate the attractiveness of traps baited with 0, 0.5, 2.5, 7.5 and 25 mg of methyl (2*E*,4*E*,6*Z*)-decatrienoate per trap and placed in different plant systems. We found that methyl (2*E*,4*E*,6*Z*)-decatrienoate and its isomers, as well as mixtures of geometric isomers, were attractive to *H. halys* males, females and nymphs. The data suggest that the presence of the *EEZ* but not *ZEZ* isomer is essential for attracting *H. halys* and other isomers do not appear to be antagonistic and may be needed for maximum attraction. We also found, regardless of plant system tested, that traps baited with high amounts of pheromone (7.5 and 25mg) caught significantly more individuals than traps baited with lesser amounts.

POSTER PRESENTATION

Age and reproduction in the parental burying beetle, *Nicrophorus orbicollis*

Stephen Trumbo

University of Connecticut-Waterbury, Connecticut, United States

Introduction: Three hypotheses have been proposed to explain enhanced reproductive performance with age: the restraint hypothesis (young individuals restrain current reproductive effort because a high level of current effort might put future reproductive opportunities at risk), the constraint hypothesis (young individuals are constrained because of a lack of skills or accumulated resources), and the selection hypothesis (there is more time for less fit individuals to be selected out of an older cohort). Burying beetles are a favorable group with which to examine these hypotheses because they have short but discrete reproductive/parental cycles during which they prepare a small vertebrate carcass as a food source for young.

Methods: Using a laboratory population of *Nicrophorus orbicollis*, we reduced adult mortality to zero, and equalized social experience during the pre-reproductive period across age groups, thereby eliminating consideration of the selection or constraint hypotheses. We then tested the restraint hypothesis by providing young (20-25 days) or old (52-58 days) single females with a breeding resource and later introducing a potentially infanticidal female (young or old).

Results: In Experiment 1, older parents were more likely to produce a brood and were faster to oviposit, and older intruders were more likely to take over a carcass. Age was not related to any measure of performance once a parent had a brood (probability of successful defense against infanticide, number and mass of larvae in original broods, number and mass of larvae in replacement broods by intruders). In a follow-up experiment using smaller carcasses (Experiment 2), age of the parent, again, was not related to successful defense of the brood, or to number and mass of larvae, suggesting that the high level of reproductive success of young females in Experiment 1 was not due to the large potential reward.

Conclusion: In *Nicrophorus orbicollis* the reproductive restraint observed in younger individuals appears to occur in a step-wise manner, inhibiting the initiation but not the continuance of reproductive attempts.

POSTER PRESENTATION

Colour learning in honeybees using a classical conditioning paradigm

Claudia Niggebrügge[1], Gérard Leboulle[1], Bernhard Komischke[1], Randolf Menzel[1], Natalie Hempel de Ibarra[2]

[1]Free University of Berlin, Berlin, Germany, [2]University of Exeter, Exeter, United Kingdom

Introduction: Bees learn colours quickly under free-flight conditions. Here we report about our success to train fixed bees to colours in a classical conditioning paradigm.

Methods: Harnessed bees with cut antennae were exposed during 10 conditioning trials to a sugar reward preceded and paired with a coloured stimulus. They learned to extend their proboscis (PER) towards the colour stimulus prior to reward and in unrewarded tests.

Results: After an absolute conditioning, accompanied by a response increase of 50-60%, bees learned the hue of the rewarded colour and showed broad colour generalisation. Differential conditioning resulted in different acquisition performances for rewarded and unrewarded stimuli, i.e. discrimination learning, only when colours were very dissimilar. Brightness contrast did not contribute to discrimination learning. Decline in responses in unrewarded trials after a training of either three or seven conditioning trials indicates that the conditioned PER is prone to extinction.

Conclusions: We conclude that colour learning occurred and memory was established within a few pairings of colour and sugar reward, similarly to free-flight conditions. We aim to implement this behavioural paradigm in the study of visual mechanisms in bees using electrophysiological and molecular-biological techniques.

POSTER PRESENTATION

Vertebrates that are victimized by an insect parasitoid: a remarkable host shift by the burying beetle, *Nicrophorus pustulatus*

Garrison Smith[2], Stephen Trumbo[1], Derek Sikes[3], Michelle Scott[4], Robert Smith[2]

[1]University of Connecticut-Waterbury, Waterbury, CT, United States, [2]University of Arizona, Tucson, AZ, United States, [3]University of Alaska Museum, Fairbanks, AK, United States, [4]University of New Hampshire, Durham, NH, United States

Introduction: Insects are well known to be parasitoids of other insects. An insect parasitoid of a vertebrate, however, is all but unknown. Recent work [Ecoscience (2000) vol. 7, 395-397] suggests that the burying beetle *Nicrophorus pustulatus* may have undergone a remarkable host shift, exploiting live reptile eggs rather than carrion as resources for breeding. We conducted behavioral and physiological experiments to test the hypothesis of a host shift and to formulate hypotheses on its origin.

Methods: From 1-5 snake or turtle eggs were provided to *N. pustulatus*, as well as to two congeners, *N. orbicollis* and *N. defodiens*, to measure the ability to produce offspring and to regulate brood size. In addition, *N. pustulatus* use of mouse carcasses vs. snake eggs was compared.

Results: Two congeners of *N. pustulatus*, *N. orbicollis* and *N. defodiens*, did not respond to snake eggs with typical breeding behavior. When *N. pustulatus* male-female pairs were presented with clutches of snake eggs the number of offspring but not the mean size of offspring varied with snake egg mass, indicating effective regulation of brood size. Turtle eggs were also utilized by *N. pustulatus*, but not as readily. *Nicrophorus pustulatus* presented with both snake eggs and a mouse carcass combined and exploited the two resources within the same nest (10 of 12 trials). Mouse carcasses and snake eggs were treated differently. Carcasses were moved, buried, and stripped of hair in a manner characteristic of burying beetles while snake eggs were not moved or buried. Females that discovered a mouse carcass also had a significantly greater juvenile hormone increase than did females discovering snake eggs. Some responses to the two resources, however, were similar. Female *N. pustulatus* oviposited rapidly in response to either a mouse carcass or snake eggs, and males elevated sex pheromone emission in response to either resource.

Conclusion: The efficient use of snake eggs, the ability to regulate brood size, and the different responses to snake eggs and to carrion suggest that *N. pustulatus* is well adapted to exploiting snake eggs for breeding. The use of eggs of vertebrates by *N. pustulatus* has potential implications for conservation of oviparous reptiles in North America.

POSTER PRESENTATION

Appearance, spreading, current status and risk assessment of invasive mosquito species of *Aedes albopictus* (Diptera, Culicidae) in Croatia

Enrih Merdić[1], Toni Žitko[2], Nediljko Landeka[3] and Sanja Merdić[1]

[1]Department of Biology, University of J.J. Strossmayer in Osijek, Croatia, [2]Health Public Institute of Split-Dalmatia county, Split, Croatia, [3]Health Public institute of Istria county, Pula, Croatia

Introduction: The invasive mosquito species of *Aedes albopictus* has been introduced in several European countries since 1975. In 2007 the species was recorded in Albania, Bosnia and Herzegovina, Croatia, Greece, France, Italy, the Netherlands, Serbia and Montenegro, Slovenia, Spain and Switzerland. It was proved that this species had the vector rule in Chicungunya virus transmission in Italy in 2007.

Methods: No European standard is currently available for vector surveillance methods, which influences the comparability of data between countries. Different surveillance methods currently used in Europe include ovitraps, carbon dioxide-baited CDC traps and larval surveys, we used them too.

Results: The first record of *Aedes albopictus* in Croatia was made in the capital city of Zagreb, in continental Croatia. The arrival is connected with companies dealing with the import of used tires. The following year, in 2005 the species appeared on the Adriatic coast: several sites on the Istria peninsula, and big cities of Zadar, Split and Dubrovnik, Findings of this species on the islands of Cres, Lošinj, Hvar and Vis, in 2007 (very attractive tourist destinations), prove that the spreading was done by yachts.

Conclusions: The risk assessment is dependent on four environmental conditions: winter temperature ≥0˚C; rainfall is at least 500mm; there is sufficient amount of summer rainfall and optimal summer temperatures (25˚C-30˚C). Local characteristics and microclimates should be considered for both establishment and abundance. The vector surveillance in Croatia must be conducted in those areas of high risk for establishment (Istria), because this species is known as high vector competence species.

POSTER PRESENTATION

Appearance, spreading, current status and risk assessment of invasive mosquito species of Aedes albopictus (Diptera, Culicidae) in Croatia

Enrih Merdić[1], Toni Žitko[2], Nediljko Landeka[3] and Sanja Merdić[1]

[1]Department of Biology, University of J.J. Strossmayer in Osijek, Croatia, [2]Health Public Institute of Split-Dalmatia county, Split, Croatia, [3]Health Public institute of Istria county, Pula, Croatia

Introduction: The invasive mosquito species of *Aedes albopictus* has been introduced in several European countries since 1975. In 2007 the species was recorded in Albania, Bosnia and Herzegovina, Croatia, Greece, France, Italy, the Netherlands, Serbia and Montenegro, Slovenia, Spain and Switzerland. It was proved that this species had the vector rule in Chicungunya virus transmission in Italy in 2007.

Methods: No European standard is currently available for vector surveillance methods, which influences the comparability of data between countries. Different surveillance methods currently used in Europe include ovitraps, carbon dioxide-baited CDC traps and larval surveys, we used them too.

Results: The first record of *Aedes albopictus* in Croatia was made in the capital city of Zagreb, in continental Croatia. The arrival is connected with companies dealing with the import of used tires. The following year, in 2005 the species appeared on the Adriatic coast: several sites on the Istria peninsula, and big cities of Zadar, Split and Dubrovnik, Findings of this species on the islands of Cres, Lošinj, Hvar and Vis, in 2007 (very attractive tourist destinations), prove that the spreading was done by yachts.

Conclusions: The risk assessment is dependent on four environmental conditions: winter temperature ≥0˚C; rainfall is at least 500mm; there is sufficient amount of summer rainfall and optimal summer temperatures (25˚C-30˚C). Local characteristics and microclimates should be considered for both establishment and abundance. The vector surveillance in Croatia must be conducted in those areas of high risk for establishment (Istria), because this species is known as high vector competence species.

POSTER PRESENTATION

Insect pests on urban greenery in Croatia

Aleksandar Mešić[1], Josip Barčić[2] and Jasminka Igrc Barčić[1]

[1]*Department for Agricultural Zoology, Faculty of Agriculture, University of Zagreb, Zagreb, Croatia,*
[2]*Department for Agricultural Engineering, Faculty of Agriculture, University of Zagreb, Zagreb, Croatia*

Introduction: Urban greenery in is attacked by different insects species. Large population of those pests usually provoke important damages on urban greenery and decrease their ecological, esthetical and other functions.

Methods: The pests of the most importance Croatia (*Aesculus hippocastanum*, *Platanus spp., Rosa spp., Acer spp., Buxus spp., Quercus spp.* and *Robinia pseudoacacia*) were researched in Zagreb and Sisak in period 2004-2007. The plant parts with symptoms of attack were evaluated in the laboratories where the pests were identified. The damages provoked by those insects were recorded and systematized.

Results: Damages on those plants were present each year. High populations of *Cameraria ohridella* were recorded each year on leaves of horse chestnuts and high populations of *Corythuca ciliata* and *Phyllonorycter platani* on plane trees. Aphids and some other insects attacked different species of roses and maple. Since 2005, total damages on leaves made by *Apethymus abdominalis* were recorded on many oaks. Small popultions of *Monarthoplpus buxi* ususaly attack *Buxus spp.*Two diffrent *Gracilariidae* species (*Phyllonorycter robiniella* and *Parectopa robiniella*) harms the black locust.

Conclusions: Each year high population of different insects provoke large damages on urban greenery. Such large populations must to be controlled by different insecticides.

POSTER PRESENTATION

Beauveria bassiana (Deuteromycotina) as a management agent for free-living ixodid ticks

Kenwyn Cradock[1], Glen Needham[2]

[1]Eastern New Mexico University, Portales, NM, United States, [2]The Ohio State University, Columbus, OH, United States

Introduction: Ticks, important disease vectors, spend much of their lives off-host. Various entomopathogenic fungi have shown potential as management agents under controlled laboratory conditions. Few studies have tested their effectiveness in the field. Unfed adult *Amblyomma americanum* were challenged with *Beauveria bassiana* GHA and placed in a field setting. The mortality of exposed ticks was compared with ticks not exposed to the fungus.

Methods: Unfed adult *Amblyomma americanum* were exposed to the entomopathogenic fungus *Beauveria bassiana* and placed in the field enclosed in BugDorm™ enclosures. Hobo data loggers were used to monitor environmental conditions both inside and outside the enclosures.

Results: Ticks exposed to the fungus experienced higher mortality than those in the control group ($p = 0.001$). The BugDorm™ enclosures did not have a biologically significant impact on environmental conditions, increased the recovery rate of study organisms, and successfully prevented unwanted organisms from removing ticks from the study.

Conclusions: *Beauveria bassiana* has potential as a useful component of tick management programs targeting off-host ixodid ticks such as *Amblyomma americanum*. It is recommended that for inclusion in a tick management program, the fungus be applied in the late evening when conditions suitable for fungal activity occur.

POSTER PRESENTATION

Physiological effects of infection with *Beauveria bassiana* (Deuteromycotina) in A*mblyomma americanum* (Ixodidae).

Kenwyn Cradock[1], Glen Needham[2]

[1]Eastern New Mexico University, Portales, NM, United States, [2]The Ohio State University, Columbus, OH, United States

Introduction: Fungal infection can result in altered behavior and physiology of infected arthropods. Although mortality may require an extended time of infection, changes in behavior due to altered physiology may still make microbial control agents effective. *Amblyomma americanum* were infected with *Beauveria bassiana* GHA to determine the effect of infection on water balance and survival relative to uninfected ticks.

Methods: Unfed adult *Amblyomma americanum* were exposed to *Beauveria bassiana*. All ticks were placed in desiccation chambers at 80%RH just below the critical equilibrium activity for the species. Change in weight was used to indicate water loss.

Results: Treated ticks survived an average of 7.2 ± 0.22 days. Control ticks survived 17.88 ± 0.73 days on average ($p = 0.01$; $df = 57$). At death, ticks exposed to the fungus had lost 25.2% ± 0.84 of their starting weight. Control ticks had lost 14.08% ± 0.85 of their starting weight (p 0.01; df = 96). Water loss was highest immediately following inoculation and then declined, although losses continued to be higher in exposed ticks.

Conclusions: This suggests that the penetration of the fungus causes sufficient damage to the cuticle to cause desiccation. Alternatively, infection may negatively impact the ticks' ability to rehydrate using water extracted from sub-saturated atmospheres, or infection increases the rate of spiracular opening resulting in increased water loss. Any or all of the impacts may cause alteration in behavior and reduce survival.

POSTER PRESENTATION

Intra- and interspecific bacterial diversity within the gut microbiota of fungus-growing termites (Macrotermitinae) from Kenya

Andreas Marten[1], Hamadi I. Boga[2], Janet Andert[2], Manfred Kaib[3], Andreas Brune[2], Roland Brandl[1]

[1]Department of Animal Ecology, University of Marburg, Marburg, Germany, [2]Max Planck Institute of Terrestrial Microbiology, Marburg, Germany, [3]Department of Animal Physiology, University of Bayreuth, Bayreuth, Germany

Termites are important decomposers in tropical ecosystem. The guts of termites harbour diverse communities of bacteria responsible for degradation of plant material. So far we have little knowledge about the variability of the gut microbiota with space as well as between closely related species.

Major workers from colonies of *Macrotermes michaelseni (*27 colonies*)*, *M. subhyalinus* (5) and *M. herus* (3) were sampled across Kenya. We constructed a clone library of the 16S rRNA gene for the gut microbiota of *M. michaelseni*. The clone library was dominated by Firmicutes (42%), Bacteroidetes (38%) and Proteobacteria (11%). Almost all clones were related to sequences isolated from guts of other termite species. Obviously the microbiota in the guts of *Macrotermes* are assemblages of bacteria specific to termites. Further, we calculated Morisita-Horn-similarity-indices and run a correspondence analysis (CA) based on t-RFLP profiles of the 16S rRNA gene to compare intra- and interspecific bacterial diversity. The CA shows no differentiation of the bacterial communities between the three termite species. Similarity-indices between communities within host species were similar to the similarity between hosts. Focussing on the similarity between colonies of *M. michaelseni* we found no consistent pattern of community composition in microbiota with space. High turnover between bacterial communities were found even between neighbouring colonies as well as low turnover between distant colonies (> 400km).

We conclude that on the limited level of taxonomic resolution of the t-RFLP method the bacterial communities of the gut within the Macrotermitinae show no species-specific differences and no spatial structure.

POSTER PRESENTATION

Foraging behaviour and reproductive strategy of *Callonychium chilense* (Apoidea: Andrenidae: Calliopsini) on *Eryngium paniculatum* (Umbrelliferae) in central Chile

Víctor Hugo Monzon[1], Luisa Ruz[2]

Pontificia Universidad Católica de Valparaíso, Valparaíso, Chile[1]
Universidad Católica del Maule, Talca, Maule, Chile[2]

Callonychium chilense (Friese, 1906) is a solitary bee that belongs to the tribe Calliopsini, within which it belongs to the most phylogenetically derived genus. The species of *Callonychium* are mostly oligolectic. Behavioural observations of *C. chilense* were made at Cobquecura, a coastal area of central Chile, (36°08'00''S - 72°47'00''W) in January, in 1991 and 1992, before the invasion of *Bombus ruderatus*. The abiotic conditions were also evaluated. The study site was sandy with medium-sized vegetation of shrubs, herbs and grasses. *C. chilense* prefers *Eryngium paniculatum* for its daily foraging and mating activities which take place from 09:00 to 18:00 h. The females arrived first at the flowers to forage. They take a position at less than 45° to the stamens, grasp the anthers with their mandibles and extract the pollen with the forelegs, which is then transferred to the posterior legs. The males patrol the inflorescences and mate with the females while foraging, but use special strategies to grasp them necessitated by their smaller size. The mating peak occurred at 11:30 to12:30 h. Mating lasted for a maximum of 20 minutes, after which the couple fly together to a different plant far away. The abundance of females at the beginning of the reproductive period did not necessarily determine short matings. The males of *C. chilense* perform only one of the known mating strategies, like *C. coquimbense* also from Chile, but not three strategies as happens in *C. petuniae* from Brasil.

POSTER PRESENTATION

The influence of temperature and aphid host at development time and parasitoid size of *Aphidius colemani* Viereck and *Aphidius transcaspicus* Telenga (Hymenoptera: Aphidiidae)

Nikolaos Garantonakis, Dionyssios Lykouressis and Dionyssios Perdikis

Laboratory of Agricultural Zoology and Entomology, Agricultural University of Athens, Iera Odos 75, 11855 Athens, Greece.

Introduction: *Aphidius colemani* Viereck and *Aphidius transcaspicus* Telenga are koinobiont solitary oligophagous aphid parasitoids. The influence of temperature and aphid host on the development time and at the size of the parasitoids *A. colemani* and *A. transcaspicus* was studied. As aphid host, *Aphis gossypii* and *Myzus persicae* was used.

Methods: On an eggplant leaf 30 individuals of second instar of *M. persicae* or *A. gossypii* were placed using a fine paintbrush and left for 1 h to settle down. Then, a female parasitoid (*A. colemani* or *A. transcaspicus*) was released in each petri dish. After the first attack on an aphid, the dish was transferred in a growth cabinet at 15, 20, 25, 27,5 or 30 ^{o}C, 65±5% R.H. and 16L:8D photoperiod. The parasitoid was allowed to forage in the dish for 30 minutes. The development time and the size of the emerged parasitoids was estimated by body length and length of the right hind tibia.

Results: The development time was found to be longer in parasitoids which developed at 15^{o}C. Longer body size was found in parasitoids which developed at 15 ^{o}C having as host the aphid *M. persicae*.

Conclusions: Both factors temperature and aphid host were found to affect the development time and size of the progeny.

POSTER PRESENTATION

Predation rate of *Macrolophus pygmaeus* (Hemiptera: Miridae) on aphid prey species

Dionyssios Lykouressis, Dionyssios Perdikis and Ioannis Mandarakas

Laboratory of Agricultural Zoology and Entomology, Agricultural University of Athens, Iera Odos 75, 118 55 Athens, Greece

Introduction: The predation rate of the polyphagous predator *Macrolophus pygmaeus* was investigated on all instar nymphs of *Aphis gossypi* when offered alone and together with nymphs of the aphids *Myzus persicae* or *Macrosiphum euphorbiae*.

Methods: Equal (10 nymphs of each instar, 40 in total) or unequal numbers (18, 13, 7 and 2 nymphs from each of 1st, 2nd, 3rd and 4th instars of *A. gossypii* alone or together with 18, 11, 8 and 3 nymphs from each instar of *M. persicae* or 19, 11, 7 and 3 nymphs from each instar of *M. euphorbiae*) were used. The aphids were placed on an eggplant leaf in a plastic Petri dish. In each dish one unstarved 5th instar nymph of the predator was introduced. The dishes were kept in a growth cabinet at 25°C, and the predation rate was recorded 24h after the introduction of the predator.

Results: Predation rates on *A. gpossypii* were similar to those on *M. persicae* but higher than *M. euphorbiae*. When equal number of nymphs of each instar of *A. gossypii* were offered alone, predation rate was similar among the instars but preference was highest for the 2nd and the 3rd instar and biomass consumption when feeding on the 3rd and 4th instars.

Conclusions: If other conditions have equal effect, *M. pygmaeus* can be more efficient in reducing *A. gossypii* numbers than *M. persicae* and *M. euphorbiae* on plants such as eggplants, where all these aphid species can occur.

POSTER PRESENTATION

Area-wide suppression of *Ceritidis capitata* and *Bactrocera dorsalis* in Kamuela Hawaii.

Roger I. Vargas[1], Eric B. Jang[1], Donald O. McInnis[1], Ernest B. Harris[1], Grant T. McQuate[1], Renato C. Bautista[3], Ronald F. L. Mau[2], Lyle Wong[3], Lester M. Klungness[1]

[1]USDA-ARS Pacific Basin Agric. Research Center, Hilo, Hawaii, United States, [2]University of Hawaii, College of Tropical Agric. & Human Resources, Honolulu, Hawaii, United States, [3]Hawaii Dept. of Agric., Honolulu, Hawaii, United States

Introduction: USDA Agricultural Research Service initiated a fruit fly suppression program for the State of Hawaii in 1999. The first suppression demonstration site was implemented in Kamuela, Hawaii in 2000.

Methods: *B. dorsalis* was suppressed with sanitation, bait spray, male annihilation using methyl eugenol, augmentation of parasitism using *F. arisanus* and the release of male sterile *B. dorsalis* in a 48 km^2 area containing urban, rural and agricultural zones. *C. capitata* females were suppressed with sanitation, bait spray and Biolure® traps.

Results: *C. capitata*: suppression techniques produced an 88.3% reduction in flies/trap/day (f/t/d) while fruit infestation declined 88.3%. *B. dorsalis*: reduction in fly captures over the 6 yrs of the treatments averaged 44.9%, but maximum reduction was 99.5% (comparing highest and lowest periods). Fruit infestation declined 60.67% over the period of bait spray application, and parasitoid augmentation, but began to increase after those treatments were suspended. The reduction in *B. dorsalis* from peak to lowest infestation was 98.1%. The 48 km^2 treatment area was compared to 3 control sites at 1, 9 and 10 km from Kamuela, over 4.64 years. The *C. Capitata* f/t/d at Kamuela was 94.7% lower and *B. dorsalis* f/t/d at Kamuela was 81.2% lower than the mean of the three control sites.

Conclusions: Combining suppression techniques in an area wide approach was effective in reducing tephritid flies below the economic threshold for crop production.

POSTER PRESENTATION

Genetic speciation of *Lutzomyia pseudolongipalpis* and *Lutzomyia longipalpis* s. l (species C2) and its vector biological- ecological implications in Venezuela.

Jazzmin Arrivillaga, Patricia Salerno

Universidad Simon Bolivar, Caracas,DF/SArtenejas, Venezuela

Reproductive isolation of two monophyletics vector species of visceral Leishmaniasis, *L. pseudolongipalpis* and *L. longipalpis* (species C2), from a sympatric area in Northwestern Venezuela was studied by mean of cross-mating experiments (homo and hetero-specific no selective cross) and isozymes diagnostic markers profile (AK and HK). The mating whereas the reciprocal mating (*L. pseudolongipalpis* females x *L. longipalpis* males) produced viable progeny (F1) and the detection of enzymatic markers codominance in the hybrids. However, fecundity and fertility were lower in comparison with co-specific mating. Asymmetric gene exchange between species (*L. pseudolongipalpis* males x *L. longipalpis* females= no eggs) and the lower production of offspring could suggest the occurrence of prezygotic and post zygotic isolation mechanisms, with re-forcing by sexual preference. In addition, the lack of natural hybrid would suggest a stronger isolation that keeps apart these species in nature than in experimental colonies.

Project S1 DID-USB to J. Arrivillaga

POSTER PRESENTATION

Oral trophallaxis between workers in the carpenter ant *Camponotus mus.*

Sarah Knish[1], Roxana Josens[2]

[1]Department of Biology, Georgia Institute of Technology, Atlanta, GA, United States, [2]Fac. of Exact and Natural Science, University of Buenos Aires, Buenos Aires, Argentina

Introduction: Sugar baits are commonly used in pest-control programs for nectivorous ants. Bait success depends on high food distribution among colony members, through mouth-to-mouth food exchanges (trophallaxis). The sugar concentration affects individual behaviours and sharing within the nest. This work analyses trophallaxis between pairs of workers as a function of the sugar concentration.

Methods: Pairs of foraging ants were isolated under controlled conditions. After an acclimation period, one ant (donor) was allowed to feed on a sucrose solution (from 10 to 60%w/w) and then returned to her partner (recipient). Time, volume, and rate were recorded for ingestion and trophallaxis.

Results: Time of both ingestion and trophallaxis, as well as volumes ingested and transferred, increased with increasing sucrose concentrations; however, 40%w/w tended to present the great proportion of load transferred. Both intake and transfer rates decreased with the concentration, but the ingestion rate decrease is more pronounced beyond 40%w/w. There is a direct relationship between intake rate and transfer rate, partially due to the effect of the viscosity on fluid dynamics (slower flow for more viscous solutions); however, this relationship is maintained within solutions of similar concentration.

Conclusions: Solution concentration affects both feeding and trophallaxis behaviours. Moreover, the correlations between crop load as well as intake rate with the transfer rate – independent of solution viscosity and the worker size – suggest that other factors must also affect transfer dynamics. Ants that fed faster demonstrated faster transfer rates. The same threshold involved in feeding responsiveness probably also affects solution-sharing behaviour.

This study was supported by CONICET PIP 5986.

POSTER PRESENTATION

Chemical ecology of the bedbug *Cimex lectularius* (Cimicidae)

Emma Weeks[1], Mike Birkett[1], Mary Cameron[2], James Logan[1], John Pickett[1]

[1]Rothamsted Research, Harpenden, Hertfordshire, United Kingdom, [2]London School of Hygiene and Tropical Medicine, London, United Kingdom

Introduction: The common bedbug, *Cimex lectularius* (Hemiptera: Cimicidae) is a major public health problem due to the biting nuisance caused when it feeds upon the blood of human hosts. Although little is known about bedbug behaviour, they are gregarious, and aggregate in response to semiochemicals. These semiochemicals could be exploited to develop monitoring tools to detect bedbug infestations. However, in order to study the response of bedbugs to semiochemicals, a suitable bioassay needs to be developed. A still air Petri-dish olfactometer, previously used to study aphid behaviour will be adapted for use with bedbugs.

Methods: A preliminary trial was completed using a volatile stimulus from intraspecific faecal material, a known aggregation signal for other Hemiptera. The stimulus was introduced into the arena, the behavioural response was observed, and the time spent active was recorded for 15 minutes per replicate. Twenty randomised replicates of experiments (stimulus present) and controls (no stimulus present), to test for bias in experimental design, were completed.

Results: Results of experiments indicated that the presence of faecal volatiles in the olfactometer caused a significant increase in time spent active when compared with controls.

Conclusions: The Petri-dish olfactometer is suitable to study the response of bedbugs to semiochemicals. The presence of faecal volatiles in the arena caused a three fold increase in bedbug activity. Further work with air entrainments, gas chromatography, electrophysiology and mass spectrometry will enable the identification of behaviourally active compounds which could be used to develop tools for bedbug monitoring and control.

POSTER PRESENTATION

Chemical ecology of the bedbug Cimex lectularius (Cimicidae).

Emma Weeks[1], Mike Birkett[1], Mary Cameron[2], James Logan[1], John Pickett[1]

[1]Rothamsted Research, Harpenden, Hertfordshire, United Kingdom, [2]London School of Hygiene and Tropical Medicine, London, United Kingdom

Introduction: The common bedbug, *Cimex lectularius* (Hemiptera: Cimicidae) is a major public health problem due to the biting nuisance caused when it feeds upon the blood of human hosts. Although little is known about bedbug behaviour, they are gregarious, and aggregate in response to semiochemicals. These semiochemicals could be exploited to develop monitoring tools to detect bedbug infestations. However, in order to study the response of bedbugs to semiochemicals, a suitable bioassay needs to be developed. A still air Petri-dish olfactometer, previously used to study aphid behaviour will be adapted for use with bedbugs.

Methods: A preliminary trial was completed using a volatile stimulus from intraspecific faecal material, a known aggregation signal for other Hemiptera. The stimulus was introduced into the arena, the behavioural response was observed, and the time spent active was recorded for 15 minutes per replicate. Twenty randomised replicates of experiments (stimulus present) and controls (no stimulus present), to test for bias in experimental design, were completed.

Results: Results of experiments indicated that the presence of faecal volatiles in the olfactometer caused a significant increase in time spent active when compared with controls.

Conclusions: The Petri-dish olfactometer is suitable to study the response of bedbugs to semiochemicals. The presence of faecal volatiles in the arena caused a three fold increase in bedbug activity. Further work with air entrainments, gas chromatography, electrophysiology and mass spectrometry will enable the identification of behaviourally active compounds which could be used to develop tools for bedbug monitoring and control.

POSTER PRESENTATION

DNA in support of tachinid taxonomy: matching the females with males in ancient described genera of Chilean Dexiini (Diptera: Tachinidae)

Antonio Rodríguez, Jose Núñez

Universidad Austral de Chile, Valdivia, XIV Region, Chile

Introduction: Tachinid taxonomy is plagued with incorrect identifications, in part due to early (s.XIX and beginning of s.XX) descriptions of species based mostly on combinations of characters too variable to be used in a classification. Furthermore, the descriptions based in more stable genitalic characters are mainly based in males, with absence of paratypes for many of the species described. The latter is the case of the related Patagonian Dexiini *Psecacera* Bigot, 1880; *Dasyuromyia* Bigot, 1885 and *Morphodexia* Townsend, 1931, after the revision of them by J. M. Aldrich in 1934.

Methods: In the course of a biodiversity inventory in the Chilean temperate valdivian forest, nine species belonging to the three genera were identified based in genitalic and first-instar larvae characters. For each of the individuals collected, total genomic DNA was extracted and COI was amplified and sequenced. A phylogeny of haplotypes was inferred to cluster together the males and females of the same species.

Results: The haplotype phylogeny shows strongly supported clades as assessed by bootstrapping, clustering together both sexes of the same species. Furthermore, allow to redescribe the species based in female genitalia and first-instar larvae, adding diagnostic characters to the description.

Conclusion: The used methodology allows us to test hypothesis about the conspecifity of the sexes inferred by the resemblance of the exemplars, and provides a powerful tool for the descriptive taxonomy.

POSTER PRESENTATION

Biology of a hyperparasitoid that disrupts biological control in New Zealand

Tara J. Murray[1,2], Sarah Mansfield[3]

[1]Scion (New Zealand Forest Research Institute Ltd), Rotorua, New Zealand, [2]Lincoln University, BioProtection & Ecology Division, Lincoln, New Zealand, [3]Faculty of Agriculture, Food & Natural Resources, University of Sydney, Sydney, Australia

The Australian hyperparasitoid *Baeoanusia albifunicle* (Hymenoptera: Encyrtidae) was discovered in the Central North Island of New Zealand in 2001. It's only known host in New Zealand is the biological control agent *Enoggera nassaui* (Hymenoptera: Pteromalidae), introduced in 1987 against the Eucalypt feeding pest *Paropsis charybdis* (Coleoptera: Chrysomelidae). In Australia, hyperparasitoids exert considerable regulatory pressure on the parasitoids of Eucalypt defoliators. There was concern therefore that in New Zealand *B. albifunicle* could disrupt the control of *P. charybdis* through its attack of *E. nassaui*. There was also some hope however that another recently arrived Pteromalid parasitoid of *P. charybdis* eggs, *Neopolycystus insectifurax*, could compensate for any decline in *E. nassaui*, as it was thought to be immune to hyperparasitoid attack.

We conducted laboratory research to determine basic biological characteristics of the hyperparasitoid to reveal its potential impact on *E. nassaui*. Data indicate that females are long lived and highly fecund with a high rate of parasitism success in the laboratory. Obligatory hyperparasitoid status was confirmed as *B. albifunicle* only developed successfully when oviposition followed parasitism by *E. nassaui*. *P. charybdis* eggs parasitised by *N. insectifurax* were occasionally accepted for oviposition but did not support hyperparasitoid development. Prior to this study it was thought that *E. nassaui* may find some refuge from the hyperparasitoid in southern New Zealand. We discuss the implications of field survey results which have indicated that *E. nassaui* has become more difficult to find and that *B. albifunicle* is now also established in the South Island.

POSTER PRESENTATION

A long-term experimental study of saproxylic beetle succession in Tasmanian *Eucalyptus obliqua* logs

Simon Grove, Dick Bashford, Marie Yee

Forestry Tasmania, Hobart, Tasmania, Australia

Concern over the conservation implications of declining availability of large logs in Tasmania's wet eucalypt production forests led to a long-term experiment examining succession of saproxylic (dead wood-dependent) beetles. This paper reports on the first sampling cycle, which spanned the first five years following the felling of six mature-aged and six regrowth-aged *Eucalyptus obliqua* trees growing in a multi-aged forest. These were felled over three seasons from May 1999 to February 2000. Five emergence traps were progressively fitted to each resultant log at roughly three-monthly intervals; and each was left in place for about three years. At total of 11546 individuals and 311 species of saproxylic beetles were sampled from the twelve logs. Twenty species made up 75% of the individuals, while 66 were represented by singletons. Seasonal patterns in abundance, species richness and assemblage composition were evident. The sampling cycle coincided with an initial pulse in abundance; the time-lag between felling and trap fitting did not noticeably influence this pattern. However, the height of the summer abundance peaks was weakly related to the date of felling. Different species showed different patterns in their annual peaks over this period. Obligately saproxylic species were more numerous than facultatively saproxylic species; species able to disperse by flight were much more numerous than crawlers; predators comprised the most abundant feeding guild; and there were roughly equal numbers of litter/surface dwelling and log interior-dwelling species. The lower collecting bottles tended to preferentially sample 'crawlers' and the upper collecting bottles 'fliers'. This paper documents the findings from merely the first sampling cycle of many that will be undertaken as the logs decay over coming decades or centuries. It provides a baseline assessment of the fauna, and gives the context for future studies, including those assessing relationships of this fauna with log size.

POSTER PRESENTATION

The effectiveness of wildlife habitat strips in maintaining mature forest carabid beetle assemblages

Simon Grove[1], Belinda Yaxley[3], Robert Taylor[2]

[1]Forestry Tasmania, Hobart, Tasmania, Australia, [2]Dept of Environment and Climate Change, Dubbo, NSW, Australia, [3]University of Tasmania, Hobart, Tasmania, Australia

A long-term research project was established in wet eucalypt forest at Tarraleah in Tasmania's central highlands, to assess the effectiveness of wildlife habitat strips (WHS) in maintaining the fauna of intact mature native forest. The present study examined carabid beetles sampled by means of pitfall traps. Samples were collected at multiple locations at one control site and two treatment sites, firstly before harvesting and then again five to six years after harvesting and regeneration and the establishment of WHS. Areas that had been logged showed decreases in abundance of carabid beetles, but great increases in species richness as pioneer or open-country species colonised. Assemblages in the control site remained essentially unchanged. Assemblages in the WHS areas remained little changed overall compared to their pre-harvest condition, but some sampling locations showed some degree of perturbation, though not always in a way comparable to the logged areas. It seems that for carabid beetles at least, WHS are largely fulfilling one of their functions of maintaining the fauna of mature native forest in a production forest landscape dominated by younger forest age-classes. Further monitoring will be required in coming decades to assess the long-term viability of WHS as a conservation strategy for these and other species of mature native forest. For instance, it is not yet apparent whether WHS can act as sources for recolonisation of surrounding regenerating forest as it matures, nor whether they can maintain their structural and functional integrity over time.

POSTER PRESENTATION

Seasonal occurrence of oriental beetle, Exomala orientalis (Coleoptera: Scarabaeidae) in Korean golf courses

Dong Woon Lee[1], Ho Yul Choo[2], Sang Myeong Lee[3], Jae Ho Kim[4], and Jong Chang Shin[5]

[1]Department of Applied Biology, Kyungpook National University, Sangju, Gyeongguk, Korea, [2]Department of Applied Biology and Environmental Sciences, Institute of Agricultural and Life Sciences, Gyeongsang National University, Jinju, Gyeongnam, Korea, [3]Southern Forest Research Center, Korea Forest Research Institute, Jinju, Gyeongnam, Korea. [4]Gimpo Seaside Country Club, Gimpo, Gyeonggii, Korea, [5]Dongrae Benest Golf Club, Gemjung, Busan, Korea.

Introduction: Oriental beetle, *Exomala*(=Blitopertha) *orientalis* is serious insect pest of turfgrasses in golf courses in Korea. Although adults of these beetles are active at night, their activity is questionable in the daytime. Therefore, monitoring of this beetle is difficult in golf courses. This study was conducted using pheromone trap to clarify seasonal occurrence of oriental beetle in Korean golf courses.

Methods: Seasonal occurrence of oriental beetle was surveyed at Gimpo Seaside Golf Club in Gimpo, Anyang Benest Golf Club in Gunpo, Gapyeong Benest Golf Club in Gapyeong, Gyeonggii province and Dongrae Benest Golf Club in Gumjung, Busan using oriental beetle sex pheromone from late May to late August. In addition, daily activity was surveyed every 2 hours on 20 June 2007 in Dongrae Benest Golf Club using pheromone trap. Soil sample was made every month with standard hole cutter from April to September in fairway and rough of Dongrae Benest Golf Club.

Results: The number of oriental beetles to pheromone trap was different depending on golf courses and holes. High numbers of oriental beetles were captured from Anyang Benest Golf Club and Dong Benest Golf Club, but none from Gapyeong Benest Golf Club. Oriental beetle was attracted to the pheromone traps from early June to middle August. The peak time was late June in Dongrae Benest Golf Club and Anyang Benest Golf Club. Oriental beetle was highly captured in pheromone trap from 20:00 to 22:00. Overwintered 3rd instar of oriental beetle pupated in May and Ist instar larva was observed at Dongrae Benest Golf Club in June. 2nd and 3rd instars were observed in July.

Conclusions: Oriental beetle adult occurred from early June to middle August and peak time was late June in Korean Golf courses. Adult was highly captured in pheromone trap from 20:00 to 22:00.

POSTER PRESENTATION

Seasonal occurrence of oriental beetle, Exomala orientalis (Coleoptera: Scarabaeidae) in Korean golf courses

Dong Woon Lee[1], Ho Yul Choo[2], Sang Myeong Lee[3], Jae Ho Kim[4], and Jong Chang Shin[5]

[1]*Department of Applied Biology, Kyungpook National University, Sangju, Gyeongguk, Korea.*
[2]*Department of Applied Biology and Environmental Sciences, Institute of Agricultural and Life Sciences, Gyeongsang National University, Jinju, Gyeongnam, Korea.*
[3]*Southern Forest Research Center, Korea Forest Research Institute, Jinju, Gyeongnam, Korea.*
[4]*Gimpo Seaside Country Club, Gimpo, Gyeonggii, Korea.*
[5]*Dongrae Benest Golf Club, Gemjung, Busan, Korea.*

Introduction: Oriental beetle, Exomala(=Blitopertha) orientalis is serious insect pest of turfgrasses in golf courses in Korea. Although adults of these beetles are active at night, their activity is questionable in the daytime. Therefore, monitoring of this beetle is difficult in golf courses. This study was conducted using pheromone trap to clarify seasonal occurrence of oriental beetle in Korean golf courses.

Methods: Seasonal occurrence of oriental beetle was surveyed at Gimpo Seaside Golf Club in Gimpo, Anyang Benest Golf Club in Gunpo, Gapyeong Benest Golf Club in Gapyeong, Gyeonggii province and Dongrae Benest Golf Club in Gumjung, Busan using oriental beetle sex pheromone from late May to late August. In addition, daily activity was surveyed every 2 hours on 20 June 2007 in Dongrae Benest Golf Club using pheromone trap. Soil sample was made every month with standard hole cutter from April to September in fairway and rough of Dongrae Benest Golf Club.

Results: The number of oriental beetles to pheromone trap was different depending on golf courses and holes. High numbers of oriental beetles were captured from Anyang Benest Golf Club and Dong Benest Golf Club, but none from Gapyeong Benest Golf Club. Oriental beetle was attracted to the pheromone traps from early June to middle August. The peak time was late June in Dongrae Benest Golf Club and Anyang Benest Golf Club. Oriental beetle was highly captured in pheromone trap from 20:00 to 22:00. Overwintered 3rd instar of oriental beetle pupated in May and Ist instar larva was observed at Dongrae Benest Golf Club in June. 2nd and 3rd instars were observed in July.

Conclusions: Oriental beetle adult occurred from early June to middle August and peak time was late June in Korean Golf courses. Adult was highly captured in pheromone trap from 20:00 to 22:00.

POSTER PRESENTATION

Molecular characterizations of a novel P450 gene encoding CYP6CE1 overexpressed in Phosphine and Dichlovos resistant strains of *Liposcelis bostrychophila* Badonnel (Psocoptera: Liposcelididae)

Hong-Bo Jiang, Jin-Jun Wang, Pei-An Tang, Yong-Qiang Xu, Feng-Ming An

Southwest University, Chongqing, China

Introduction: In China, *Liposcelis bostrychophila* Badonnel (Psocoptera: Liposcelididae) is a dominant species in stored products and the resistance to PH_3 and other insecticide has been a severe problem. In order to reveal whether P450 enzymes were involved in the resistance to PH_3 and DDVP or not, a novel P450 gene encoding CYP6CE1 was isolated. And the mRNA expression levels in different strains were determined.

Methods: The degenerate primers derived from the conserved domain of CYP6 family: 5'-CGGARACNHYNMGNAARTAYCC-3' and 5'-CGGGNCCNKCNCCRAANGG-3' were used to amplify the P450 fragments. The 5'-RACE and 3'-RACE were applied to obtain the full-length cDNA. Searching of similar sequences was performed using BlastP on the NCBI website. Deduced protein sequence was analyzed by the ProtParam program and a phylogenetic tree was constructed by DNAMAN. The mRNA expression levels were determined by Real-time PCR using the $\Delta\Delta CT$ method and the data was statistical analyzed.

Results: The complete CYP6CE1 (GenBank accession number, EF421245) cDNA sequence are comprised of 2025 bp with an open reading frame of 1581 bp encoding 527 amino acid residues, 215 bp 5' untranslation regions and 226 bp 3' untranslation regions, respectively. Putative cytochrome P450 CYP6CE1 is highly similar to several insect CYP6s that are responsible for increased detoxification to pyrethroid insecticides. The mRNA levels in DDVP- and PH_3-resistant strains were 1.74 and 1.41 folds higher than susceptible strain, respectively.

Conclusions: The results implied that overexpression of cytochrome P450 probably contributed to the resistance to PH_3 and DDVP in psocids.

POSTER PRESENTATION

Establishment of new insect cultured cell lines and insect cell bank in NIAS

Shigeo Imanishi

National Institute of Agobiological Sciences, Tsukuba, Ibaraki, Japan

Introduction: Cultural technique is not adequately established for all kind of insect species and their tissues. However, cell lines derived from Lepidoptera, Coleoptera, Hemiptera, and Diptera can be tool for analyzing molecular biological phenomena.

Methods: Materials for the primary culture are derived from the tissues of embryo, ovary, testis and fatty body of these species' insects. MX medium is being registered in the USA'Patent. Primary culture was done for approximately three months by exchanging half medium on every two weeks under 25C temperature. The established cell lines were registered at NIAS Genebank.

Results: MX30, including 30% volume of FBS in the MX medium, could accelerate a migration and multiplication of the cells from testis tissues of *Bombyx mori*, and could shorten the primary culture period in several months. I established the *Plautia stali* cells derived from embryo, of *Anomala cuprea* cells from fatty body, of *Agrius convolvuli* cells from fatty body, of *Bombyx mandarina* cells from fatty body, of *Bombyx mori* cells from fatty body, ovary, and embryo and of *Culicoides oxystoma* cells from embryo. One cell line is being used as a large scale culture *in vitro*. The other cell lines are confirmed that *Bombyx* cell line can keep *Wolbachia*, some *Bombyx* cell lines maintain a certain kind of plant disease viruses, and one cell line reacts typically to insect hormone.

Conclusions: These cell lines are promoting the development of insect molecular research. Cell lines registered as "active collection" can be distributed under BIOLOGICAL MATERIAL TRANSFER AGREEMENT (MTA).

POSTER PRESENTATION

Life history strategies of the armored Rambutan scale insect, *Aulacaspis alisiana* (Hemiptera: Diaspididae) on the Japanese silver tree in Fukuoka, Japan

Charles Midega, Keiji Takasu

Kyushu University, Fukuoka, Japan

Introduction: *Aulacaspis alisiana* is a pest species host-specific to the Japanese silver tree. We studied its life history strategies at Ino and Nakakubara forests in Fukuoka Japan.

Methods: Fecundity was determined by counting the number of crawlers that emerged from female scales twice a week for three weeks from twenty trees at both sites. Generation time was determined by weekly observing *A. alisiana* at the initial crawler stages on randomly selected leaves until adults emerged. Physical characteristics of the trees such as height, branch, leaf position and predator abundance were recorded and infestation rates by the pest assessed for any relationships. Impact of natural enemies was determined by natural enemy exclusion procedures using nets and insect trap adhesive.

Results: Each *A. alisiana* female produced an average of 55.8 eggs at Ino and 67.4 eggs at Nakakubara. The generation time ranged from 64 to 76 days, and the generations were overlapped. The potential natural enemy guild in both forests comprised mainly ants, spiders and beetles (coccinelids), with an average of 28.6 and 19.8 individuals per tree at Ino and Nakakubara respectively. Disappearance of *A. alisiana* nymphs was significantly higher on control than on exclusion branches at both sites (Ino: Exclusion 15.1%, control 26.1%. Nakakubara: Exclusion 11.5%, control 21.0%). Infestation rates of *A. alisiana* were not influenced by physical characteristics of trees and natural enemy presence or absence.

Conclusion: *A. alisiana* has three overlapping generations in Fukuoka with relatively high female fecundity and moderate natural mortality.

POSTER PRESENTATION

Good-bye Scydmaenidae: fully resolved phylogeny of the Staphylinine Group, or why the ant-like stone beetles should become Staphylinidae *sensu latissimo* (Coleoptera)

Vasily Grebennikov[1], Alfred Newton[2]

[1]Entomology Research Laboratory, Ontario Plant Laboratories, Canadian Food Inspection Agency, K.W. Neatby Bldg., 960 Carling Avenue, Ottawa, Ontario K1A 0C6, Canada, [2]Zoology Department, Field Museum of Natural History, 1400 South Lake Shore Drive, Chicago, Illinois 60605, United States

Ant-like stone beetles (Coleoptera: Scydmaenidae) include more than 4850 described species in about 90 genera maintained as a separate cosmopolitan family since 1815. Recent authors have hypothesised that Scydmaenidae might be rooted deep inside rove-beetles (Staphylinidae). To test this hypothesis we analysed 206 parsimoniously informative larval and adult morphological characters scored for 38 taxa: Leiodidae (1 terminal), Agyrtidae (1), Silphidae (3), Scydmaenidae (6), Omaliinae (1), Tachyporinae (1), Piestinae (1), Apateticinae (1), Trigonurinae (1), Oxyporinae (1), Megalopsidiinae (1), Solieriinae (1; larva unknown), Leptotyphlinae (3), Steninae (2), Euaesthetinae (4), Pseudopsinae (3), Paederinae (3) and Staphylininae (4).

Twelve analyses utilised three datasets (larval, adult and combined) each treated under four sets of assumptions (successively weighted/unweighted and multistate characters ordered/unordered). Strict consensus topologies from the shortest trees in all 12 analyses consistently placed Scydmaenidae as sister to (Steninae + Euaesthetinae) in a monophyletic Staphylinine Group (with or without Oxyporinae). The single fully resolved and most consistently supported topology maintains a monophyletic Staphylinine Group consisting of Oxyporinae + (Megalopsidiinae + ("Scydmaenidae" + (Steninae + Euaesthetinae)) + (Leptotyphlinae + (Pseudopsinae + (Paederinae + Staphylininae))))); Solierius lacks larval data and is ambiguously placed within the Group.

Preliminary analyses of 18S rDNA data for 93 members of Staphylinoidea under parsimony, neighbour-joining and Bayesian approaches were inconclusive, and largely conflicting with the morphological results.

Our results strongly suggest that ant-like stone beetles do not form an independent family, but are morphologically modified members of Staphylinidae and, consequently, should be treated as a 32nd subfamily within the megadiverse Staphylinidae sensu latissimo.

POSTER PRESENTATION

Beetle-Bits 101: Imaging Staphyliniformia & Scarabaeiformia for the Beetle Tree of Life project

Margaret Thayer, José-Cristian Martínez

Field Museum of Natural History, Chicago, Illinois, United States

Introduction: The Staphyliniformia TWiG (Taxonomic Working Group) of the multi-investigator, multi-institutional project BToL (Assembling the Beetle Tree of Life) is producing digital images of whole-body habitus and structural features of both adults and larvae of 32 exemplar taxa belonging to the series Staphyliniformia (Hydrophiloidea, sensu lato, plus Staphylinoidea) and 16 taxa of Scarabaeiformia. The images consist of 66 standard views selected by all participants in the project to document for each taxon the states of approximately 600 morphological characters of adults and larvae. These data will be combined with extensive DNA sequence data to perform phylogenetic analyses of the entire order Coleoptera.

Methods: We use primarily a Microptics ML Macro XLT digital imaging system incorporating a Canon EOS 1D Mark II camera. Some images of smaller specimens require using a compound microscope (Leitz Dialux 20 with a Spot Insight Color digital camera) or a scanning electron microscope (LEO EVO 60®). Most final images are composites of a series of up to 26 individual images taken in multiple focal planes, combined using either CombineZM (public domain) or Auto-Montage (©Syncroscopy) software. Imaging specimens ca. 1 to 35 mm long and parts thereof presents a variety of logistical challenges, our solutions to some of which we present here.

POSTER PRESENTATION

Managing Bt-resistance development in maize: Are stem borer populations in refugia still susceptible?

Johnnie Van den Berg, Marlene Kruger

North-West University, Potchefstroom, South Africa

Introduction: Genetically modified (Bt) maize is used for control of *Busseola fusca* (Lepidoptera: Noctuidae) and *Chilo partellus* (Lepidoptera: Crambidae) in South Africa. Resistance of this species to Bt maize has recently been reported in South Africa. The high dose/refuge strategy for resistance management is prescribed is South Africa. The aim of this study was to investigate whether *B. fusca* populations in "refugia" were still susceptible to Bt maize.

Methods: *B. fusca* larvae were collected from the resistant population and on conventional maize at several sites. Larvae were reared on Bt- or conventional maize until moths appeared. Eggs were collected from these rearing colonies and, after hatching, neonate larvae were inoculated onto conventional and Bt maize plants. Larval survival and mass were determined until the pupal stage was reached.

Results: When larvae originating from susceptible colonies were put on Bt plants 100% mortality was observed within 12 days while normal development occurred on conventional maize. Larvae collected from the reportedly resistant population survived on Bt and susceptible plants, all be it at a lower percentage. Larvae originating from the "refugia" associated with the resistant stem borer population survived on Bt maize up to the pupal stage but at low levels.

Conclusion: Stem borer populations in conventional maize refugia in the area where resistant populations have been reported is less susceptible to Bt than populations from conventional maize in other areas.

POSTER PRESENTATION

Morphological studies of *Cissococcus fulleri* (Hemiptera: Coccidae), a unique gall-inducing soft scale insect in South Africa, and evidence of a closely related new species

Ian Millar[1], Penny Gullan[2], Chris Hodgson[3]

[1]ARC Plant Protection Research Institute, Pretoria, South Africa, [2]University of California, Davis, United States, [3]The National Museum of Wales, Cardiff, United Kingdom

Cissococcus fulleri Cockerell is an unusual South African scale insect species that induces galls on species of *Rhoicissus* (Vitaceae). It was described by Cockerell in 1902, and *Cissococcus* has remained a monotypic genus ever since. It has very unusual morphology and its familial placement has been uncertain. Cockerell considered *Cissococcus* to belong to the Eriococcidae when he described it. However, Hodgson believed it was a soft scale (Coccidae), in his overview of world Coccidae genera, and the present studies of male and crawler morphology support the view that *Cissococcus* is a soft scale, although it is the only known member of this family to induce complex coverings or enclosed galls.

Studies on the adult female stage by Hodgson in 1994 revealed the existence of a separate "form" which differed morphologically from *C. fulleri*, and which could represent an undescribed species. Observations on recently-collected samples of *Cissococcus* show that two different types of galls are induced by *Cissococcus*; and the available material indicates that each of the two morphological "forms" lives inside its own characteristically-shaped gall. So far, samples of the "typical form", representing *C. fulleri*, have been found on *Rhoicissus tridentata*, whereas the "non-typical form" occurs on *R. digitata*. Our samples show that the geographical ranges of the two morphological "forms" of *Cissococcus* overlap but molecular data from each of the two different "forms" strongly support the hypothesis that they are separate species.

POSTER PRESENTATION

Developmental changes in cholorplast of three cecidomyiid galls indicated by confocal imagery

Meng-Yuan Huang[1], Yung-Ta Chang[1], Man-Miao Yang[2], Chi-Ming Yang[3]

[1]Department of Life science, National Taiwan Normal University, Taipei, Taiwan, [2]Department of Entomology, National Chung-Hsing University, Taichung, Taiwan, [3]Research Center for Biodiversity, Academia Sinica, Taipei, Taiwan

Introduction: Multiple changes in response to gall inducers have been found in host plant tissues. While much attention has been focused on the morphology and anatomy of insects or their induced galls, relatively little work has been done on the chloroplast of galls and its photosynthesis. Therefore, the aim of this research was to test a hypothesis that leaf-derived cecidomyiid galls alter the distribution of chloroplast.

Methods: Confocal laser-scanning microscopy was applied to investigate the distribution of chloroplast in three cecidomyiid galls derived from *Machilus thunbergii* and *Litsea acuminata* leaves.

Results: Stronger characteristics of chloroplasts are found in host leaves than in leaf-derived galls in terms of number, size, and fluorenscence intensity for all the types of gall tested. While the three characteristics of chloroplasts are homogeneously throughout the tissues of all host leaves, in contrast, these features in all gall tissues gradually decrease from outside toward the larval chamber direction. In other words, the deeper center the gall tissue is, the less the number, the smaller the size and the weaker the fluorescence intensity will be found.

Conclusions: The results indicate that different species of herbivorous insect dramatically alter the photosynthetic characteristics of chloroplast in their host leaves. The galls are life time deficient in some biophysical and biochemical characteristics of chloroplasts which are normally found in host leaves.

POSTER PRESENTATION

Phylogenetic patterns of brachyptery in the cicada Tribe Tettigomyiini (Hemiptera: Cicadidae) in the Eastern Cape.

Benjamin Price, Terence Bellingan, Martin Villet, Nigel Barker

Rhodes University, Grahamstown, South Africa

The Tettigomyiini is endemic to Africa, having diversified predominantly within East and South Africa and particularly within the Eastern Cape. The tribe currently consists of nine genera, of which six have not been reviewed since description (1904 – 1980). In addition, the phenomenon of female brachyptery (rudimentary wings rendering the organism flightless) occurs in some species within the tribe. This female-only brachyptery may be a result of two factors: 1) obligate inheritance from a recent common ancestor; 2) recurrent adaptation through brachyptery in stable habitats, allowing the partition of greater resources to egg production. A phylogenetic study of the tribe was conducted using two mitochondrial genes (CO1 & 16S) from sixteen species, representing six of the seven genera to test the monophyly of the described genera with respect to the brachypterous trait. Furthermore the phylogenetic estimation was related to the biogeography of the tribe and patterns of diversification within the Eastern Cape. It was found that the monophyly of *Paectira*, *Stagea* and *Stagira* was well supported whereas the genera *Xosopsaltria*, *Bavea* and *Tettigomyia* formed a paraphyletic group. Brachyptery was demonstrated to have no particular orientation within the tree, and to occur independently in *Xosopsaltria, Tettigomyia* and *Stagira*. This result suggests that brachyptery evolved more than once in association with savanna grassland, possibly as a result of decreasing habitat heterogeneity. It is suggested that the generic taxonomy of the Tettigomyiini be reviewed.

POSTER PRESENTATION

Effects of neo-nicotinoid insecticides on feeding behaviour of *Myzus persicae* (Homoptera: Aphididae) with EPGs

M.K. Kang, M.J. Seo, E.J. Kang, H.B. Seok, D.H. Lee, H.J. Lee, Y.M. Yu, Y.N. Youn

Chungnam National University, Daejon, Republic of Korea

The green peach aphid, *Myzus persicae* is a pest which has been found on more than hundreds of host plants in over 40 plant families all over the world. *M. persicae* causes wilting and reducing growth rate of plant and it's honeydew causes sooty mold at plant. It is difficult to control with contact insecticides because aphids often positioned under the leaves and less volatilization under 20℃. For these reasons, systemic insecticides are much effective at cool temperatures. Neo-nicotinoid insecticide class is one of the new insecticides. Three neonicotinoid insecticides were used, imidacloprid, thiamethoxam and dinotefuran. After 1 hour of feeding behaviour recording, each insecticide were treated by 1/5, 1, and 5 fold of recommended concentration by manufacturer. EPGs were recorded for 7 hours and recorded aphids were regularly checked feeding or not. In order to compare with feeding behaviour and inflow concentration of insecticide, HPLC analyze was used. Total time could not suggest specific data, but result showed that high concentration showed a long non-penetration and a short feeding pattern compare with lower concentration. Also, different feeding time in same concentration categories was shown. It might due to different traits of each insecticide. Each insecticide and each concentration was seemed to similar feeding behaviour, but inflow concentrations were considered, each insecticide may have different characteristic. Specifically, inflow concentration of imidacloprid was drastically lower than other insecticides but strong anti-feeding or repellent phenomenon was showed.

POSTER PRESENTATION

Control methods for agricultural insect pests in Japan during the Edo period (17th - 19th century)

Taro Adati, Takuya Kawase

Department of International Agricultural Development, Faculty of International Agriculture and Food Studies, Tokyo University of Agriculture, Sakuragaoka 1-1-1, Setagaya-ku, Tokyo 156-8502, Japan

The control of agricultural insect pests was economically important in Japan in the Edo period as it is today, and there are many descriptions of old methods of pest control. Some of those control methods, including use of plant-derived insecticides and insect repellents, are both biorational and environmentally friendly from the viewpoint of modern entomology. Here, we review three remarkable pest control methodologies described during the Edo period, and reassess their effects on pests in light of the latest knowledge in entomology and pest management science:

Pouring oil into rice paddies: To control leaf- and plant-hoppers, farmers poured oil on the water surface of rice paddies. Rice plants were submerged by a bamboo stick so that hoppers drop on the surface of water and are smothered because the oil chokes their spiracles. The oils were both of animal and plant origin, but whale oil was used primarily after the remarkable insecticidal effect of whale oil was discovered.

Plant-derived insecticides and insect repellents: More than twenty plant species were claimed to be effective against insect pests if the plants were under-ploughed or their extracts were poured into the paddy water. Among those plants, about ten species have not yet been analyzed for their active components.

Bonfires: During the Edo period, Japanese farmers knew that bonfires could attract and kill insect pests. The latest knowledge suggests that temporary lighting causes behavioural suppression for nocturnal insect pests, thus disrupting their reproduction.

POSTER PRESENTATION

Differences in gene expression level of endogenous cellulase in young xylophagus cockroaches and termites

Keisuke Shimada, Kiyoto Maekawa

University of Toyama, Toyama, Japan

Introduction: Xylophagy is an important trait for the evolution of sociality in termites and cockroaches. Recent phylogenetic studies strongly suggest that the xylophagous and subsocial cockroach genus *Cryptocercus* is a sister group to termites. There are many similarities, including symbiotic protozoa and long-lasting biparental care which includes parental feeding. Sociality in *Cryptocercus* and termites thus seems to have a common origin. However, the blaberid genus *Salganea* (Panesthiinae) is also xylophagous, with biparental subsociality that includes parental feeding; their social structure, parental behavior, and ecology are convergent with those of *Cryptocercus*. The xylophagous blaberid *Panesthia angustipennis* (Panesthiinae), however, has a gregarious social structure, without parental care. Because the cellulose based diet of these taxa may be difficult for young nymphs to process, wood-digestion abilities of first instars may vary with social structure in these cockroaches and termites.

Methods: We compared the wood-digesting ability of first-instar nymphs among four xylophagous and three non-xylophagous species by analyses of endogenous cellulase gene expression using real-time quantitative PCR.

Results: The results showed that first-instar nymphal expression levels are strikingly low in relation to adults in biparental species (termites: *Zootermopsis nevadensis*, cockroaches: *Cryptocercus punctulatus*, *Salganea esakii*), expression levels in gregarious *Panesthia angustipennis* are quite high. In non-xylophagous, gregarious cockroaches (*Periplaneta fuliginosa*, *Elliptorhina* sp., *Blattella germanica*), first-instar nymphal expression levels are low, but higher than those of biparental species.

Conclusions: These results suggest that there is a clear correlation between first-instar nymphal wood-digesting ability and social structure in xylophagous cockroaches and termites.

POSTER PRESENTATION

Species composition and population dynamics of spider mites on Kudzu vine, *Pueraria lobata* (Fabaceae)

Tetsuo Gotoh

Ibaraki University, Ami, Ibaraki 300-0393, Japan

Introduction: Identification of spider mites based on morphological characters is often difficult because differences can be subtle. Therefore, I developed a method based on the enzymes, esterase and phosphoglucomutase (PGM), to tell apart the 13 known *Tetranychus* species in Japan [Gotoh et al. (2007) Appl. Entomol. Zool. 42: 579-585 and 685-692]. Using this method, I describe the composition and population dynamics of the tetranychid mites on Kudzu vine.

Methods: At two sites a ground area of 10 x 10 m was subdivided into 100 1 x 1 m plots each. Kudzu vine leaves are composed of three leaflets, one of these was sampled from each plot at 10-day intervals from April to November during the three successive years. All adult female mites sampled were placed individually onto leaf discs of common bean (*Phaseolus vulgaris*) and allowed to lay eggs for three days (for using morphological study), and then females were used for electrophoresis.

Results: Five *Tetranychus* species were sampled on Kudzu vine: *Tetranychus puerariсola, T. ludeni, T. parakanzawai, T. kanzawai* and *T. piercei*. Most abundant in each of the three years was *T. puerariсola* (76-97% of mites). Populations peaked in June and/or September-October. Most colonies (defined as areas surrounded by silky spider-mite threads) consisted of only one species, but some (10%) had two or three species.

Conclusions: Isozyme analysis proved a useful tool to elucidate population development of the five Japanese *Tetranychus* species on Kudzu vine.

POSTER PRESENTATION

Phylogenetics and biogeography of the Australian Colletidae

Pelin Kayaalp, Michael Schwarz

Flinders University, Adelaide, South Australia, Australia

Introduction: Colletid bees are most prevalent in the southern hemisphere, in particular in Australia and South America. Preliminary results looking at the patterns and timings of biogeographical events will be presented, with emphasis on diversification of the Australian colletids.

Methods: One mitochondrial (CO1), and two nuclear genes, (EF1α and LW Rhodopsin) are used to analyse phylogenetic relationships among the southern hemisphere colletids via Bayesian and maximum parsimony methods, and r8s and DIVA are used to examine biogeographical scenarios and divergence times within Australia.

Results: Previous work by Eduardo Almeida has suggested a sister-group relationship between the Australian subfamily Euryglossinae and the southern African Scrapterinae, and the mainly Australian Hylaeinae with the South American Xeromelissinae. Molecular analyses of the Australian Hylaeinae and Euryglossinae infer times and patterns of radiation of the Australian components of these groups and divergence times from the non-Australian groups.

Conclusion: The richness of the Hylaeinae and Euryglossinae in Australia, and the restriction of Euryglossines to Australia, is probably due to both recency of origin and to the abundance and diversity of Myrtaceae. Because these two bee groups are short-tongued they are easily able to access the nectar in the shallow cups presented by the Myrtaceae. This may be indicative of two clades that have undergone a recent radiation with the rise of Myrtaceae in Australia. While earlier studies suggested that the dominance of colletid bees in Australia may reflect retention of an ancient Gondwana bee fauna, our results suggest a more recent explanation for this abundance and diversity.

POSTER PRESENTATION

Biotic communities in *Protea infructescences*: Examples of mutualism, commensalism and antagonism

Francois Roets[1], Michael Wingfield[1], Brenda Wingfield[1], Léanne Dreyer[2]

[1]Forestry and Agricultural Biotechnology Institute (FABI) University of Pretoria, Gouteng Province, South Africa, [2]Department of Botany and Zoology, Stellenbosch University, Western Cape Province, South Africa

Introduction: The flowers of the African endemic plant genus *Protea* mature into infructescences that remain on the plants for several years. During this period, they are colonized by numerous arthropods and fungi. We investigated the interactions between these organisms focusing on the ophiostomatoid fungi (*Ophiostoma* and *Gondwanamyces*) and their associated arthropods.

Materials and methods: *Protea*-fungus interactions were investigated using fungal competition studies. Mite-fungus interactions were assessed using food preference studies, microscopy, molecular methods and direct isolations. Mite-arthropod interactions were assessed using scanning and light microscopy.

Results: The ophiostomatoid fungi from *Protea* are saprophytic and dominate fungal communities in infructescences. They appear to exclude fungal decomposers that break down the internal tissues of infructescences, leading to premature release and consequent predation of the seeds. *Protea*-associated *Ophiostoma* serve as a food source for various mites. E.g., when *Trichouropoda* mites were fed these fungi, they had significantly higher reproductive rates that when their diet was composed of other fungi. Mites were shown to disperse ophiostomatoid spores between infructescences. These mutualistic interactions resulted in evolutionary adaptations in both the mites (specialized spore-carrying structures) and the fungi (sticky spore-drop for attachment to arthropods). Long-distance dispersal of the mites and the ophiostomatoid fungal spores that they carry was shown to be achieved through phoresy on beetles (e.g. *Genuchus hottentottus*) that feed on *Protea* seeds.

Conclusions: The interactions between biotic communities within *Protea* infructescences are complex and they include examples of mutualism, commensalism and antagonism. *Protea* infructescences clearly represent mini-ecosystems including various trophic levels and feeding guilds.

POSTER PRESENTATION

Mapping and distribution modeling of individual flea species (Siphonaptera) and flea's species diversity in the Negev Desert

Georgy Shenbrot, Boris Krasnov, Sergey Burdelov

Mitrani Department of Desert Ecology, Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, Midreshet Ben-Gurion, Israel

Introduction: Detailed knowledge on distribution and abundances of blood-sucking ectoparasites is essential for understanding processes in the natural foci of zoonotic diseases. However, such a data are scarce and irregularly distributed spatially. Distribution modeling is increasingly in use for evaluation of distribution patterns of free-living organisms but rarely used for ectoparasites whose distribution depend on hosts and abiotic environment.

Methods: Rodents and fleas were randomly sampled in the area of 9,200 sq km of the north-central part of the Negev Desert with sampling intensity of one sampling point per 100 sq. km. For each rodent species and for each flea species within each host rodent species we composed distribution model based on environmental (climate, topography, soil and vegetation) and presence/absence and abundance data using MAXENT and step-wise multiple regression analysis. Individual species models were projected into the geographic space and presented as the maps of distribution and abundances. Maps of individual species were overlaid to get the map of species diversity.

Results: Distributional models were constructed for 18 rodent host species and 12 flea species. Based on these models, we compiled the maps of distribution and abundances for each flea species and integral maps of general abundance and species diversity of fleas.

Conclusions: Modeling of ectoparasite distribution can be used as a powerful tool for estimation of areas of high epidemiological risk.

POSTER PRESENTATION

Malaria vector control and insecticide resistance

Maureen Coetzee[3], Richard Hunt[2], Lizette Koekemoer[1], Basil Brooke[1]

[1]Vector Control Reference Unit, National Institute for Communicable Diseases, School of Pathology, Division of Microbiology, University of the Witwatersrand, Johannesburg, South Africa, [2]School of Animal, Plant & Environmental Sciences, University of the Witwatersrand, Johannesburg, South Africa, [3]NRF Chair in Medical Entomology & Vector Control, University of the Witwatersrand, Johannesburg, South Africa

Introduction: Effective malaria vector control interventions have been available for over 60 years but are seldom applied efficiently or appropriately. Research across Africa has shown that the vectors are not homogeneous, they adapt to different environments in various ways and respond differently to insecticidal pressure. Control programmes must be tailored to address the specific needs of each situation and to do this, entomological surveys are required. We present data from three African countries where vector control is being implemented and discuss the problems faced by these programmes.

Methods: Mosquito surveys were carried out in Sudan, Ghana and South Africa. Specimens were identified by PCR, examined for parasite infectivity, assessed for susceptibility to insecticides approved for vector control by WHO and where applicable, processed for the *kdr* mutation.

Results: Sudan: *Anopheles arabiensis* was 1% parasite positive, resistant to pyrethroids, DDT and organophosphates and susceptible to carbamates. The West African *kdr* mutation was found at a high frequency and did not correlated with the bioassay data.

Ghana: *Anopheles gambiae* 'S' form was 5% parasite positive, susceptible to organophosphates and resistant to pyrethroids, carbamates and DDT. *An. funestus* was 2% parasite positive, susceptible to pyrethroids and organophosphates but resistant to carbamates and DDT. The West African *kdr* mutation was found at low frequencies in *An. gambiae*.

South Africa: *An. funestus* was 5% parasite positive, susceptible to DDT and organophosphates, and resistant to pyrethroids and carbamates. *An. arabiensis* was resistant to DDT but susceptible to pyrethroids.

Discussion: All three localities are using indoor residual house spraying (IRS) for vector control. South Africa implements a mosaic resistance management strategy using DDT and pyrethroids. Ghana is using organophosphates in an integrated vector management (IVM) programme. Sudan uses a carbamate for IRS as well as ITNs. Each programme has tailored its strategy in the light of the above results.

POSTER PRESENTATION

The possible mechanisms of Spinosad resistance in *Bactrocera dorsalis*

Ju-Chun Hsu[1], Guo-Cih Lin[1], Chin-Gi Huang[2], Hai-Tung Feng[1]

[1]*Taiwan Agricultural Chemicals and Toxic Substances Research Institute, Taichung, Taiwan,* [2]*Department of Entomology, Taipei, Taiwan*

Introduction: The oriental fruit fly (*Bactrocera dorsalis*), disturbed throughout Southeast Asia and the Pacific, is a major pest in orchard crops and one of the most prominent quarantine pests in the world. Currently, spinosad is considered an effective insecticide for control of various fruit flies, however, the oriental fruit fly could be highly resistant to spinosad after successive selections. The purpose of this study is to find out the possible mechanisms evolved in spinosad resistance of *B. dorsalis*.

Methods: Bioassays were carried out by using synergists, S,S,S-tributyl phosphorotrithioate (DEF), piperonyl butoxide (PBO) and diethyl maleate (DEM) with spinosad in spinosad-resistant and susceptible lines. The activities of metabolic enzymes including esterases (ESTs), glutathione-S-transferase (GSTs), and mixed function oxidases (MFOs) were assayed and compared between these two lines. Finally, to elucidate the possible target site alteration, the susceptibilities to other neurotoxic insecticides, fipronil and imidacloprid, were assayed and compared between the two lines.

Results: DEF showed significant synergistic effect toward spinosad in susceptible flies. In resistant flies, the synergism was not conclusive because the highest dose of spinosad (100 mg/mL) in use only caused less than 10% mortality. The resistant line exhibited a slightly higher ESTs activity than in susceptible flies and appeared to be cross-resistant to imidacloprid but not to fipronil.

Conclusions: In *B. dorsalis,* both esterases and imidacloprid-related nicotinic acetylcholine receptors might have mild influences in the resistance to spinosad. The major resistance mechanism of spinosad, probably altered target site, needs to be ascertained in the future.

POSTER PRESENTATION

Initial assessment of *Trichogrammatoidea lutea* (Hymentopera: Trichogrammatidae) as a biological control agent of codling moth (*Cydia pomonella*, Lepidoptera: Tortricidae) in apple and pear orchards under sterile insect release (SIR)

Nadine Wahner, Matthew F. Addison, Alicia Timm

University of Stellenbosch, Stellenbosch, WC, South Africa

Codling moth, *Cydia pomonella*, is the major pest of apples and pears in the Western Cape, South Africa. *Trichogrammatoidea lutea* (Hymentopera: Trichogrammatidae) is an indigenous egg parasitoid of False Codling Moth as well as Codling Moth that has previously been found to have considerable parasitism potential.

For secure identification of *Trichogrammatoidea lutea* and its distinction from the morphologically similar local species *T. cryptophlebiae* (an indigenous False Codling Moth parasitoid on citrus) the ITS 2 sequences of both species have been determined and species specific primers have been developed. The efficacy and population sustainability of released *T. lutea* were investigated in several field studies. Trials took place in apple and pear orchards that formed part of an area-wide sterile Codling Moth release program. Inoculative, as well as inundative releases were carried out within blocks of up to 1 ha. The square grid of up to 36 monitoring trees per block allowed spatial distribution analysis, as well as population density estimation throughout the season. Toxicity studies, concerning some of the most often sprayed pesticides in the Western Cape elucidated the potential effects of chemical sprays in orchards on released parasitoids. Life table studies of *T. lutea* gave an indication of how population cycling and reproduction in the field is influenced by the ambient temperatures.

According to the results of above studies, *T. lutea* shows potential for broad-scale releases against Codling Moth, within a broader integrated pest management program.

POSTER PRESENTATION

Initial assessment of *Trichogrammatoidea lutea* (Hymentoptera: Trichogrammatidae) as a biological control agent of codling moth (*Cydia pomonella*, Lepidoptera: Tortricidae) in apple and pear orchards under sterile insect release (SIR)

Nadine Wahner, Matthew F. Addison, Alicia Timm

University of Stellenbosch, Stellenbosch, WC, South Africa

Codling moth, *Cydia pomonella*, is the major pest of apples and pears in the Western Cape, South Africa. *Trichogrammatoidea lutea* (Hymentoptera: Trichogrammatidae) is an indigenous egg parasitoid of False Codling Moth as well as Codling Moth that has previously been found to have considerable parasitism potential.

For secure identification of *Trichogrammatoidea lutea* and its distinction from the morphologically similar local species *T. cryptophlebiae* (an indigenous False Codling Moth parasitoid on citrus) the ITS 2 sequences of both species have been determined and species specific primers have been developed. The efficacy and population sustainability of released *T. lutea* were investigated in several field studies. Trials took place in apple and pear orchards that formed part of an area-wide sterile Codling Moth release program. Inoculative, as well as inundative releases were carried out within blocks of up to 1 ha. The square grid of up to 36 monitoring trees per block allowed spatial distribution analysis, as well as population density estimation throughout the season. Toxicity studies, concerning some of the most often sprayed pesticides in the Western Cape elucidated the potential effects of chemical sprays in orchards on released parasitoids. Life table studies of *T. lutea* gave an indication of how population cycling and reproduction in the field is influenced by the ambient temperatures.

According to the results of above studies, *T. lutea* shows potential for broad-scale releases against Codling Moth, within a broader integrated pest management program.

POSTER PRESENTATION

Seasonal abundance of fleas on stray dogs and cats in Taipei, Taiwan

Chin-Gi Huang, Mauricio E. Alarcón, Wen-Jer Wu

National Taiwan University, Taipei, Taiwan

Introduction: Flea is the most abundant and problem-causing ectoparasite of cats and dogs especially in stray animals. Although the pet owner can treat fleas at home, fleas always infect and attack animals from outdoor. Surveying flea from stray animals may help us more clearly in control programs.

Methods: From March 2006 to February 2008, we surveyed fleas monthly from stray dogs and cats collected in different administrative division of Taipei city. Animals were checked for 10 minutes using flea comb. Fleas were examined and identified under microscope.

Results: In last two years, fleas were detected on 519 (44.4%) out of the 1169 dogs (976) and cats (193) surveyed. A total of 5490 fleas was sampled and only one species, *Ctenocephalides felis* (Bouché), was found. *Ctenocephalides canis* (Curtis) was not found in our survey. The male to female cat flea ratio is 1:2.9. In spite of seasonal fluctuation in flea prevalence, the trend line of flea index in current survey was lower than that of in 1990. There were 2 peaks of the flea index in the year. In addition, we found that 14.4% (792/5490) of flea midgut were infected with trophozoites of a gregarine (Apicomplexa).

Conclusions: Only one flea species *Ctenocephalides felis* (Bouché) was found in dogs and cats in Taipei City, and there are 2 peaks of flea prevalence.

POSTER PRESENTATION

Damage evaluation of the olive insect pest *Rhynchites cribripennis* (Coleoptera: Attelabidae)

Dionyssios Perdikis[1], Nikolaos Garantonakis[1], Antonios Paraskevopoulos[2], Dionyssios Lykouressis[1], Athanassios Giatropoulos[1]

[1]Laboratory of Agricultural Zoology and Entomology, Agricultural University of Athens, Athens, Greece, [2]Directorate of Rural Development, Trifylia, Kyparissia, Greece

Introduction: *Rhynchites cribripennis* (Desbr.) has a wide distribution in the Mediterranean region and has been reported to cause significant yield losses on olive orchards.

Methods: The damage potential of this pest was investigated in an olive groove of var. "Koroneiki" in the area of Kyparissia, near Kalamata, western Greece, in 2007. Shoots with fruits were enclosed in mouslin cages (25cm diameter and 70cm length) along with adult weevils at the end of the flowering period (May 22, 2007). In each cage 2 or 4 adults introduced and cages without any weevil were used as controls. All the treatments were situated on shoots developed from a single main twig. In each cage the number of olives on the shoots, the dropped olives and the feeding holes on olive fruits were recorded on June 18, August 4 and September 4.

Results: The total percentage of the dropped fruits was highest (53%) in the cages with the high pest density (i.e. 4 adults) followed by that observed in the cages of the low pest density (i.e. 2 adults) (37%) whereas in the controls it was 16%. The damage severity (feeding holes) on the fruits was proved to depend on the time and the pest density, being significantly higher at the highest pest density.

Conclusions: These results indicate that *R. cribripennis* can create significant damage mainly due to the drop of a high percentage of the fruits. In addition, the damage level on the fruits that are harvested can be serious.

POSTER PRESENTATION

Fumigant toxicity of essential oil from *Tanacetum balsamita* L. against *Callosobruchus maculatus* (F.) (Coleoptera:Bruchidae)

Nouraddin Shayesteh[1], Farzaneh Attighi[2], Shahram Aramide[2], Adel Khashaveh[2]

[1]Islamic Azad University, Branch of Mahabad, mahabad/West Azarbaijan,, [2]Urmia University, Urmia/West Azarbaijan, Islamic Republic of Iran

Introduction: The fumigant activity of essential oil vapors distilled from *Tanacetum balsamita* (Compositae) was tested against adults and eggs of *Callosobruchus maculatus*. *T. balsamita* growing wild in North Iran. (Elburz area, near Kandovan Tonel).

Methods: A sufficient quantity of *T. balsamita*, extracted by water steam method, was obtained from Golbahar Co. Urmia, Iran. Experiments were carried out at 27±2°C and 65±5% R.H. adopting a factorial design. Essential oil at 5.12, 7.23, 10.19, 14.36 and 20.24 µl/lair for adults and 5.3, 8.5, 10.8, 13.7 and 17.4 µl/lair for eggs of *C. maculatus* was used. For each concentration four replications that each replication including thirty one day old adult**s** or thirty 0-24 h eggs. Different concentrations of the essential oil applied on filter paper, were kept in 0.5-liter glass jars with the insects kept in the fumigation jars. Mortality was recorded after 24, 48 and 72 h. The percent mortality was corrected using Abbot's formula (1925). Data were subjected to Duncan's multiple range test.

Results: Increasing the essential oil concentrations increased the effects of essential oil on mortality of adults and eggs of *C. maculatus*. The percentage mortality after 72 h, received to 75.20 % of adults at higher dose (20.24 µl/lair), and 49.06 % of eggs at higher dose (17.4 µl/lair) of T. *balsamita.* The LC50 values after 72 h, on adults and eggs of *C. maculatus*, were observed (1.96 µl/lair), and (21.29 µl/lair), respectively.

Conclusions: Fumigant activity of this essential oil was more effective against adults of *C. maculatus*.

POSTER PRESENTATION

Displacement among exotic herbivorous insects on introduced tall goldenrods

Yoshino Ando[1], Shunsuke Utsumi[1], Timothy Craig[2], Takayuki Ohgushi[1]

[1]Center for Ecological Research, Kyoto University, Otsu, Shiga, Japan, [2]Department of Biology, University of Minnesota, Duluth, Minnesoa, United States

Introduction: The exotic aphid *Uroleucon nigrotuberculatum* was one of most dominant species on introduced tall goldenrods at a common field in Japan. Recently, the aphid markedly decreased on tall goldenrods at the field. In the same year, the exotic lacebug *Corythucha marmorata* was frequently observed on tall goldenrods. We hypothesized that lacebug colonization decreased the formally established aphid.

Methods: We set lacebug-attacked plants and lacebug-free plants in greenhouse and then inoculated the aphids. Behavior, colonization density, and survival of the aphid were compared between treatment plants. Distribution and density of both exotic herbivorous insects on tall goldenrods were recorded in five local areas. Also, we took census of their natural enemies found on tall goldenrods.

Results: There was no direct interference between these herbivorous species. Also, the aphid density and survival did not differ between treatments. However, the alate type of the aphids repelled leaves attacked by the lacebug, suggesting that the lacebug affected host selection of alate aphids through plants. On the other hand, predators decreased survival of the aphid. There were many kinds of predators of the aphids in the field, although there were few predators of the lacebug. The lacebugs occurred on most of tall goldenrods at high density, while the aphids locally distributed on tall goldenrods in a small colony size.

Conclusion: Not only colonization of the exotic lacebugs but also predation decreased the exotic aphids on tall goldenrods.

POSTER PRESENTATION

Nestmate discrimination in the harvester termite *Hodotermes mossambicus* in the Namib desert

Felix Hager[1], Joh Henschel[2], Wolfgang H. Kirchner[1]

[1]Ruhr-University, Department of Biology and Biotechnology, Bochum, Germany, [2]Gobabeb Training and Research Centre, Gobabeb, Namibia, [3]University of the Witwatersrand, School of Animal, Plant and Environmental Sciences, Johannesburg, South Africa

Nestmate and kin recognition in social insects have been studied extensively in social hymenopterans. Much less is known about nestmate recognition and the underlying mechanisms in termites. In the African harvester termite *Hodotermes mossambicus* it has been recently shown in laboratory experiments that they are able to discriminate between nestmates and non-nestmates using cues provided by the colony-specific composition of the intestinal flora. Aim of the present study was to investigate nestmate discrimination in this species under natural conditions.

Termites were collected close to the Gobabeb Training and Research Centre in the Namib-Naukluft Park, Namibia. Pairs of nestmate or non-nestmate termites taken from colonies which were up to 2 km apart were observed in Plexiglass arenas. All interactions were recorded for two minutes.

Discrimination between nestmates and non-nestmates was significant at all distances between nests tested ranging from 13m to 2100m. The probability of agonistic behaviour was significantly distance dependent. The reactions to non-nestmates were generally much more aggressive than in previous laboratory studies.

The results confirm previous laboratory studies on nestmate discrimination in *Hodotermes mossambicus.*

POSTER PRESENTATION

A peripheral circadian clock controls the cuticle deposition rhythm in *Drosophila melanogaster*.

Chihiro Ito[1], Shin Goto[1], Sakiko Shiga[1], Kenji Tomioka[2], Hideharu Numata[1]

[1]Graduate School of Science, Osaka City University, Osaka, Japan, [2]Graduate School of Natural Science and Technology, Okayama University, Okayama, Japan

Introduction: Insect endocuticle thickens after adult emergence by daily alternating deposition of two chitin layers with different orientation. Although the cuticle deposition rhythm is known to be controlled by a circadian clock in many insects, the site of the driving clock, the photoreceptor for entrainment, and the oscillatory mechanism remain elusive. In the present study, we investigated them in *Drosophila melanogaster*.

Method: The cuticle growth layers in the furca, which is the thoracic apodeme attached to inner muscles, were observed. Wild type (Canton-S) and clock mutant flies (per^{01}, tim^{01}, cyc^{01}, Clk^{Jrk} and cry^{b}) were used.

Results: The cuticle deposition rhythm in wild-type fly free-ran in constant darkness and was entrained to light-dark cycles. The cuticle deposition rhythm also free-ran and was entrained to light-dark cycles when the whole thorax was cultured *in vitro*. These results suggest that it is controlled by a peripheral circadian oscillator. In most per^{01}, tim^{01}, cyc^{01} and Clk^{Jrk} flies, the endocuticle was thickened without distinct growth layers under constant darkness. In cry^{b} flies, the cuticle deposition rhythm free-ran but was not entrained to light-dark cycles. Entrainment ability of cry^{b} was restored by *act-Gal4*-mediated *cry* expression.

Conclusions: The circadian clock for the cuticle deposition rhythm is in the peripheral tissues and composed of the same clock genes as the central clock regulating locomotor activity rhythm. Unlike other peripheral circadian rhythms of *Drosophila*, CRYPTOCHROME is not involved in generation of the circadian oscillation for the cuticle deposition rhythm.

POSTER PRESENTATION

Immunological challenge promotes dispersal in a territorial damselfly *Calopteryx virgo*

Suhonen Jukka, Honkavaara Johanna, Rantala Markus J.

University of Turku, Turku, Finland

Introduction: Dispersal is an important determinant of gene flow, and thus subject to strong natural selection. Parasites can also have important fitness consequences, and increased rates of dispersal from areas with high infection risk could reflect parasite avoidance behaviour.

Methods: We tested whether experimental activation of immune system has an effect on dispersal behaviour of *Calopteryx virgo* males collected from three populations in southern Finland. For immune-challeged group, we inserted a nylon monofilament in an abdominal segment, for sham-manipulated group a puncture was made in the same segment, and the control group was captured and handled without a puncture or an implant. The damselflies were released back to nature, and their dispersal behaviour was monitored.

Results: Immune-challenged males exhibited increased levels of dispersal rate and dispersal distance. Sham-manipulate males also dispersed more readily compared to control males, but for shorter distances than males with implants.

Conclusions: Activation of the immune system enhances dispersal behaviour in *C. virgo* males. Dispersal might reduce risk of further infections if activation of the immune system indicates high infection risk in the present habitat. Further, increased risk of parasites might incur an increased infection risk also to offspring and dispersal might reduce this risk, too. Moreover, immune defence might deplete energy reserves, amount of which is an important determinant of territory holding capacity in these insects. If a male cannot defend a territory due to activation of immune system, it might be more prone to disperse in order to find a non-vacant territory elsewhere.

POSTER PRESENTATION

Influence of feeding frequency on a life cycle of the antlion, *Myrmeleon formicarius* (Neuroptera: Myrmeleontidae)

Toshiaki Matsura

Kyoto University of Education, Kyoto, Japan

Larvae of *Myrmeleon formicarius* are common antlions that make a conical pit on the dry sand. Since antlion larvae seldom relocate their pits, prey consumption of them possibly varies among individuals. To clarify how the variation of prey consumption affects their life cycles, third instar larvae of *M. formicarius* were reared under various feeding conditions using chironomid larvae as a prey. All larvae reached adult stage in the second year from their egg-hatching, although it has been said that *M. formicarius* needs at least two years to complete one generation because the third instar larva must experience a short day length after having experienced a long day length in order to form a cocoon. This experiment demonstrated that *M. formicarius* can potentially become univoltine if the larva has grown under a rich feeding condition. Moreover it was shown that the difference of feeding rate caused a variation in adult size but their periods of the final instar stage were nearly constant. As a result the adult eclosion was synchronous.

POSTER PRESENTATION

An investigation into the potential of entomopathogenic nematodes for control of banded fruit weevil, *Phlyctinus callosus* (Schoenherr) (Coleoptera: Curculionidae)

Tiarin Ferreira, Antoinette Malan

University of Stellenbosch, Stellenbosch, South Africa

Introduction: The banded fruit weevil, *Phlyctinus callosus* (Schoenherr), is the most important weevil pest on apples and nectarines in South Africa. Control of weevils is important due to damage caused to fruits, leaves and roots and also regarding export because of phytosanitary regulations. Current control of weevils in orchards is mainly targeted at the above ground adult. The use of South African species of entomopathogenic nematodes (EPN) against different life stages of the weevil were investigated in laboratory assays.

Methods: In this study *Steinernema khoisanae*, *Heterorhabditis zealandica* and *H. bacteriophora* were used to test the efficacy of the nematodes against adults and larvae of weevils in the laboratory. The nematodes were cultured on *Tenebrio molitor* and used within one week of harvesting. Adult weevils were collected from cardboard bands around the trunks of apple trees. Eggs were collected from adults that oviposited on wet cotton wool. Larvae used were either sieved from soil or reared on an artificial diet. The insects were inoculated with infective juveniles in 24 well plates and kept in a growth chamber at 25 ºC. Insect adults and larvae were individually dissected to determine infection with nematodes.

Results: After a period of 14 days all adults in the controls and inoculated wells were dead. Up to 75% of inoculated adults were infected with nematodes. All weevil larvae were found to be infected by the three nematodes species used.

Conclusion: Two stages of the banded fruit weevil, the adult and larvae, have been shown to be susceptible to three EPN species in laboratory conditions.

POSTER PRESENTATION

Assessment of termite biodiversity in Kakamega forest (Kenya) using DNA barcodes

Zipporah B. Osiemo[1], Godfrey H. Kagezi[2], Johanna P.E.C. Darlington[3], Andreas Marten[1], Manfred Kaib[4], Linus M. Gitonga[5], Hamadi I. Boga[6], Roland Brandl[1]

[1]Department of Animal Ecology, University of Marburg, Marburg, Germany, [2]Kawanda Agricultural Research Institute, Kampala, Uganda, [3]Zoology Department, University of Cambridge, Cambridge, United Kingdom, [4]Department of Animal Physiology, University of Bayreuth, Bayreuth, Germany, [5]Department of Zoology, Jomo Kenyatta University of Agriculture & Technology, Nairobi, Kenya, [6]Department of Botany, Jomo Kenyatta University, Nairobi, Kenya

Termites are among the most important decomposer in tropical ecosystems, where they can make up to 95% of the insect biomass in soil. The taxonomy as well as the determination of termites to the species level mostly relies on characters of soldiers. However, workers are the most frequently sampled caste during ecological surveys. Therefore, the diversity of termites is poorly understood, especially in tropical forests. Recently it was suggested to use DNA-sequences (barcoding) for inventories of hyper-divers taxa as well as taxa, which are difficult to determine. Here we present a first approach towards establishing a DNA barcode library to termite species identification and biodiversity assessment using sequences of the mitochondrial COII gene.

Kakamega Forest is the most eastern extension of the Kongolian forest block reaching western Kenya. This isolated forest is a hotspot of biodiversity in Kenya, however, threatened by the increasing human population. We sampled termites across a gradient from primary forests to farmland to assess the regional pool of termite species. A first morphological assessment of almost 250 samples suggested that at least 16 morphospecies occur along the gradient. A first analysis of 100 sequences suggested that more than 20 termite species may occur along the habitat gradient. Furthermore, the assignment of samples to morphotypes corresponded not always to the sequence analysis. Obviously barcoding provides a more comprehensive picture of the diversity of termites. We will use barcoding to estimate the total richness of termites in the Kakamega forest.

POSTER PRESENTATION

Assessment of on-farm stored maize losses in the highland areas of Bungoma district, Kenya

Kimondo Mutambuki, Christopher N. Ngatia

National Agricultural Research Laboratories, Nairobi, Kenya

Introduction: A simulation trial to assess losses in crib and in-house maize storage practices was conducted.

Methods: Three cribs were constructed and 180kg maize in two bags treated with 1.6% pirimiphos methyl and 0.3% permethrin stored in one. In the other, a similar quantity of untreated maize in two bags was stored while in the third crib, 4 bags of cob maize were placed. Another 4 bags, two treated and two untreated were placed on dunnage separated by a 2-meter path in the living house. Samples were analysed at 4-week interval for 24 weeks and pest damage was used to calculate percent weight loss. Grain from selected farmers was also analysed for comparison.

Results: Crib trial had 53% and 20% pest damage in untreated and treated maize compared with 56% and 16% for in-house storage after six months. Cumulative weight loss averaged 20.6% and 9.7% for untreated and treated maize. The figures are markedly higher than 5% criterion for effective pest control measures. Weight loss on farmer stocks compared well with untreated maize and grain damage varied from 5.4% to 27%, translating to 0.5% and 16.8% cumulative loss.

Conclusion: These results suggest ineffective pest control measures by Bungoma farmers. The results contrast with Kitui ones in an earlier study where *Prostephanus truncatus* is endemic and contributed to 10% cumulative loss above the Bungoma level. Efforts should be made to reduce grain damage to below 5% to realise food security at farm level.

POSTER PRESENTATION

Biological and ecological studies of the leucaena bruchid (*Acanthoscelides macrophthalmus*)

Li-Hsin Wu, Wen-Jer Wu, Chiao-Pin Wang

Department of Entomology, National Taiwan University, Taipei, Taiwan

Introduction: *Leucaena leucocephala* (Lam.) de Wit is a powerful invasive weed plant can cause serious ecological problems such as destruction on local vegetation diversity. A new recorded bruchid beetle (*Acanthoscelides macrophthalmus*) attacking the seeds of leucaena was found in Taiwan in 2004.

Method: We studied the effect of temperature on developmental rate of each life stage and the influences of food supplement and mating on the population growth rate. In addition, the shelter and other host plant surveys were proceeded simultaneously in the field.

Results: The developmental zero temperature is 8.769□, the effective cumulative temperature is 706.471 DD (degree days), their developmental rate gradually increased with the temperature, while maximum survival rate reached 66% in 27□ and further population growth rate parameters were also described. In the field, leucaena bruchid can complete their life cycle on pods that we manipulated underground or within canopy, and their population number fluctuates with the phenology of mature leucaena pods; we also found leucaena bruchid can feed on *Albizzia falcataria*, a new host plant in 9 legume species surveyed.

Conclusion: Our study provides several developmental parameters of leucaena bruchid which can help us to evaluate the feasibility for using them as a biocontrol agent of *Leucaena leucocephala*.

POSTER PRESENTATION

Biological and ecological studies of the leucaena bruchid (*Acanthoscelides macrophthalmus*)

Li-Hsin Wu, Wen-Jer Wu, Chiao-Pin Wang

Department of Entomology, National Taiwan University, Taipei, Taiwan

Introduction: *Leucaena leucocephala* (Lam.) de Wit is a powerful invasive weed plant can cause serious ecological problems such as destruction on local vegetation diversity. A new recorded bruchid beetle (*Acanthoscelides macrophthalmus*) attacking the seeds of leucaena was found in Taiwan in 2004.

Method: We studied the effect of temperature on developmental rate of each life stage and the influences of food supplement and mating on the population growth rate. In addition, the shelter and other host plant surveys were proceeded simultaneously in the field.

Results: The developmental zero temperature is 8.769□, the effective cumulative temperature is 706.471 DD (degree days), their developmental rate gradually increased with the temperature, while maximum survival rate reached 66% in 27□ and further population growth rate parameters were also described. In the field, leucaena bruchid can complete their life cycle on pods that we manipulated underground or within canopy, and their population number fluctuates with the phenology of mature leucaena pods; we also found leucaena bruchid can feed on *Albizzia falcataria*, a new host plant in 9 legume species surveyed.

Conclusion: Our study provides several developmental parameters of leucaena bruchid which can help us to evaluate the feasibility for using them as a biocontrol agent of *Leucaena leucocephala*.

POSTER PRESENTATION

Influence of temperature on some developmental stages of *Culex quinquefasciatus* Say.

Vijaylakshmi Swain

University of Delhi, Delhi, India

Introduction: Temperature is an intrinsic factor of the environment which exhibits variations and fluctuations. It influences all living organisms and alters certain physiological characteristics. Vector mosquitoes pose a threat to mankind due to their capacity to transmit disease, genetically inherited trait of development of resistance against common insecticides and their observed adaptability to varied ecological changes including thermal adaptation. An attempt has been made to evaluate the effect of temperature on insecticide susceptible and resistant strains of some developmental stages *of* the filarial vector, *Culex quinquefasciatus*.

Methods: Malathion resistant (RR) and susceptible (SS) laboratory strains of *Culex quinquefasciatus* were exposed to a range of temperatures (35-42℃) to determine sub-lethality. Replicates of 4^{th} instar larvae were pooled and subjected to sub-lethal temperature, then allowed to recover and proceed with their life cycles. Rate of pupation, adult emergence and longevity were closely monitored along with the control.

Results: In malathion (RR) strain there was increased longevity in adult females but a substantial decrease in case of males. The males were more sensitive and succumb to stress and hence there is increased mortality. There was late onset of pupation, higher larval mortality and diminished adult eclosion in the thermal adapted strains.

Conclusions: The ability to tolerate thermal exposure and get adapted is reported to be a homeostatic response to protect the insect and confers adaptive thermotolerance.

POSTER PRESENTATION

Role of the salicylic acid signalling pathway in the *Mi-1*-mediated resistance of tomato to whitefly *Bemisia tabaci*.

Gloria Nombela[1], Clara I. Rodríguez[1], Isgouhi Kaloshian[2], Mariano Muñiz[1]

[1]Institute for Agricultural Sciences - Spanish National Research Council (CSIC), Madrid, Spain, [2]Department of Nematology (University of California, Riverside), Riverside, United States

Plant defense responses to pests, pathogens or wounding are usually dependent on either the salicylic acid (SA) pathway or jasmonic acid (JA) and ethylene-dependent pathways. In Arabidopsis, the B-biotype of *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) induced SA defenses and suppressed JA defenses. In tomato, resistance to *B. tabaci* is mediated by the *Mi-1* gene, which also regulates resistance to potato aphid *Macrosiphum euphorbiae* and 3 species of root-knot nematodes (*Meloidogyne* spp.). A role for the SA signaling pathway in *Mi-1*-mediated resistances to root-knot nematodes and aphids has been previously identified.

In the present work, the *NahG* transgene that eliminates endogenous salicylic acid (by degradation to catechol) was used to test the role of the SA pathway in the resistance mediated by *Mi-1 gene* to *B. tabaci* (B and Q biotypes). The tomato genotypes used were VFN (*Mi-1/Mi-1*), Moneymaker (*mi-1/mi-1*), the transgenic tomato expressing *NahG* in Moneymaker background, and the cross VFN x *NahG* to introduce *NahG* in the *Mi-1* background. In no-choice assays under controlled conditions, 5 female whiteflies were confined in a clip-cage attached to the abaxial surface of a leaflet per plant. Females were allowed to oviposit for 6 days. Then, females and clip-cages were removed and the number of eggs was counted. Twenty one days later, the numbers of L3, L4 and new adults on each plant were recorded. The resistance was lost in the cross VFN x *NahG*, which indicates that SA signaling pathway is required for the *Mi-1*-mediated resistance to *B. tabaci* in tomato.

POSTER PRESENTATION

Effects of host plant and temperature on *Aphidius colemani* (Hymenoptera: Braconidae) intrinsic rate of population increase

Rostislav Zemek[1], Vojtech Jarosik[2], Jan Havelka[1], Fernando Chihale[1]

[1]Biology Centre of Academy of Sciences of the Czech Republic, Institute of Entomology, Ceske Budejovice, Czech Republic, [2]Charles University, Faculty of Natural Sciences, Prague, Czech Republic

Introduction: *Aphidius colemani* is a generalist aphid endoparasitoid commonly used in augmentative biological control of *Myzus persicae* in vegetable greenhouses. The aim of this paper was to investigate the aphid-mediated effects of plant on *A. colemani* life-history characteristics.

Methods: *A. colemani* was reared on *Myzus persicae* using either *Nicotiana tabacum* or *Vicia faba* as a host plant for aphids. The experiments were carried out at four constant temperatures 18, 22, 26 and 29 °C. The intrinsic rate of increase as well as other derived parameters, were estimated from the life table data by means of the computer program. The standard error of the parameters was estimated using a Jackknife sub-sampling method.

Results: The highest mean total number of offsprings per female was found when parasitoids were offered to *M. persicae* grown on bean at 22 °C. The lowest mean total number of offsprings was found at 29 °C when tobacco was used as a host plant. Survivorship of females was significantly higher on tobacco than bean at 26 °C while at the other temperatures no differences were found. The intrinsic rate of increase was higher for *A. colemani* parasitizing aphids on bean than tobacco although significant differences were found only at optimal temperature 22 °C.

Conclusions: The obtained results corroborated our hypothesis that the host plant is important factor in an aphid-parasitoid relationship. Plant toxins are probably the cause of lower rate of population increase in *A. colemani* developed on tobacco-reared aphids.

Acknowledgments: This work was supported by MSMT grants No. 2B06005, 21620828 and LC06073.

POSTER PRESENTATION

Grapevine leafroll-associated virus 3 (GLRaV-3) extraction from grapevine and mealybugs (Hemiptera: Pseudococcidae) for quantitative real-time PCR

Nicoleen Douglas, Glen P. Malherbe, Kerstin Krüger

Department of Zoology and Entomology, University of Pretoria, Pretoria, South Africa

Introduction: The integrity of purified RNA is critical for reliable diagnostic use in quantitative real-time reverse transcription polymerase chain reaction (real-time RT-PCR). Sampling, storage and extraction method affect the integrity and purity of extracted RNA. *Grapevine leafroll-associated virus 3* (GLRaV-3) has been associated with one of the most economically important viral diseases of grapevines. An important vector is the vine mealybug *Planococcus ficus*. For the development of a quantitative real-time RT-PCR for GLRaV-3, the efficiency of different extraction methods was evaluated using plant material and mealybugs.

Methods: Initially five extraction methods were compared: Qiagen RNeasy Mini, Promega SV total RNA Isolation System, Gentra Purescript RNA Isolation Kit, Phenol-chloroform method and QiaZol extraction method. Of the five extraction techniques tested, the Gentra, QiaZol and Phenol-chloroform techniques were selected based on cost involved. Extractions were tested for GLRaV-3 presence using nested reverse transcription PCR (nested RT-PCR) and efficiency was compared using real-time RT-PCR to determine relative concentrations of GLRaV-3.

Results: The PCR results showed 60-70% of the Phenol-chloroform, 80-90% of the Gentra and 90-100% of the QiaZol plant material samples to be positive for GLRaV-3. The number of GLRaV-3 - positive mealybug samples was 60-70% for Phenol-chloroform, 60-90% for Gentra and 79-100% for QiaZol extractions.

Conclusion: Overall, the QiaZol technique was selected as the preferred method, based on cost and time involved. The Phenol-chloroform and Gentra techniques also produced good results. However, the former is time-consuming and the latter is no longer commercially available.

POSTER PRESENTATION

Integrated production and durable management of a reproduction sericultural family farm

Matei Alexandra[1], Popescu Agatha[2], Sladescu Viorica[3], Talpes Marilena[4], Dan Mioara[5], Androne Magda[1]

[1]Commercial Society Sericarom-Research department, Bucharest, Romania, [2]University of Agricultural Sciences and Veterinary Medicine, Bucharest, Romania, [3]National University of Fine Arts Bucharest – Textiles Arts Department, Bucharest, Romania, [4]Institute of Research and Development for Aquatical Ecology, Fishing and Aquaculture, Galati, Romania, [5]National Institute of Research and Development for Textiles and Leather Goods, Bucharest, Romania

Introduction: The paper presents a management system of the sericultural activities in family farms based on the principle of integration between the main activities, respective the production of reproduction biological material, with the processing of the waste products and the production of secondary products obtained from the main activity. The project is based on the long experience existing in sericulture in the country, on the high value silkworm races and hybrids, mulberry varieties and on the tradition in the domestic silkworm rearing and cocoon processing.

Methods: Techniques and methods: specific for producing biological reproduction biological reproduction material (selection based on biological and technological criteria, pure breed reproduction or inbreeding), for achieving new textile structures of natural silk and other fibres (mohair, wool), for processing unreeling cocoons, for determining the nutritive value of the forage recipes and food conversion in body weight at fishes.

Results: The project can be applied in family farms, more exactly in households having at least 1 ha arable land (0.5 ha mulberry plantation and 0.5 ha mulberry nursery), 150 s.m. buildings as silkworm rearing houses and 2-3 family members dealing with the activities stipulated in the project. The main product is represented by silk cocoons. The yearly production capacity of the family farm is 400 kg cocoons. The cocoons can be partially used for obtaining silkworm eggs (1000 boxes)) or can be sold to specialized reproduction units. Other cocoons could be processed in silk fibres and traditional handy-crafts. The expectations for the average technical performances are the following ones: 6000 kg leaf yield production/0.5 ha plantation, 35 kg raw cocoon production/box, 400 kg raw cocoon production/0.5 ha mulberry plantation, 15 kg leaf consumption/kg cocoons, 80% pupation rate, 2.0 g raw cocoon weight, 0.400 g shell weight and 1200 m filament length.

Conclusions: The major project objective is to establish the scientific and economic fundamentals for setting up a family sericultural reproduction farm under the conditions of integrated production and management.

POSTER PRESENTATION

Molecular tools for improving insecticide resistance management in the whitefly *Bemisia tabaci* (Homoptera: Aleyrodidae)

John Vontas[1], Emmanouel Roditakis[2], Ralf Nauen[3], Mark Paine[4], Shai Morin[5], Anastasia Tsagkarakou[2]

[1]Laboratory of Pesticides Science, Agricultural University of Athens, Iera Odos 75, 11855 Athens, Greece, Greece, [2]Laboratory of Entomology and Agricultural Zoology, National Agricultural Research Foundation, Heraklion (N.AG.RE.F.),, Kastorias 32A Katsampas, 71003 Heraklio, Greece, Greece, [3]Bayer CropScience AG Research Insecticides, Insect Toxicology and Resistance Building 6220 Alfred Nobel Str. 50 D-40789 Monheim, Germany, [4]Vector Group, Liverpool School of Tropical Medicine, Pembroke Place, Liverpool, L3 5QA, United Kingdom, [5]Department of Entomology, Faculty of Agricultural, Food and Environmental Quality Sciences, Hebrew University of Jerusalem, P.O.Box 12, Rehovot 76100, Israel

Introduction: The whitefly *Bemisia tabaci* is responsible for significant yield losses in numerous protected and field crops. Growers rely on insecticides, however many of those no longer effectively control these pests, due to the appearance of insecticide-resistant populations. Early detection and monitoring of insecticide resistance and knowledge of the population genetic structure are crucial for the implementation of insecticide management tactics.

Methods: Insecticide resistant strains and field populations are collected from the island of Crete (Greece). Simple PCR based detection assays, appropriate for low tech laboratories, are being designed for the detection of characterised markers, such as those associated with target site insecticide resistance (MACE, kdr) and *B. tabaci* biotypes. Antibody detection assays, based on artificially synthesized specific peptides are used for the diagnosis of metabolic resistance.

Results: We developed simple PCR–RFLP and PASA agarose gel visualization based assays for monitoring the L125I, T129V pyrethroid resistance mutations in the IIS4-IIS6 region of the para sodium channel gene and a MACE organophosphate resistance mutation of the Ace gene. A PCR-RFLP and a diagnostic PCR based on mitochondrial DNA differences were developed for the reliable discrimination between different biotypes, while higher resolution gene flow analysis is performed using microsatellite markers. Finally, a specific antibody assay was produced for the detection of a CYP6 cytochrome P450 which is associated with Imidacloprid resistance in both B and Q biotypes of *B. tabaci*. The assay is being simplified into a diagnostic format.

Conclusions: A number of applicable simple molecular tools have been developed, which can be used to improve insecticide resistance management in the whitefly *B. tabaci.*

POSTER PRESENTATION

Changes of mosquito diversity: Vectors of pathogenic agents in relationship to weather changeability in inundated areas of the Czech rivers Morava and Dyje

Ivan Gelbic, Jiri Halouzka

[1]Biological Centre AS CR, Ceske Budejovice, Czech Republic, [2]Institute of Vertebrate Biology, Brno, Czech Republic

Introduction: The global climate change is well known phenomenon for several years. The annual mean temperature in the last decade is 1-2°C higher than long-term normal and rain-falls are less regular. Temperature is sizeable fluctuated, especially in spring and summer and dry and hot weeks are changed by rainstorms causing local and sometimes catastrophic floods, practically in all European countries during the last decades.

Methods: This phenomenon together with increased temperature in spring and summer months causes changes in biodiversity of mosquito communities as well as in the density of mosquito species connected with calamitous situations. The study is dealing with mosquito populations and their changes in an inundated area of the Morava and Dyje rivers after flood in 1997.

Results: Rainstorms and following floods dramatically increased mosquito density. However, subsequent year showed rapid decrease of species biodiversity but on the contrary multiple growth of only some mosquito species density including the known main vector of *West Nile* virus – *Culex pipiens*. The global change is also probably responsible for emergence of new arboviruses in Europe, for example originally African *Usutu* virus. Species with seasonal regular overcrowding having epidemiological importance are *Aedes vexans*, *Ochlerotatus sticticus*, Oc*. cinereus* and Oc*. cantans*. During the last year also more numerous populations of *Anopheles claviger* and *Culex modestus* species on some Moravian localities were observed.

Conclusions: In the past decade the changes in the number and species composition of the mosquito fauna were observed. The species preferring lower temperature subsequently disappear and species developing in higher temperature occurs.

POSTER PRESENTATION

Spectral sensitivity and colour choice in the pollen beetle, *Meligethes aeneus*

Thomas Döring[1], Samantha Cook[2]

[1]Imperial College London, Ascot, United Kingdom, [2]Rothamsted Research, Harpenden, United Kingdom

Introduction: The pollen beetle, *Meligethes aeneus* is a serious pest of oilseed rape (OSR, *Brassica napus*) in Europe. Resistance levels to insecticides have increased dramatically over the last few years and the OSR acreage is rapidly expanding. Alternative control methods are therefore urgently needed. As a first step towards exploring the potential use of coloured traps for monitoring and the use of cultivars with petal colours other than yellow for pollen beetle control, physiological and behavioural experiments were conducted to elucidate their response to colours.

Methods: Spectral sensitivity was measured in 6 animals using the electroretinogram technique: light flashes (100 ms) at varied wavelengths (340-660 nm, 10 nm steps) and at different light intensities were applied to the eye after dark adaptation. Water traps of 140 colours (from yellow to green to blue with varying amounts of white and black added) were set out in the field in May 2007.

Results: The mean spectral sensitivity curve peaked at 520 nm; however, a model template fitted to the long wavelength tail of the observed curve revealed a peak around 535-540 nm. A secondary sensitivity peak was observed in the UV (370 nm). In the coloured traps, a total of 159 pollen beetles were found. Yellow traps with small amounts of white added caught the most, while the second highest catch was observed in pure yellow traps.

Conclusions: Our results confirm that pollen beetles prefer yellow over other colours, however more trap experiments are needed that include varied reflectance in the UV.

POSTER PRESENTATION

Frequency patterns in empty and occupied ovipositional patches in blowflies

Luciane Galindo, José Passos, Liciana Silveira, Wesley Godoy

Universidade Estadual Paulista, Botucatu, São Paulo, Brazil

Introduction: In this study, the ovipositional behavior in blowflies was investigated focusing the patches occupation, with the purpose of verifying whether the previously occupied patches influence the ovipositional habit by females.

Methods: The collections were done by using suspended traps in trees during four days. Each trap had ground meat and 100 larvae of *C. albiceps*, *C. megacephala* and *C. putoria*. As the control, a container without larvae was included.

Results: 34.561 dipterous were obtained with Accumulated Frequency, estimated inside and among treatments. *Chrysomya megacephala* was the most numerous species, followed by *Lucilia* ssp., *Chrysomya albiceps* and *Ophyra chalcogaster*. The control traps were the most attractive, accordingly to the results of a previous study in the laboratory.

Conclusions: The high number of *C. megacephala* suggests that the species might not carry influence from the occupation and it indicates good larval performance under competition for food in the previously occupied patches. *Lucilia* ssp., showed a larger ovipositional inhibition due to the occupation, and *C. albiceps* did not inhibit the oviposition in general. The preference for not occupied patches suggests that the insects choose to lay eggs under this condition, but the mechanism by which the females are able to detect other species is still unknown. A more complete analysis, including results obtained in the following months, might indicate clearer trends for the confirmation of the suggested result.

POSTER PRESENTATION

‘Exite’-like structures on the thoracic appendicular bases of the mayfly *Bleptus fasciatus* Eaton (Ephemeroptera: Heptageniidae)

Koji Tojo, Ken Miyairi

Shinshu University, Matsumoto, Nagano, Japan

Insects account for three quarters of all animal species, and more than 99 percent of them are wing-acquired insects. Pterygotans have achieved spectacular prosperity and radiation, and elucidating their evolution and groundplans is a most interesting subject. With regard to the ‘origin of wings’, which has been argued over for a long period, various hypotheses have been proposed. Of these hypotheses, presently, the ‘epicoxal exite (outer lobe or podite of the most basal leg segment) theory’ is the most widely accepted. Furthermore, the epicoxal exite hypothesis for the origin of wings can be reconciled readily with other theories on related topics. That is to say thatwings derive from tracheal gills of an ancestral aquatic “protopterygote”. According to this theory, the abdominal winglets (or gills) of the protopterygote are serially homologous with thoracic wings, and also the gill itself is a modified epicoxal exite of a hypothetical, basal leg podite.

When verifying the direct homology of the wing to the epicoxal exite, it becomes important to compare the serial homology between wings with other proximal exites (e.g., subcoxal, coxal, trochanteral and prefemural). Recently, we could find the remaining structures of subcoxal and coxal exites in a heptageniid mayfly. Furthermore, in these exites, tracheation can be clearly observed. The remnants of these structures are a new discovery amongst present Pterygotans. This discovery amongst present Pterygotans, provides long required research opportunities to verify the serial homology discussed above using various newly available techniques.

POSTER PRESENTATION

Biology and feeding capacity of anthocorid predator, *Orius maxidentex* Ghauri (Hemiptera: Anthocoridae) as a biological control agent of thrips

Oraphan Kernasa, Athitiya Kaewpradit, Wiwat Suasa-Ard

[1]NBCRC CRC, Nakhon Pathom, Thailand, [2]Kasetsart University, Nakhon Pathom, Thailand

Introduction: Anthocorid predator, *Orius maxidentex* Ghauri (Hemiptera: Anthocoridae) was a new recorded as biological control agent of thrips and sap-sucking insects in chili plantations in Thailand, during 2006. Biology and feeding capacity of *O. maxidentex* were since then investigated in laboratory condition at National Biological Control Research Center, Central Regional Center, Kasetsart University, Kamphaeng Saen Campus, Nakhon Pathom.

Methods: Investigation of biology and efficiency of *O. maxidentex* against thrips were conducted by individually reared first instar nymphs in petri dishes on small piece of egg plant leaf, 3x3 cm that was infected by thrips. Daily observation of developmental growth in each stage and number of thrips feeding were recorded.

Results: This assessment revealed that female adult laid the eggs singly in tissue of leaf vein of eggplant leaf. The egg translucent and looked like jar. The incubation period was 3.83 ± 0.38 days. The nymphal stage consisted of 4 instars. The developmental period of nymphal stage was 12.73 ± 0.74 days. The longevity of adult male and female were 10.36 ± 1.96 and 19.05 ± 4.36 days, respectively. Feeding capacity of *O. maxidentex* nymphs on thrips revealed that the total nymphal stage fed about 27.56 ± 2.82 thrips. Male and female fed about 40.73 ± 8.17 and 87.16 ± 14.31 thrips, respectively.

Conclusion: *Orius maxidentex* should be an promising natural enemy as biological control agent of thrips in Thailand.

POSTER PRESENTATION

Diversity of insecticide resistance profiles in pyrethroid-resistant *Triatoma infestans* (Hemiptera: Reduviidae) from Argentina and Bolivia

Mónica Germano, Claudia Vasssena, Pablo Santo Orihuela, Eduardo Zerba, María Inés Picollo

Centro de Investigaciones en Plagas e Insecticidas (CONICET-CITEFA), Buenos Aires, Argentina

Introduction: *Triatoma infestans* is the main vector of Chagas Disease in South América. Chemical control by insecticides has been successful for the elimination of domestic infestation and consequently the reduction of vectorial transmission. Recently, high resistance to pyrethroids was reported in northern Argentina and southern Bolivia. Additionally a decrease in the effectiveness of field treatments was found in two Andean areas of Bolivia. In this work we studied the susceptibility profile to non-pyrethroid insecticides in resistant populations from Salta (Argentina) and Yacuiba, Sucre and Mataral (Bolivia)

Methods: Toxicity test were done by topical application of insecticides (0,2 µl) on first nymphs (3- 5 days old). Activity of cytochrome P-450 mono-oxygenase was measured in individual first nymphs through ethoxycoumarine-o-deethylase.

Results: Resistant ratios (RRs) demonstrated lower deltamethrin resistance for Andean populations (RR Sucre 31.3; RR Mataral 17.4) than Salta (RR 133.1) and Yacuiba (RR 154.4). Moreover, remarkable differences were found in resistance profile to fipronil in Andean and non-andean populations. Sucre and mataral showed very high RRs (585.5 and 386.9 respectively) to fipronil, while Salta and Yacuiba were susceptible to this insecticide. Additional studies demonstrated that all populations were susceptible to the organophosphorus fenithrotion. Activity of mono-oxygenases showed noticeable differences in the distribution of activities between susceptible and resistant populations. The total percentage of insects below 0.48 pmol of 7-OH coumarine/m/l was lower for susceptible strain (36%) than for resistant populations

Conclusions: The differential pattern of susceptibility to insecticides and the relative contribution of mono-oxygenases, suggest an independent evolution of resistance in the studied populations of *T. infestans.*

POSTER PRESENTATION

Phenotypic characterization of races from native genetical stock of the silkmoth *Bombyx mori* L.

Matei Alexandra[1], Androne Magda[1], Popescu Agatha[2]

[1]Commercial Society Sericarom-Research department, Bucharest, Romania, [2]University of Agricultural Sciences and Veterinary Medicine, Bucharest, Romania

Introduction: The importance of gene bank existence as an essential condition for breeding programs elaboration is unanimously known for every plant and animal species, from which the permanent concern for its diversification and maintaining by appropriate preservation procedures "in situ" or "ex situ". This way, the loss of biological material, especially of the local races resisting to diseases and adapted to environmental conditions is avoided. This study aims the analysis of phenotypic characters variability within the genetic stock of *B. mori,* in accordance with its biological development stages (egg, larva and pupa). Native genetic stock of silkmoth *B. mori* resulted from the identification of gene sources from local populations, bilateral exchange of biologic material with similar foreign institutes, creation of new genotypes using specific breeding methods. Within its structure, the genetical stock of silkmoth includes 72 races.

Methods: The silkworm specific experimental technique has been applied, differentiated by technological and biological development stages (Grekov D., 2005). The sample size used as the base for phenotypic parameters determination as well as the working methods correspond to sericulture technical standards.

Results: The main phenotypical and quantitative parameters of the races that represent the gene stock of *B. mori* have the following values: fecundity (230-710 eggs/laying), hatchability (80.6-100%), larval stage duration (26-32 days), larvae weight (4.2-5.7 g), larvae pupation (80.8-96.6%), raw cocoon weight (1.445-2.361 g), cocoon shell weight (0.240-0.520 g), fiber length (746-1356 m), metric number of fiber (2917-3764 m/g).

Conclusions: Depending on the quantitative parameters value, the silkworm races are differently used, the entire genetic stock being destined for various technological levels, as follows: 4 active races (parents of hybrids), 4 candidate races for parents of hybrids, 64 races in preservation.

POSTER PRESENTATION

Ovicidal effect of monoterpenoids against permethrin-resistant human head louse (Phthiraptera: Pediculidae)

Ariel Toloza, Claudia Vassena, María Inés Picollo

Centro de Investigaciones en Plagas e Insecticidas, CONICET-CITEFA, Buenos Aires, Argentina

Introduction: The human head louse *Pediculus humanus capitis* De Geer is an important cosmopolitan pest affecting school-aged children. Previous works of our laboratory have detected populations in Buenos Aires with high resistance levels to pyrethroids in both adult and egg stages (RR>80). In the search of new insecticides, monoterpenoids seem to be good control alternative candidates because they are environmental friendly and not acutely toxic to mammals. The purposes of this work were to develop a methodology employed to detect the ovicidal effect of 23 monoterpenoids against *P.humanus capitis* from Buenos Aires, and to compare it with the activity previously reported on adults.

Methods: Eggs were collected from heads of children 5-12 yr old, using an anti-louse comb. Groups of 15-20 late development eggs were exposed to the vapours of the evaluated monoterpenoids in an enclosed chamber. The number of emerged nymphs was counted, and those with incomplete emergence were considered as dead.

Results: There were highly significant differences among the evaluated monoterpenoids ($p<0.0001$). Ten of the monoterpenoids produced mortality above 80%. The most effective monoterpenoids were hydrocarbons and ethers, followed by ketones, alcohols, phenols and esters. Regression analysis revealed a statistically significant relationship between ovicidal mortality and adulticidal knockdown of the same evaluated monoterpenoids at the 99% confidence level.

Conclusion: This study demonstrated the ovicidal activity of monoterpenoids in concordance with their effectiveness on nymphs and adults. The potential use of mono-terpenoides as ovicides and adulticides in novel pediculicide formulations is discussed

POSTER PRESENTATION

Developing a laboratory rearing technique for the litchi moth*, Cryptophlebia peltastica* (Lepidoptera: Tortricidae).

Willem P. Steyn, Pieter S. Schoeman

Agricultural Research Council, Institute for Tropical and Subtropical Crops, Nelspruit, Mpumalanga, South Africa

Introduction: The litchi moth, *Cryptophlebia peltastica* (Meyrick) (Lepidoptera: Tortricidae) is a quarantine pest of litchi, *Litchi chinensis* Sonnerat in South Africa. Litchis are exported from South Africa but countries such as the USA, which is climatically suitable for litchi moth establishment, impose quarantine restrictions against countries likely to carry new pest species across their boundaries. The female moth lays her eggs on the skin of the fruit and newly hatched larvae eat through the skin and into the fruit flesh and seed. The aim of the present study was to rear high numbers of the litchi moth in captivity for future research, to establish quarantine measures that will prevent the accidental distribution of this pest to foreign countries.

Methods: Infested litchi fruit was collected in the Nelspruit area of the Mpumalanga province in South Africa during the growing season. Final instar larvae found in the fruit were placed in plastic containers with sand at the bottom for the larvae to pupate in. Pupae found were placed in gauze cages to emerge and adult moths were kept in these cages at room temperature to reproduce. Eggs laid were placed into honey flasks with a steam sterilized maize meal medium and kept at room temperature.

Results: The eggs hatched and the first generation of *C. peltastica* was successfully reared through all life stages. Currently eggs of the second generation are on medium.

Conclusions: From these results, it would appear that a viable technique for the rearing of litchi moth has been developed and that a laboratory colony of this quarantine pest can now be established.

POSTER PRESENTATION

The fate of the clock protein PERIOD in the *Drosophila melanogaster* ovary

Joanna Kotwica[1], Maureen Larson[2], Piotr Bebas[1], Jadwiga M. Giebultowicz[2]

[1]Univeristy of Warsaw, Department of Animal Physiology, Warsaw, Poland, [2]Oregon State University, Department of Zoology, Corvallis, United States

Introduction: The clock protein PER undergoes cycles of accumulation, phosphorylation, nuclear translocation and degradation in *Drosophila melanogaster* clock cells. One exception to this pattern is in follicular cells enclosing previtellogenic ovarian follicles. In these cells, PER remains high and cytoplasmic at all times of day. Here, we studied PER levels and subcellular localization in older vitellogenic follicles. We also investigated whether DBT, a kinase known to affect PER in clock cells, interacts with PER in ovarian follicular cells.

Methods: Levels of PER and DBT proteins were assessed by Western blotting and immunocytochemistry. Expression of *dbt* was driven into wild type ovarian follicular cells using the *tim*-Gal4/UAS-*dbt* system.

Results: In wild type flies, PER levels decreased in follicular cells of vitellogenic follicles compared to younger follicles. Nuclear PER was detected in stage 9 follicles, while PER was completely absent in stage 10 follicles. DBT was absent in previtellogenic follicular cells, but present in stage 9 follicular cells. Surprisingly, overexpression of DBT led to higher levels of ovarian PER than in control ovaries. Experiments are under way to verify these data using different GAL4 lines, directing expression of *dbt* into specific follicle stages.

Conclusions: The absence of *dbt* expression in the follicular cells of previtellogenic follicles is the likely reason for stable and cytoplasmic expression of PER in these cells. Onset of *dbt* expression in vitellogenic follicles coincides with nuclear localization and subsequent decline in PER protein. The functional significance of the interplay between ovarian PER and DBT levels is under investigation.

POSTER PRESENTATION

Mapping the cellular network of the circadian clock in two cockroach species

Chih-Jen Wen, How-Jing Lee

Department of Entomology, National Taiwan University, Taipei, Taiwan

Introduction: *Blattella germanica* and *B. bisignata* are sibling species with similar *period* sequence but distinctive circadian rhythm in locomotion. Period (PER), Pigment Dispersing Factor (PDF), and Corazonin (CRZ) are three clock-related proteins whose antibodies are used to map the cellular network of the circadian clock.

Methods: The cell distribution and connection of immunoreactivity (ir) against PER, PDF and CRZ were compared between the two cockroach species.

Results: Three major PER-ir cell groups are located in the optic lobes, which are the sites of the major circadian clock. The output signal, PDF, is co-localized with PER in all groups of cells. Only two CRZ-ir cells and their axons are found in the optic lobes and they are not co-localized with PER-ir or PDF-ir cells and axons. A group of 3-4 PER-ir cells in the protocerebrum display typical characteristics of neurosecretary cells. In addition, there are numerous, small PER-ir and PDF-ir co-localized cells in the pars intercerebralis, which have direct connections with CC through PER-ir and PDF-ir axons.

Conclusions: Since the overall distribution pattern of the clock cells are the same for *B. germanica* and *B. bisignata*, the possible explanation for the differential expression of locomotor circadian rhythm between the species depends on downstream genes of *per, pdf*, and *crz*.

POSTER PRESENTATION

Differential testing laboratory conditions for *Pediculus humanus humanus* and *Pediculus humanus capitis (*Phthiraptera: Pediculidae)

Anabella Gallardo, Gastón Mougabure cueto, María Inés Picollo

Centro de Investigaciones en Plagas e Insecticidas, CONICET-CITEFA, Buenos Aires, Argentina

Introduction: Human pediculosis is a prevalent parasitic infestation occurring in both developed and underdeveloped nations. It is produced by *Pediculus humanus humanus* and *Pediculus humanus capitis*, two obligate ecto-parasites who affect the body or the head of the host. A laboratory strain of the body lice was adapted to a rabbit host in the 1940s and was maintained without feeding on humans in laboratories from different countries. Experimental evidence has proved that body lice are an appropriate test organism for testing products for the control of its sub-species, the head lice. This study compared the optimal environmental conditions for females and males of *P humanus humanus* and *P humanus capitis* at laboratory level.

Methods: For the tests, we used separately females or males of body or head lice. Insects were kept for 24 h in closed chamber at different measured temperatures (18, 24 and 28 ºC) and humidities (50-60 and 95- 100 % RH). Mortality of lice was recorded at 18 and 24 h.

Results: There was a significant differential response to changes in temperature and humidity between body and head lice. All *P humanus humannus* exposed to different combinations of temperature and humidity, showed high survival (90- 100%). In contrast, survival of *P humanus capitis* was clearly dependant on temperature and humidity. Mortality of males and females increased as the temperature increased or the humidity decreased. The optimal laboratory conditions for head lice were 18ºC and 95- 99% RH, where average survival of males was 90% and females 85%.

Conclusions: At laboratory, head lice required more special conditions of temperature and humidity than body lice for the survival of control insects. Thus, optimal head lice conditions (18ºC and 95- 99% RH) can be used for both sub-species in comparative toxicological tests for evaluating pediculicide activity

POSTER PRESENTATION

Bioecology of the fruit gall system in strawberry guava

Anamaria DalMolin[1], Gabriel Melo[2], Rosy M. S. Isaias[3], Jose Henrique Pedrosa-Macedo[2]

[1]Texas A&M University, Department of Entomology, College Station, TX, United States, [2]Universidade Federal do Parana, Curitiba, PR, Brazil, [3]Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brazil

Introduction: This work presents basic biological aspects of the gall-maker – plant interaction in fruit galls induced by the chalcid wasp *Prodecatoma carpophaga* in the weedy tree strawberry guava (*Psidium cattleianum*).

Methods: We characterized the gall as to the associated wasp species and their ecological roles, gall ontogeny, fruit infestation at different localities in Southern Brazil (Parana State First Plateau and littoral), and resistance of a possible alternative host, *Psidium longipetiolatum*. The morphoanatomic alterations were described through anatomical staining and histochemical tests. The comparison of fruit infestation levels were made with quantitative parasitological indicators such as prevalence (number of galled fruits), intensity (number of galls per infested fruit) and aggregation. *P. longipetiolatum* resistance was compared to *P. cattleianum* by testing plant acceptability as oviposition site and suitability for gall development.

Results: The gall results from modified cells from ovary, placenta and funicle internal epiderm in the early stages and from tissue reorganization induced in the fruit by larvae. There is a greater prevalence of infested fruit in the plateau localities, in the comparison to the coastal ones. Infested fruits produce less seeds than non-infested ones. Although both *P. cattleianum* and *P. longipetiolatum* were accepted by the ovipositing females, the latter tends to abort the infested buds and shows a practically null level of infestation.

Conclusions: The gall has a significant impact in the reproductive potential of the host plant and should be further investigated for its use in biocontrol for specificity and the causes of differential infestation levels.

POSTER PRESENTATION

The effects of rapid phase-shifting on adult lifespan and reproduction of the German cockroach

Shu-Chi Tsao, How-Jing Lee

Department of Entomology, National Taiwan University, Taipei, Taiwan

Introduction: Desynchronization between internal clocks and environment time signals can affect the well-being of organisms. Longevity and reproduction of the German cockroach are investigated as the long term effect of circadian timing desynchronization by rapid phase-shifting schedules.

Method: With a 12 hours light-dark reversal in every 3 or 7 days schedules were used to monitor the adult lifespan and fecundity.

Result: The longevity of male cockroaches was significantly reduced by rapid phase-shifting. Furthermore, the shorter interval between phase-shifting enhanced the effect of lifespan reduction. The females did not show lifespan and offspring reduction under the 7 days phase-shifting schedule. However, the 3 days phase-shifting schedule did cause lifespan and offspring reduction, even though the effect was significantly smaller than that of males.

Conclusion: Rapid phase-shifting causes detrimental effects on longevity and reproduction of the German cockroach. But it induced different level of impact between males and females, suggesting the existence of sexual dimorphism in circadian regulation.

POSTER PRESENTATION

Preliminary study: The analyses of blowfly larval crops for the presence of host genomic DNA

Theo Viljoen, Theuns van der Linde, Karen Ehlers

University of the Free State, Bloemfontein, South Africa

Introduction: The DNA technology subsection of forensic entomology is primarily emphasized in cases where there are insects present at a crime scene but no decedent. DNA typing can also be used to test if the larvae on the decedent are related to the crime scene or to rule out an alternative food source. The aim of this study is to determine if DNA from the food source can be extracted from the larval crops.

Methods: Three extraction methods were tested for efficiency namely the QIAamp mini kit tissue extraction protocol (Qiagen®), the phenol-chloroform extraction protocol and the salt-chloroform extraction protocol. *Calliphora vicinia* Robineau-Desvoidy, *Chrysomya albiceps* (Wiedemann), *Lucilia cuprina* (Wiedemann) and *Lucilia sericata* (Meigen) larvae were fed on fresh bovine liver (*Bos taurus*) and the alimentary canal removed. The bovine primers INRA023, SPS115 and ETH225 were used to test whether the DNA extraction was successful.

Results: The salt-chloroform extraction proved to be the most effective extraction method due to the amount of DNA delivered. The bovine DNA from the larval crops showed a decrease in peak size relative to the standard. This could be contributed to the quality of the extracted DNA due to activity of digestive enzymes. The bovine DNA extracted from the larval crop was successfully amplified at locus ETH225 in both the third instar and post-feeding larvae.

Conclusions: The genomic DNA from the larval crops was successfully extracted using the salt-chloroform extraction, but the quality of the DNA was only sufficient enough to produce a partial DNA profile.

POSTER PRESENTATION

Study of embryogenesis's abnormalities for *Morus* sp. plants cultivated for sericulture

Tanase Doina, Nicolae Toma, Motoc Rozalia

[1]Commercial Society Sericarom-Research department, Bucharest, Romania, [2]National Institute of Biology, Bucharest, Romania

Introduction: The present paper work presents modifications within *Morus* sp. plants' embryogenesis (the only nutritional source for *Bombyx mori* L. silkworms) made by traffic air-l pollution with Pb and surpass of the heavy metals content (Pb, Ni, Cr, Co)**.**

Methods: The distinguish of mineral elements translocation from soil and environment to Morus sp plants was made by soil profile method. The biological samples were roots, leaves and fruits from different development stages, of plants belonging to M. alba and M. multicaulis varieties. The samples for photonic microscopy were realised through paraffin technology and analysis with Fluowal microscope and a microphotographic system. The electron microscopy was made by syntetic resins including technology, and the ultra sections grills were analysis with a TEM Philips 2001, details from photonic samples drew on a clear room for jugal embryogenesis.

Results: The heavy metals Pb, Ni, Cr, Co content from traffic pollution site, are over the reference value, for fruits samples (5,0 ppm, 7,2 ppm, 1.5 ppm and 2,7 ppm) and leaves samples (9.1 ppm, 10.6 ppm, 2.1 ppm and 10.1 ppm). The photonic microscopy data, distinguished the anomalies apparition during the zygotic embryogenesis process for the fruits samples within traffical pollution (some processes unsynchronization, atypical endosperogenesis, uncomplet development, polyembryony). Electron microscope researches for leaves samples, distinguish anomalies upon ultrastructure organisation of chromatine, cloroplasts and mitocondries (decrease of cellular components volume and decrease of membranes electronic density)

Conclusions: The traffic pollution may affect in a visible way the embryogenesis for Morus sp. fruits and determine the appariton of some anomalies upon the ultrastructural organisation of different cells and cellular components types for the Morus sp leaves.

POSTER PRESENTATION

Microsatellite DNA markers to study genetic differentiation and dispersion capacities in three Calliptaminae species (Orthoptera, Acrididae)

Elodie Blanchet, Alex Franc, Christine Pages, Laurence Blondin, Antoine Foucart, Jean-Michel Vassal, Michel Lecoq

CIRAD, Montpellier, France

Introduction: Global changes have an impact on the habitat of endangered species as well as pests. Some grasshopper pests, like the *Calliptaminae* species, in the North Mediterranean Basin, can be affected. In certain regions such as Languedoc (France), landscape has undergone modifications for a long time, particularly an important fall of agricultural practices which has closed landscapes. The present study expects to verify if alterations of vegetation cover have an impact on genetic diversity and dispersion capacities of three *Calliptaminae* species, with different habitats and dispersion capacities, observed in this region: *Calliptamus barbarus*, *C. italicus* and *C. wattenwylianus*.

Method: We sampled 1200 specimens from the three species, on two sites (72 km²) that were 40 kilometres apart. For each specimen, we took geographic coordinates (GPS point) so having possibility to cross individual sample site and spatial data of landscape structure on these sites. To develop microsatellite bank, DNA were extracted with CTAB protocol and an enriched method was used.

Results: In total, we isolated 11 polymorphic markers, among which three amplified on the three species, five on *C. barbarus* and three on *C. italicus*. Hitherto we observed more than four alleles for each primer, but genotyping and analysis are in progress.

Conclusion: Associated with spatial characterisation of the environment, these new markers may allow us to develop spatial genetic studies on this genus and to have a better evaluation of their dangerousness. This method already used in conservation could be applied on different locusts.

POSTER PRESENTATION

Multiplex ITS1 PCR for identification of two species of the genus *Phorbia* (Anthomyiidae: Diptera), pests on wheat

Ventsislav Ventsislavov, Hristina Krasteva, Olia Karadjova

Plant Protection Institute, Kostinbrod, Bulgaria

Introduction: *Phorbia fumigata* (Meigen, 1826) and *Phorbia haberlandti* (Schiner, 1865) are economically important pests on wheat in Bulgaria. Because of their similar morphology, the correct identification of both species is of great importance for the pest management. Currently these pests are being identified using morphological differences, which is suitable for the adult, but is very difficult or even impossible for the eggs and larvae.

Methods: The abdomens of collected male specimens were treated with KOH and species were determined following Hennig (1976) using stereomicroscope. DNA extraction was performed with High Pure PCR Template Preparation Kit (Roche, Germany), according to the protocol of the manufacturer. PCR with universal and specific primers was performed (annealing temperature - 50 ^{o}C). *Opomyza florum* (Fabricius, 1794) was used as a control for primer specificity.

Results: Total DNA from the two species was extracted and subjected to amplification of Internal Transcribed Spacer 1 (ITS1), 5.8S rRNA gene and Internal Transcribed Spacer 2 (ITS2) with universal primers ITS1 and ITS4. The amplicons were cloned and sequenced in both directions. Sequences were analyzed and three specific primers (two forward and one reverse) annealing on ITS1 region, differentiating the two species were designed. The performed Multiplex PCR showed clear differentiation of the two species, resulting in specific bands of 350 bp for *Ph. fumigata* and 610 bp for *Ph. haberlandti*.

Conclusions: For the first time new specific primers are developed, which are very reliable for identification of all stages of *Ph. fumigata* and *Ph. haberlandti*.

POSTER PRESENTATION

Possible function of norharmane in egg-laying by ergatoids and nymphoids of the lower termite, *Reticulitermes speratus* (Kolbe)

Shuji Itakura, Satoshi Kawabata, Hiromi Tanaka, Akio Enoki

Kinki University, Nara, Japan

The aromatic ß-carboline norharmane, which is located in the fat body of *Reticulitermes speratus*, stimulated the activity of juvenile hormone epoxide hydrolase (JHEH) of larva, ergatoid, and nymphoid homogenates. JHEH activity of ergatoid (16.67 ± 1.30 µU/termite) and nymphoid (20.94 ± 1.64 µU/termite) homogenates fortified with 0.1 mM norharmane was significantly higher than that of ergatoid (9.84 ± 1.69 µU/termite) and nymphoid (16.99 ± 0.60 µU/termite) homogenates to which no norharmane was added. Egg-laying by ergatoids and nymphoids, which ingested norharmane by feeding on norharmane-treated filter paper, was observed in 3 weeks. During rearing on filter paper without norharmane, egg-laying by ergatoids was observed in 5 weeks, whereas no egg-laying by nymphoids was observed throughout the incubation period of 8 weeks. Norharmane seems to be involved in egg development of ergatoids and nymphoids of *R. speratus*.

POSTER PRESENTATION

Host plants of the genus *Mussidia* (Lepidoptera: Pyralidae) in Kenya

Benjamin Muli[1], Johnnie van den Berg[2], Schulthess Fritz[1]

[1]International Centre of Insect Physiology and Ecology, Nairobi, Kenya, [2]North West University, Potchefstroom, South Africa

Introduction: The ear-borer, *Mussidia nigrivenella*, is one of the most important pests of maize in West Africa. Several species of the genus *Mussidia* have been reported from different regions of the world attacking different host plants. In east Africa, for example Kenya, the *Mussidia* spp. diversity and their hosts have not been explored hence little is known about them. Consequently, as part of the efforts to fill this knowledge gap, and probably explain why *Mussidia* spp. have not acquired pest status in the region.

Materials: Fruits were sampled in an attempt to investigate the diversity of *Mussidia* spp. and associated host plants in Kenya. Mature fruits were collected from trees, shrubs and vines suspected to harbor *Mussidia* spp. and were kept in the laboratory until insects in them emerged. The spatial distribution of *Mussidia spp.* was done on selected host plants during the study.

Results: Eight plant spp. (*Kigelia africana, Adansonia digitata, Afzelia quanzensis, Tamarindus indica, Strychnos spinosa, Strychnos madagascariensis, Canavalia cathartica* and *Canavalia ensiformes*) were found to host *Mussidia* spp. *Mussidia* spp were aggregated on *C. cathartica* and *S. madagascariensis* respectively while it was regular distribution on *K. africana*.

Conclusion: Different *Mussidia* spp. exist in Kenya and attack a variety of host plants. However, maize has not been exploited by the borer as a host as it is in west Africa.

POSTER PRESENTATION

Leptocybe invasa (Hymenoptera: Eulophidae) now in South Africa

Gudrun Dittrich-Schröder[1], Bernard Slippers[1], Stefan Neser[1], Zvi mendel[2], Michael J. Wingfield[1]

[1]Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, Gauteng, South Africa, [2]Department of Entomology, Agricultural Research Organization, 50250 Bet Dagan, Israel

The *Eucalyptus* gall wasp, *Leptocybe invasa* (Hymenoptera: Eulophidae) was initially discovered on species of *Eucalyptus* in the Middle East and Mediterranean region in 2000. This wasp is native to Australia although its discovery there was only noted after infestations in introduced environments. Although *L. invasa* is not problematic in Australia, *Eucalyptus* plantations in other countries have experienced significant damage. Since the initial reports, the wasp has spread extremely fast and today it covers the eucalyptus planting areas of the Mediterranean basin, southern Europe, northern and eastern Africa, and southern Asia from Iraq to India and Vietnam. Most recently it has also been reported from South Africa. Adults of *Leptocybe invasa* are small, ranging from 1.1 –1.4 mm, and are thus not easily seen in the field. Symptoms of *L. invasa* are, however, easily recognizable as galls present on the midrib, petiole and twigs of trees. After oviposition, five stages of gall development can be identified. As the gall matures its colour changes from green to a dark pink with slight variations depending on whether the gall is on the midrib, petiole or shoot and the exposure to the sun. The wasp attacks new growth of all age ranges of the tree, including nursery stock. Heavy galling causes the leaves to warp and in extreme cases may stunt the growth of the tree. A number of *Eucalyptus* species have shown susceptibility to *L. invasa*, including *E. botryoides, E. bridgesiana, E. robusta, E. saligna, E. tereticornis and E. viminalis. Eucalyptus camaldulensis* (and other members of the Exsertaria section), however, seems to be the most susceptible. Preliminary work suggests that control of this wasp will have to rely mainly on biological control of the galler and on an integrated approach of sylvicultural measures and breeding for resistance.

POSTER PRESENTATION

Effect of wavelengths on the *N*-acetyltransferase activity in *Dianemobius nigrofasciatus* (Orthoptera: Grillidae)

Norimitsu Izawa, Takeshi Suzuki, Makio Takeda

Kobe University, Kobe city, Japan

N-acetyltransferase (NAT) is known as the output system of the circadian rhythms and constitutes a large family of enzymes, found in a variety of organisms, which catalyze the transfer of an acetyl moiety from acetyl-CoA to monoamine substrates. Most of NAT family shows a feature whose activity is inhibited by light from. NAT is involved in many physiological functions in insects: inactivation of biological amines, formation of *N*-acetyldopamine and *N*-acetyloctopamine, an agent important for sclerotization of the cuticle, formation of puparium, tanning of oviposited eggs and synthesis of melatonin.

Deguchi (1981) showed effect of various intensities of monochromatic light on the night-time increase of NAT activity in organ cultures of chicken pineal organ. It was reported that NAT has a high sensitivity to light of around 500 nm wavelength. Later, Okano et al., (1994) clarified that there were two kinds of photoreceptors, pinopsin and iodopsin. Pinopsin was sensitive to blue light and iodopsin was sensitive to red light. Pinopsin had higher expression level than iodopsin. Hence, it was clarified that the highest NAT sensitivity shifted to middle wave length light.

It was clarified that NAT activity depended on light in *D.nigrofasciatus* head. NAT activity in nighttime was higher than daytime as in mammals and birds. Effect of wavelengths on NAT activity was measured in *D. nigrofasciatus*. The following monochromatic light was employed; 350, 400, 450, 500, 550, 600 and 650 nm. *D.nigrofasciatus* had the highest sensitivity to light of around 450 nm and 550 nm wavelengths. 450 nm Wavelength light had higher sensitivity level than 550 nm wavelength light. Hence, it was clarified that the most important light affecting NAT activity was blue light. Blue wave sensitive photoreceptors, blue wave (BW) opsin and cryptochrome which were therefore the candidates of photoreceptor that had the highest effects on NAT activity. Next plan is immunohistochemistry of BW opsin and cryptochrome to compare the expression position of NAT.

This study aims at developing human and eco-friendly pest control systems by targeting insect NAT.

POSTER PRESENTATION

The effects of different temperature conditions on the colony characteristics of *Bombus terrestris* L.

Fehmi I Gurel, Ayhan Gosterit

Akdeniz University Department of Animal Science, Antalya, Turkey

Introduction: In this work our aims were to compare the effects of three temperature regimes (24°C, 27°C and 30°C) on the colony development characteristics of *B. terrestris* and to find out optimal temperature condition for mass rearing of bumblebee.

Methods: A total of 300 queens which had been over wintered in artificial conditions were used. Queens were subjected to one of three temperature treatments at 24±0.5 °C, 27±0.5 °C or 30±0.5°C under constant humidity of 60 ± 5 %. All queens and colonies were furnished with unlimited amounts of sugar solution and fresh pollen collected from honeybee colonies.

Results: There were significant differences among treatments in terms of egg laying, colony production, saleable colony production and progeny queen production ratios, the colony initiation time, the number of egg cells in first brood, and the first worker emergence time. The highest egg laying, colony production and saleable colony production ratios were found at the 30°C treatment (86, 48, 34 %) followed by 27°C (42, 19, 13 %) and 24°C (43, 14, 12 %) treatments respectively. Similarly, at the 30°C queens developed more egg cells (4.72±0.22) in the first brood and started egg laying (12.47 ± 0.78 days) earlier than in the other treatments.

Conclusions: The results show that 30°C is the best temperature condition for colony development of *B. terrestris.*

POSTER PRESENTATION

Biology of *Trichogrammatoidea lutea* (Hymenoptera: Trichogrammatidae), a potential biological control agent for *Helicoverpa armigera* (Lepidoptera: Noctuidae)

Khethani V. Mawela[1], Kerstin Krüger[2], Rami Kfir[3]

[1]University of Pretoria, ARC-Plant Protection Research Institute, Pretoria, South Africa, [2]University of Pretoria, Pretoria, South Africa, [3]ARC-Plant Protection Research Institute, Pretoria, South Africa

Introduction: The African cotton bollworm *Helicoverpa armigera* is a major pest in many parts of the Old World. The egg parasitoid, *Trichogrammatoidea lutea,* is indigenous to South Africa and an important natural enemy of *H. armigera*. We assessed the life-history parameters of *T. lutea* on *H. armigera* to determine its potential as a biological control agent.

Methods: Forty pairs of *T. lutea* were each supplied daily with 20 UV-radiated *H. armigera* eggs. These were collected daily and incubated at 25°C. Age-specific fecundity and longevity of parents, and sex ratio of offspring were recorded. In addition, percent parasitism, development time and sex ratio on *H. armigera* eggs at five different constant temperatures (18–30°C) were determined.

Results: Mean longevity of male and female *T. lutea* was 5.6 and 8.6 days, respectively. *Trichogrammatoidea lutea* did not show a pre-oviposition period. The reproduction period lasted for up to 14 days. Females produced on average 52 offspring. Daily fecundity and parasitism per female were highest on the day of eclosion; both parameters decreased with age of females. The sex ratio changed with age of females from female- to male-biased after 3 days. The overall sex ratio of *T. lutea* progeny was 1:1. Parasitism and rate of development of *T. lutea* were highest at 27°C. The sex ratio was similar at all temperatures.

Conclusion: The study provides important information on the biology of *T. lutea* on *H. armigera* eggs as well as for mass rearing of this potentially promising biological control agent.

POSTER PRESENTATION

Stingless bees (Meliponini) and their nests in the Balsas savannah ("cerrado"), Ma, Brazil

Marcia Rego[1], Patricia Albuquerque[1], Giorgio Venturieri[2]

[1]Federal University of Maranhaonhão, Sao Luis,MA, Brazil, [2]EMBRAPA Amazonia Oriental, Belem, PA, Brazil

Introducion: The majority of stingless bees nest in hollows of trees, alive or dead.

Methods: The Meliponini nests were looked for from July/2006 to November/2007 in a cerrado area (07° 42' 58.5" S and 46° 11' 19.8" W), numbered and mapped with the aid of a GPS receiver. Nest characteristics like its height above the ground, stem diameters at breast height (DBH) of the trees and or branches diameters were annotated, as soon as the popular name of floral species, where the nests were found.

Results: A total of 110 stingless bee nests of 21 species were located. Among those, *Scaptotrigona* was the most abundant genus (36.4% of nests), followed by *Oxytrigona* (15.5%) and *Frieseomellita* (12.7%). The bees known as "tubi" (two belonging to *Scaptotrigona* genus), "tataíra" (2 *Oxytrigona*), "mané-de-abreu" (*Frieseomellita flavicornis*), "borá" (*Tetragona quadrangula*) and "jataí" (*Tetragonisca angustula*) were the most common species. The nests were found mainly in main trunks and branches of "sucupira-amarela" (*Pterodon aff. polygalaeflorus* - Fabaceae), "piqui" (*Caryocar brasiliense* - Caryocaraceae) and "puçá" (*Mouriri grandiflora* - Melastomataceae). Trees with larger diameter of the main trunk and bigger hollows were preferentially selected by bigger bees, like "uruçu" species (*Melipona flavolineata*) and "tiúba" (*Melipona fasciculata*), both not so abundant in the Maranhao cerrado anymore.

Conclusion: The stingless bees from Maranhão cerrado nest in some tree species with hollows in their trunks, but the environment destroyed by human action has been slowing down the nesting places and threatening these important insects.

POSTER PRESENTATION

Are females attracted by wound volatiles to cane splits? Early stages in the development of a plant derived attractant for raspberry cane midge

Carolyn Mitchell[1], Tom Shepherd[1], Nick Birch[1], Stuart Gordon[1], Jerry Cross[2], David Hall[3]

[1]SCRI, Dundee, United Kingdom, [2]East Malling Research, East Malling, Kent, United Kingdom, [3]Natural Resources Institute, Chatham Maritime, Kent, United Kingdom

Introduction: The raspberry cane midge, *Resseliella theobaldi,* is an important pest of red raspberry (*Rubus idaeus*) in the UK and much of north and central Europe. The adult midge lays eggs in the splits of young canes, either caused by natural splitting or by mechanical injury. The larvae feed on the pith causing lesions which allow entry of a range of diseases such as cane blight fungus and midge blight. There has already been a great deal of research into the development of female sex pheromone traps for local monitoring of male midges. However, advancement of this monitoring and mass trapping technology to aid the control of midge numbers requires an attractant to lure the females as they emerge from the soil in early spring (first generation) and during the second generation (coinciding with fruit harvest and the main time of fungal colonisation). The early stages in the identification of a plant volatiles released from cane wounds are discussed.

Materials and methods: Two separate methods are currently being used to identify possible attractants. (1) Behavioural assays observing the females preferences over split and unsplit canes. (2) Entrainment of volatiles from the cane splits and identification of these volatiles.

Results: Preliminary observations indicate that the presence of a split affects the behaviour of the female midge prior to oviposition. Entrainment shows variation in the wound volatiles released from the split and unsplit canes.

Discussion: The preliminary results are encouraging and provide ideas on how this will shape future work.

POSTER PRESENTATION

Selective antennal receptors for pheromone, non-host, and host compounds govern behavioural responses in a bark beetle

Martin N. Andersson, Mattias C. Larsson, Fredrik Schlyter

Department of Plant Protection Biology, Swedish University of Agricultural Sciences, Alnarp, Sweden

Host selection by conifer-inhabiting bark beetles is mediated by pheromones from conspecifics and kairomones from host trees. The response to attractive odours is modulated by non-host volatiles (NHV), originating from angiosperm trees. The spruce bark beetle, *Ips typographus*, uses aggregation pheromone and NHV in host location, but the role of kairomones in host attraction is unclear. Several repellent NHV are known, some with redundant, others with synergistic effects.

By means of single-sensillum recordings, we investigate the proportions of olfactory receptor neurons (ORNs) that respond to pheromones, host, and non-host volatiles, respectively, and we study if the behavioural pattern of redundancy and synergism among NHV could be explained by ORN response specificity.

We have recorded from 150 sensilla and obtained powerful responses to synthetic chemicals from more than 100 ORNs. Most receptor neurons respond specifically to one or a few compounds and dose-response trials show that specificity is highest at low doses. Four ORN classes responding to NHV have been characterised and these neurons occupy a surprisingly large proportion of sensilla. The response specificities of these neurons explain much of the behavioural redundancy and synergism observed among NHV. One neuron does not distinguish between three redundant GLV alcohols while synergizing compounds (verbenone and *trans*-conophthorin) are perceived by different ORNs. Six ORN classes that respond to host compounds have been characterised, suggesting that kairomone might be relevant in host tree location. Our results provide a basis for how different attractive and inhibitory signals are encoded by the insects' peripheral olfactory system.

POSTER PRESENTATION

Pathogenicity of *Metarhizium anisopliae* and *Beauveria bassiana* to the pea leafminer *Liriomyza huidobrensis*

Lorna N. Migiro[1], Nguya K. Maniania[1], Johnnie Van den Berg[2], Adenirin Chabi-Olaye[1]

[1]International Centre of Insect Physiology and Ecology (ICIPE), Nairobi, Kenya, [2]North West University, Potchefstroom, South Africa

Introduction: The pea leafminer, *Liriomyza huidobrensis*, is a polyphagus pest of vegetable and ornamental crops. Chemical control has shown to be ineffective. Entomopathogenic fungi are being considered as an alternative for its control.

Methods: Twenty 1-2 day-old adult *L. huidobrensis* were contaminated through a velvet cloth placed inside of a cylindrical plastic tube. They were allowed to walk for one minute, after which they were transferred to Perspex cages and fed on 10% sugar solution. The number of conidia picked by a single fly was determined by selecting 5 flies at random and vortexed to dislodge the conidia. Control insects were exposed to fungus-free velvet cloth. Mortality was recorded daily for 11 days.

Results: The number of conidia picked by single fly varied between 2.3-2.8 x 10^5 conidia ml^{-1}. All the fungal isolates tested were pathogenic to adult *L. huidobrensis*. However, there were significant differences in mortality between the fungal isolates, with the least pathogenic isolate causing mortality of 39.9% and 100% with the most virulent isolate. The lethal time to 50% mortality (LT_{50}) values varied between 5.5 days for the less virulent isolates, and 2.6 days for the most virulent isolates.

Conclusions: *Beauveria bassiana* and *M. anisopliae* are pathogenic to *L. huidobrensis*. However, the challenge is how to apply the fungus in the field. Studies are underway to design and test different contamination devices that could be used in the field.

POSTER PRESENTATION

Biological control of *Plutella xylostella*: role of generalist predators and enemy-enemy interactions

Freddy Miranda[2], Christer Bjorkman[1], Helena Bylund[1], Riccardo Bommarco[1]

[1]*Department of Ecology, Swedish University of Agricultural Sciences, Uppsala, Sweden,* [2]*Universidad Nacional Agraria, Managua, Nicaragua*

Introduction: The diamondback moth (*Plutella xylostella*) is a major pest in large parts of the world. It has developed resistance against almost all known insecticides, including Bt. Efforts to develop biological control have mainly focused on parasitoids. Less emphasis has been on the role of generalist predators.

Methods: The density of natural enemies (predators and parasitoids) and level of parasitism was estimated on farms using or not using insecticides in Nicaragua. The level of damage by *P. xylostella* on cabbage plants was estimated on the same farms. An exclosure experiment was performed, on semi-organic farms, to estimate the relative importance of different nataurel enemy types (flying vs. ground-dwelling).

Results: The density of generalist predators and parasitoids was higher on farms not using insecticides than on farms using insecticides. This difference translated into a lower damage of cabbage on farms not using insecticides. The exclosure experiment showed that flying and ground-dwelling natural enemies predated upon *P. xylostella* larvae to a similar extent, when either of them was excluded. However, when both types were allowed to act as enemies, there was a significant negative interaction between them.

Conclusions: Generalist predators, especially wolf spiders (Lyocsidae), but also rove beetles (Col.; Staphylinidae), jumping spiders (Salticidae) and damsel bugs (Heteropt.: Nabidae), are important natural enemies of *P. xylostella* and should be considered when developing biological control programs. The possible negative interaction between different types of natural enemies needs to be explored further to reduce the risk of counterproductive efforts when developing biological control methods.

POSTER PRESENTATION

Vibrational communication in the predaceous spined soldier bug *Podisus maculiventris* (Say) (Pentatomidae: Asopinae)

Alenka Zunic[1], Andrej Cokl[1], Meta Virant Doberlet[1], Jocelyn G. Millar[2]

[1]Department of Entomology, National Institute of Biology, Ljubljana, Slovenia, [2]Department of Entomology, University of California, Riverside, United States

Introduction: The predatory bug *Podisus maculiventris* has received extensive attention as a potential biological control agent. Numerous studies have examined predator-prey interactions but little is known about vibrational communication in this species. Mating behaviour of *P. maculiventris* was observed, and vibrational signals used in intraspecific communication were recorded and analyzed.

Methods: Vibrational signals were recorded from adults placed on a non-resonant loudspeaker membrane, and by laser vibrometry of bugs placed on a plant cutting. Behaviour was observed on a freshly cut plumbago shoot. In playback experiments, bugs were stimulated by pre-recorded males' signals, or by pre-recorded vibrations produced by a female walking on a plant.

Results: Males produced vibrational signals by different mechanisms: vibration of the abdomen (MS-V), percussion with the front legs (MS-P), or tremulation of the body (MS-T). Observations of mating behaviour and playback experiments showed that MS-V signals had long range calling and short range recognition functions. MS-T signals were emitted at close range and were essential for copulation to occur. In the courtship phase of mating behaviour, males emitted combined pulse trains composed of a MS-V pulse following a MS-T pulse. MS-P signals were not emitted in a particular behavioural context; they were emitted during both calling and courtship phases. In male-male interactions, signals were produced by only one male, and no regular alternation of signalling was recorded.

Conclusions: Compared to phytophagous Pentatomidae, *P. maculiventris* produce vibratory signals by three different modes. The signals are emitted only by males, and females search for the calling male.

POSTER PRESENTATION

Molecular phylogeny of Apoidea (Hymenoptera) with special emphasis on sphecid wasps

Volker Lohrmann[1], Michael Ohl[1], Lars Podsiadlowski[2], Christoph Bleidorn[3]

[1]Museum für Naturkunde der Humboldt-Universität zu Berlin, Berlin, Germany, [2]Freie Universität Berlin, Institut für Biologie, Chemie, Pharmazie – AG Evolution und Systematik der Tiere, Berlin, Germany, [3]Universität Potsdam, Institut für Biochemie & Biologie – AG Evolutionsbiologie / Spezielle Zoologie, Golm, Germany

Introduction: Within the aculeate Hymenoptera the monophyly of the Apoidea [bees and digger wasps (=Sphecidae sensu lato)] is well supported but its basal phylogeny is still controversial discussed.

Methods: Sequences from the nuclear long-wavelength-rhodopsin and the mitochondrial cytochrom-c-oxidase (subunit I) from different representatives of the aculeate Hymenoptera, with special emphasis on digger wasps, were analysed using maximum parsimony, maximum likelihood and Baysian inference methods.

Results & Discussion: Compared with previous phylogenetic studies based on morphology, the results of the molecular analyses are controversial but correspond in the absence of support for the Sphecidae s. l (sensu BOHART & MENKE). The relationships within the Sphecidae sensu stricto correspond largely with recent morphological studies. There is circumstantial evidence that the Ampulicidae and Sphecidae s. str. together form a monophyletic group, whereas the relationships within this taxon are still uncertain. Although there is no evidence for a definitive phylogenetic position of the Heterogynaidae; it can be excluded that they are the sistertaxon to all other Apoidea. Instead, they are probably a derived group within the Crabronidae. In conflict to the majority of current morphological studies, the molecular analyses provide no support for the Crabronidae and Bembicinae. Some molecular analyses imply a close relationship between Philanthinae and the monophyletic bees.

Since the phylogeny of the Crabronidae as the phylogenetic position of the Heterogynaidae (and other questions) remain uncertain, further studies should be made including more taxa and using more genes.

POSTER PRESENTATION

Insecticidal and plant growth regulator effects of some botanical materials

Ersin Polat[1], Fedai Erler[2], Halil Demir[1], Huseyin Cetin[3], Tugba Erdemir[2]

[1]Akdeniz University, Department of Horticulture, Antalya, Turkey, [2]Akdeniz University, Department of Plant Protection, Antalya, Turkey, [3]Akdeniz University, Department of Horticulture, Antalya, Turkey, [4]Akdeniz University, Department of Biology, Antalya, Turkey, [5]Akdeniz University, Department of Plant Protection, Antalya, Turkey

Introduction: The major pests of mushroom are cecidomyiid, sciarid and phorid flies; *Megaselia halterata* (Wood) (Diptera: Phoridae) being the most common species in Turkey. In the present study, five hot water plant extracts, namely; *Origanum onites* L., *Inula viscosa* (L.), *Melisa officinalis* L., *Ononis natrix* L., *Teucrium divericatum* Sieber, and two commercial neem-based products, Neemazal-T/S® and Greeneem® oil, were tested for insecticidal activity against *M. halterata* and for plant growth regulator (PGR) effect on the white button mushroom (*Agaricus bisporus* L.).

Methods: Experiments were conducted in a mushroom house in the campus of Akdeniz University (Antalya, Turkey) in three successive growing periods. The concentrations were 50 g/l water for all hot water plant extracts, and 5 ml/l water for both neem-based products. Only one application was made by soil drench at the spawn-runned stage in each growing period. The insecticidal activity of test materials was evaluated by measuring larval damage and counting the emerging adults of the pest in each treatment. Their PGR effects were evaluated by measuring cap and stalk size (cm), yield per bag (kg) and stalk length (cm).

Results: All test materials caused significantly reduction in mean number of emerging adults and larval damage compared to water-treated controls. All botanical material treatments significantly increased yield and were better in visual quality parameters.

Conclusion: Overall results suggest that all botanical materials can be used for the control of mushroom phorid fly and may also be used to enhance the yield and other quality parameter of white button mushroom.

POSTER PRESENTATION

Character displacement of calling songs in *Euterpnosia varicolor* and *Euterpnosia alpine* (Hemiptera: Cicadidae) from Taiwan

Chen-Hsiang Chen, Shiuh-Feng Shiao

Department of Entomology, National Taiwan University, Taipei, Taiwan

Introduction: Calling songs of most *Euterpnosia* species don't share a common general pattern, and it is considered as a good character for species identification. *Euterpnosia varicolor* and *Euterpnosia alpina* are two closely-related species; evidences show the character displacement of calling songs between these two species may play an important role in reinforcement of reproductive isolation in sympatric area (Guanwu, Hsinchu County, Taiwan).

Methods: Calling songs were recorded in the field using a digital recorder with a shotgun microphone. The microphone was placed as close to the insects as possible, generally not far away from 5 M, The calling song were analyzed using BatSound Pro and Avisoft-SASLab Pro. Molecular analysis using mitochondrial cytochrome oxidase subunit I (COI) sequences was performed to further compare the population differences.

Results: The dominant call pitch (frequency) is approximately at 5.1-5.8 kHz in *E. varicolor*, and at about 10.3 kHz in allopatric *E. alpine.* The dominant call pitch of *E. varicolor* increases from 5.1-5.8 kHz to 11.9 kHz; meanwhile, the frequency increases from 10.3 kHz to 12.3 kHz in sympatric populations of *E. alpina* (overlapping zone). The group of pulses in *E. varicolor* increases from 1-1.5 per sec to 2.5 per sec, and decreases from 29 per sec to 22 per sec in sympatric *E. alpina* population.

Conclusion: The increase of call pitch and the changes of pulse group for *E. varicolor* and *E. alpina* in sympatric area meet the criteria for reproductive character displacement. And the molecular data also reveal that two sympatric *Euternosia* species have not yet evolved to new species from their conspecific but allopatric populations based on their genetic distances.

POSTER PRESENTATION

Integrated control of *Lobesia botrana* by using IGRs, *Bacillus thuringiensis* products and neonicotinoid; relationship between the insect infestation and development of *Botrytis cinerea*

Thomas Thomidis, Emmanouel Navrozidis, Zisis Michailides

A.T.E.I. Thessaloniki, Sindos Thessaloniki, Greece

Introduction: *Lobesia botrana* (Denis & Schiffermueller) (Lepidoptera: Tortricidae) is the major grape berry moth in vineyards of southern Europe. IThe caterpillars gnaw the almost ripe fruits and various moulds, in particular *Botrytis*, develop very rapidly on the wounds. The main aim of this study was to investigate the effectiveness of two insect growth regulators Lufox 105EC (lufenuron + fenoxycarb) and Cascade 10WDC (flufenoxuron), two commercial products of *Bacillus thuringiensis* (XenTari DF, Dipel 150 Dust) and thiamethoxam (Actara 25WC) in managing *L. botrana*.

Methods: The growth regulators were applied in the beginning of the second flight, *B. thuringiensis* products were applied one week after the beginning of the second flight, while deltamethrin was applied in the peek of the second flight.

Results: The results showed that the insect growth regulators were the most effective. There was no significant difference between flufenoxuron and lufenuron+fenoxucarb. Less effective were *B. thuringiensis* and the insecticide thiamethoxam.

In addition, the relationship between the percentage of attacked fruits from *L. botrana* and rotted berries from *B. cinerea* was examined in the experimental field where the above insectices were applied. In all treatments, a relationship between the percentage of attacked berries from *L. botrana* and the rotted berries from *B. cinerea* was found. Also, it was noticed that larvae were grown, pupated and adult-emerged independent from the percentage of fungal infection.

Discussion: This study showed the possible use of the insect growth regulators against *L. botrana* and the relationship between the insect infestation and development of *B. cinerea.*

POSTER PRESENTATION

Scots pine felling debris as a substrate for development of saproxylic beetles

Jiri Foit

Faculty of Forestry and Wood Technology, Mendel University of Agriculture and Forestry in Brno, Brno, Czech Republic

It is widely known, that felling debris is potential substrate for many species of saproxylic beetles. The aim of this study was to find out, which species of saproxylic beetles use different types of Scots pine (*Pinus sylvestris* L.) felling debris for their development, how do the season of felling and the different ways of treatment of felling debris (concentrating to the mounds and cross-cutting) affect species composition, abundance, and success of development. The research was carried out in planned mature cutting, thinning in stands older than 40 years, and in juvenile thinning. In chosen stands many elaborately designed felling measures took place to produce required felling debris. From 2006 to 2008 colonization of this felling debris by saproxylic beetles and their development were thoroughly studied. The season of felling and the way of treatment of the felling debris has significant impact on species composition, abundance and success of development of saproxylic beetles. Felling debris produced during winter and spring supports development of high abundances of important insect pests, above all *Pityogenes chalcographus* (L.), and *Ips acuminatus* (Gyll.). On the contrary felling debris produced in later summer (August and/or September) does not allow above mentioned insect pests to develop there. The felling debris situated in the inner parts of the felling debris mounds is significantly less attractive for the most species of saproxylic beetles than felling debris left dispersed or situated on the surface of the mounds.

This study was supported by the project VaV MZP CR TARMAG SP/2D4/59/07

POSTER PRESENTATION

Extinction of the genus *Neurohelea* (Diptera: Ceratopogonidae) in Europe?

Andrea Tóthová

Masaryk University, Brno, Czech Republic

Introduction: The species *Neurohelea luteitarsis* (Waltl, 1837) is the only representative of the genus *Neurohelea* Kieffer in Europe. So far it has been reported from 4 EU countries - Great Britain, Belgium, Ireland and Germany; however in Germany was lately proclaimed extinct.

Material and Methods: About 40 specimens of *Neurohelea* were collected during years 2005-06 in PLA Jizerské hory (Czech Republic) using Malaise traps. The chosen specimens were mounted into microscope slides, measured and examined.

Results: While processing the collected specimens of *N. luteitarsis*, we observed some morphological features that have not been described before. We observed 3 fully developped spermathecae in all female specimens. There is an indication that the number of spermathecae not an abberation and this fact might support the potential phylogenetic relation of *Neurohelea* to *Physohelea.* We have also found in females abdominal saccules of unknown function; puffy, pale but clearly visible formations turn to residuals after the slides are mounted. These structures are known only within Palpomyiini+Stenoxenini tribes and their presence in Heteromyiini might show new relations between these tribes. The other unique morphological feature we observed is the interruption of the vein r-m observed in both sexes of all specimens of our collection.

Conclusions: We consider the report of *N. luteitarsis* and its new features an important reference of a species that has been proclaimed extinct in the neighbouring Germany. The study has been supported by the Ministry of Education grant MSM No. 0021622416.

POSTER PRESENTATION

Mushrooms appearing from insects in Japan

Hiroki Sato[1], Sayaka Ban[2], Hayato Masuya[3], Tsuyoshi Hosoya[4]

[1]Forestry and Forest Products Research Institute, Kumamoto, Japan, [2]NITE-NBRC, Kazusa, Japan, [3]Forestry and Forest Products Research Institute, Tsukuba, Japan, [4]National Museum of Nature and Science, Tsukuba, Japan

Insects are killed by several kinds of microorganisms. Some fungal groups make infection to insects, kill them, and produce curious mushroom on the cadavers. Dr. Kobayasi was one of the most active mycologists who studied entomopathogenic fungi in Japan and described more than 150 species mainly in *Cordyceps* and *Torrubiella,* showing approximately 30% of species in those genera were by his description. Japan is rich in entomopathogenic fungal flora that may have wide source for controlling insect pests. Insect cadavers showing mushrooms collected in the field must be identified, and should be compared with type specimen in detail for identification. However, the information of preservation is obscure about specimens of Dr. Kobayasi. During the total re-arrangement of the fungal specimens in National museum of nature and science in the last two years, many specimens of entomopathogenic fungi, both registered and non-registered, including *Cordyceps, Torrubiella* were found out mainly immersed in liquid formalin. We evaluated those specimens for their type status referring to their original descriptions and their current condition under preservation. More than one hundred specimens were found out for the candidates of holotype specimens, and to date, we judged nineteen specimens of *Torrubiella* as holotype: *Torrubiella alboglobosa, T. aurantia, T. corniformis, T. ellipsoidea, T. formosana, T. fusiformis, T. globosostipitata, T. longissima, T. mammillata, T. minutissima, T. miyagiana, T.neofusiformis, T. oblonga, T. ooaniensis, T. pallida, T. rosea, T. ryogamimontana, T. ryukyuensis, T. superficialis.* Most of all the specimens found out very good condition.

POSTER PRESENTATION

Agronomic techniques to control *Lobesia botrana*

Zisis Michailides, Aikaterini Vartholomeou, Emmanouel Navrozidis, Christopher Payne, Georgios Salpiggidis

A.T.E.I. Thessaloniki, Sindos, Thessaloniki, Greece

Introduction: The grapevine moth *Lobesia botrana* (Denis & Schiffermuller) (Lepidoptera: Tortricidae) is a key pest of grapevines in Greece. As part of a broader study on integrated pest management, we investigated the effects of different cultural methods on the establishment and survival of *L. Botrana*.

Methods: Application of different nitrogen levels (30 and 100 N units applied as Ammonium Sulphate or 70 N units applied as Agrobiosol); summer leaf and shoot pruning; application of growth regulators (Regalis, prohexadione-calcium or Falgro, gibberellic acid).

Results: The results showed that there were significant differences among the three levels of N application. The lowest *L. botrana* infestation rates were found in plots treated with 30 units of N applied as Ammonium Sulphate and plots that received some summer pruning. Following the application of plant growth regulators, the lowest *L. botrana* infestation levels were found in the plots treated with Regalis or Falgro at manufacturers recommended concentrations. On vines where growth regulators had been applied, the clusters had fewer berries than those not treated with growth regulators.

Discussion: This study suggests the use of the growth regulators Regalis and Falgro reduced the *L. botrana* infestation. Reduction of the *L. botrana* infestation is also possible by application 30 units' ammonium sulfate. Summer pruning is recommended in reducing *L. botrana*'s infestation.

POSTER PRESENTATION

Chemical characterization of the pheromone trail in *Reticulitermes lucifugus.*

Valeria Tubiolo[1], Claudio de Pasquale[2], Giuseppe Alonzo[2], Ezio Peri[1], Alfonso Agrò[1], Stefano Colazza[1]

[1]Department S.EN.FI.MI.ZO, Università di Palermo, Palermo, Sicilia, Italy, [2]Department ITAF, Università di Palermo, Palermo, Sicilia, Italy

Reticulitermes lucifugus (Rossi) is a subterranean termite present in Italy where is a serious pest of wooden human structures, historic buildings and cultural heritage. *Reticulitermes spp* , in the search for food, react to chemical trail pheromones laid from abdominal sternal glands. Here we report the results of behavioural tests and the chemical investigations of trail pheromone in workers of *R. lucifugus.* Experiments were conducted in an open arena. A video tracking and motion analysis system was used to evaluate the behaviour of *R. lucifugus* in the presence of naturally laid trails, or in the presence of trails prepared with hexane extracts of the sternal glands (4°-6° abdominal segment), and, as a control, hexane extracts of the 6°-8° abdominal segment. Termites followed either naturally laid trails and trails made by solvent extracts of the sternal glands. While, they did not reacted to trails made by control solvent extracts. Hexane extracts of the sternal glands were then analyzed by GC-MS. The mass spectra of sternal gland hexane extracts were recorded from 42 to 550 m/z. Commercial NIST 98 mass spectra library search on the diagnostic of relative intense ions, and the determination of Kovats indices according to the linear long chain hydrocarbon standard compounds, allowed to identify alcoholic, aldehydic and linear and branched hydrocarbon in the solvent extracts.

POSTER PRESENTATION

Soybean rust protection using the Integrated Pest Management Pest Information Platform for Extension and Education (ipmPIPE)

Kitty Cardwell, Martin Draper, Dennis Kopp, Elizabeth Li

USDA, Washington, DC, United States

Introduction: In late 2004, aerobiological models predicted that Asian soybean rust (SBR) might be introduced to the continental U.S. from South America. Soon after Hurricane Ivan's landfall, SBR was reported in nine states. No damage resulted from SBR in 2004, but uncertainty about 2005 weighed on producers. The pathogen was expected to survive along the US southern coast on kudzu, potentially compromising 75 million acres of soybeans in 2005. To avoid unnecessary spraying of fungicides in 2005, an education and extension system was launched to provide timely, web-based information about SBR risk to soybean producers. The system is now known as *ipm*PIPE.

Methods: Field observers in every soybean producing state monitor sentinel plots and submit weekly data on disease presence/absence and management recommendations in their respective states. The information system, a partnership of private and public sector agricultural scientists and grower organizations, maps field observations and visualizes the movement of soybean rust throughout the year, apprising soybean producers of risk and management options.

Results: In `05 and `06, *ipm*PIPE saved soybean producers an estimated $299 million/year in fungicides not applied. By 2007, 74% of fungicide application decisions to manage SBR were based on *ipm*PIPE advisories, valued at $100 million dollars in decision support.

Conclusions: The *ipm*PIPE is a coordinated effort of agricultural industry, scientists, extension specialists, and educators. In addition to SBR, the *ipm*PIPE facilitates pest risk management by monitoring movement and delivering timely expert advice to growers for other invasive and migratory pests across Mexico, the U.S. and Canada.

POSTER PRESENTATION

Differentiation of follicular cells in panoistic ovarioles of *Gryllus bimaculatus* (Insecta: Orthoptera)

Janusz Kubrakiewicz

Zoological Institute, University of Wroclaw, Wroclaw, Poland

In *Gryllus* ovarioles three distinct zones can be recognized along their anterior-posterior axis: terminal filament, germarium and vitellarium. Germarium houses oogonia and early meiotic oocytes, while vitellarium is formed by a linear array of ovarian follicles (oocytes covered by somatic follicular epithelium) in progressively advanced stages of oogenesis. Germ cells in the germarium are accompanied by few somatic prefollicular cells (pFCs). Some of the pFCs are located peripherally and adhere to the ovariole basal lamina, while others can be found inside the ovariole, among the germ cells. In the previtellogenic follicles somatic cells stretch over the surface of the growing oocytes to form follicular epithelium. Single follicular cells (FCs) can be found inside the ovariole, at the border of neighboring ovarian follicles. FCs proliferate intensively until the advanced stages of previtellogenesis. Those on the surface of the oocyte (main body FCs) become cuboidal with bilobate nuclei. The “excess” of FCs crowd in between the ovarian follicles thus forming interfollicular stalks. During vitellogenesis main body FCs change their shape, become rounded and not tightly apposed to each other so that the follicular epithelium becomes patent. In the late stages of vitellogenesis a few, single FCs located on the ventral side of the ovarian follicle form short processes towards the oocyte surface. These processes mould canals of the micropyles. FCs in panoistic ovarioles of *Gryllus* do not exhibit any migratory activity. Changes in their positions and shape result exclusively from their proliferative activity and reorganization of the cytoskeleton.

POSTER PRESENTATION

Cuticular hydrocarbon profiles of inquiline–host pairs of ants: a search for patterns

Kari Vepsäläinen[1], Riitta Savolainen[1], Toshiharu Akino[2], Pekka Punttila[3]

[1]University of Helsinki, Helsinki, Finland, [2]National Institute of Agrobiological Sciences, Tsukuba, Japan, [3]Finnish Environment Insitute, Helsinki, Finland

Introduction: Social-parasitic ant species must trespass the semiochemical defence of their host. This may be achieved if the host and parasite ants are related chemically, or if callow parasites are odourless and acquire the host-colony odour when invading the nest. Here we test the alternative hypotheses.

Methods: We assessed cuticular hydrocarbon (CHC) profiles of *Myrmica* species: three inquiline–host pairs, *karavajevi–scabrinodis*, *hirsuta–sabuleti* and *microrubra–rubra* (inquiline recently synonymized with its host), and six additional *Myrmica* species. We collected ten virgin queens from one nest per species (of two *hirsuta* nests). Additionally, we included established, old *hirsuta* queens found in the nest, and lab-mated queens; virgin queens from two nests were cross-mated with males from the opposite nest. We analysed the samples using non-metric multidimensional scaling (NMDS).

Results: NMDS ordinated the samples to species-specific clusters, such that each inquiline and its host grouped as neighbours. The *hirsuta* samples mostly clustered by queen status and age, with lab-mated nests at opposite ends of the NMDS space.

Conclusions: The semiochemical similarity of inquiline and host concur with phylogenetic studies suggesting sympatric speciation of some inquilines within their host colonies. Distinctiveness between *rubra* and its inquiline agrees with population-genetic studies implying that *microrubra* is a good species at least *in statu nascendi*. To understand better the role of semiochemicals in inquiline–host relationships, analyses of details of CHC profiles are needed to find possible key compounds—and their origins— that enable the inquiline to integrate with the host colony.

POSTER PRESENTATION

Artificial diet with tomato juice for larvae of *Bactrocera oleae* (Diptera: Tephritidae)

Emmanouel Navrozidis, Minos Tzanakakis

A.T.E.I. Thessaloniki, Sindos, Thessaloniki, Greece

Introduction: In nature, oviposition and larval growth of the olive fruit fly *Bactrocera oleae* (Rossi) (Diptera: Tephritidae) occur only in the mesocarp of fruits of the genus Olea, including the cultivated olive.

Methods: Larvae of *B. oleae* were reared on Rey's (1970) reference artificial diet in which the water was replaced by canned tomato juice, and the nutritive components were gradually reduced or omitted altogether one by one maintaining the pH at 4. The criteria for comparison and selection of diets were the duration of the larval stage, pupal weight, yield in adults and adult fecundity and fertility.

Results: The diet finally selected was consisted of: tomato juice (Sekove) 51.5 ml, cellulose powder 21.5 g, brewer yeast (Schwechat, Vienna) 8 g, chickpeas seedlings (*Cicer arietinum*) 15 g, potassium sorbate (Merc) 0.05 g, methyl-p-hydroxybenzoate (Merc) 0.1 g and HCL 2N 3 ml to a pH of 4.The yield of this diet in adults over neonate larvae was 69.7 %, the mean pupal weight 6.4 mg and larval development was completed in 9.6 days at 25 ± 1^{o} C. The female in F_3 generation produced 15.3 eggs per day from 7^{th} until 17^{th} day of their lives and the eclosion was 94.1 %.

Discussion: The suggested solid artificial diet was simpler and contained 25% less chickpea seedlings and 20% less brewer yeast than Rey's reference artificial diet.

POSTER PRESENTATION

Distribution of saproxylic insects on standing Scots pine trees with the relation to diameter, thickness of the bark, and height above the ground

Jiri Foit

Faculty of Forestry and Wood Technology, Mendel University of Agriculture and Forestry in Brno, Brno, Czech Republic

The aim of this study was to examine the composition of coenosis of saproxylic insects developing on the standing Scots pine trees (*Pinus sylvestris* L.), to evaluate home ranges of particular species, and to assess impact of the basic factors (section of the tree, thickness of the bark, diameter of the trunk/branch, and height above ground) on the composition of insect communities. Eighty randomly chosen freshly dead standing pine trees were thoroughly analyzed during the spring 2006 in the area of Drahanska Highlands. Thirty-five species of saproxylic insects were found. Preferred home ranges for the development of all abundant species were evaluated along the transect from the tree base to the thinnest branches. At least four well separated guilds of species were found by means of the Correspondence Analysis. Three of these guilds can be described as typical for the specific part of the tree. All examined environmental factors (see above) have significant impact on the composition of studied communities. Factor “section of the tree” explains almost all explained variance of the species data itself. However, this factor can be largely substituted by combination of pure metrical parameters (thickness of the bark, diameter of the trunk/branch, and height above ground). The most significant of these parameters is thickness of the bark. Although examined factors have undisputed impact on the composition of studied communities, major part of the variance of the species data must be attributed to other factors.

This study was supported by the project VaV MZP CR TARMAG SP/2D4/59/07

POSTER PRESENTATION

Evaluation of mini-barcodes for the identification of tephritid fruit flies (Diptera, Tephritidae)

Jeroen Van Houdt[2], Floris Breman[2], Massimiliano Virgilio[1], Thierry Backeljau[3], Marc De Meyer[1]

[1]Entomology Section, Royal Museum for Central Africa, Tervuren, Belgium, [2]Joint Experimental Molecular Unit, Brussels/Tervuren, Belgium, [3]Dept Recent Invertebrates, Royal Belgian Institute of Natural Sciences, Brussels, Belgium

The family of Tephritidae is composed of more than 4,000 species and more than 350 are of economic importance (EI). Because of the user interest and the reasonable taxonomic knowledge the Tephritid Barcoding Initiative (TBI) was initiated in 2006. TBI aims at obtaining DNA barcodes for all EI species and the majority of their congeners. Most of the source material originates from museum collections and is often not suitable for the generation of full DNA barcodes (650bp). The full length barcode could be amplified for most specimens (88%) collected after 2001. However, this success rate dropped dramatically to less than 50% for older specimens. Therefore we evaluated the applicability of mini-barcodes for the identification of tephritid fruit flies in 88 specimens collected between 1961 and 2007. We developed DNA barcodes of different lengths, being 450 bp, 340 bp and 220 bp. The 450 bp marker had a slightly higher success rate compared to the full DNA barcode. However, the amplification success of the 340 bp marker was substantially higher. A 100% success rate for specimens collected after 1990 was obtained, but this decreased to 40% for specimens collected between 1990 and 1980. More than 95% of the latter specimens and almost 60% of the oldest specimens (before 1980) rendered a PCR product for the 220 bp marker. The power of these mini-barcodes to discriminate tephritid fruit fly species is evaluated and discussed.

POSTER PRESENTATION

Synopsis of the genus *Chloropepla* Stål with a phylogenetic analysis of the species (Hemiptera: Heteroptera: Pentatomidae)

Jocelia Grazia, Caroline Greve, Cristiano Schwertner

Universidade Federal do Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil

Introduction: In this paper, a cladistic analysis based on morphological data of the genus *Chloropepla* is presented. Redescription of the genus and a key for all species are also done. *Chloropepla* was first described to include *Loxa vigens* Stål, 1860 (Stål 1867). Currently the taxon is composed by nine species, distributed exclusively on South America.

Methods: The data matrix comprised ten species: nine of *Chloropepla* and *Mayrinia curvidens* (Mayr, 1864), defined as outgroup based on literature. Only adult general and genitalia morphology characters were included.

Results: The analysis of 20 informative characters, seven of general morphology, two of female and eleven of male genitalia morphology resulted in one most parsimonious tree that shows *Chloropepla* as a monophyletic taxon. The monophyly were sustained by six synapomorphies: 1) jugae slightly overlapping clypeus at apex, 2) mesosternal carina strongly developed, 3) long evanescent ostiolar rugae, 4) marginal process of dorsal rim of pygophore present, 5) reduced membranous conjuntiva, almost totally obscured by phallotheca and 6) collar process on base of vesica. The relationships found among the species are: (*C. aurea*, *C. pirani*) (*C. vigens*, *C. paveli*) (*C. lenti C. stysi C. rolstoni C. tucuruiensis*, *C. dollingi*). The clade formed by *C. stysi + C. rosltoni + C. dollingi + C. tucuruiensis* is the best supported one, all characters corresponding to morphology of male and female genitalia. This group includes species distributed on Amazonian region only, revealing probably a congruence between the area and taxon history.

POSTER PRESENTATION

Dynamics of intraspecific interactions in blowflies under the influence of phenobarbital: Ecological applications in the forensic context

Juliana Gião, Wesley Godoy

Universidade Estadual Paulista; Julio de Mesquita Filho;- UNESP, Botucatu, São Paulo, Brazil

Introduction: We evaluated the effect of phenobarbital on the population dynamics of *Chrysomya albiceps*, in an attempt to compare behaviour patterns in species of forensic importance by using a population growth model.

Methods: An oligidic diet containing powdered milk, agar, yeast, nipagin, casein and chicken hearts was used as a rearing medium. Scramble larval competition was established in the laboratory by setting up six larval densities. A larval setting was maintained in 50 g of the oligidic diet as a control, and another in the same diet including phenobarbital (150 mg/Kg). Fecundity was estimated by counting the number of eggs per female, and survival by recording the emergent adults in each larval density. A population growth mathematical model was used to analyse the dynamic behaviour of flies, comparing the control diet with the diet containing the drug.

Results: The population dynamics of *C. albiceps* was slightly changed as a response to addition of phenobarbital to the artificial diet. Apparently, this drug produced destabilising effects, anticipating bifurcations and consequently the occurrence of cycles and chaos. No qualitative change in dynamic behaviour was found after the introduction of the drug, but quantitative changes were observed.

Conclusions: Studies such as this are important in terms of forensic entomology because they characterise patterns of dynamic behaviour inherent to different taxonomic groups, by mixing empiricism and population theory.

POSTER PRESENTATION

Presence of cytokinin-producing *Wolbachia* in different plant-leafminer systems and associated plant physiological alterations

Wilfried Kaiser[1], Elisabeth Huguet[1], Céline Commin[1], Carlos Lopez-Vaamonde[2], Jérôme Casas[1], David Giron[1]

[1]*Institut de Recherche sur la Biologie de l'Insecte, CNRS- University of Tours, Tours, France,* [2]*National Institute of Agronomic Research (INRA), Orléans, France*

Introduction: The nutrition hypothesis states that galling or mining, two major forms of endophytophagy in insects, provide enhanced nutrition over other external-feeding modes, and allow endophagous organisms to avoid major plant defences. This behaviour can also be reinforced by manipulating the plant physiology and leafminer insects have been shown to create an "optimal" nutritional micro-environment through cytokinin production by their endosymbiotic partners. This study aims to explore the presence of cytokinin-producing *Wolbachia* in different plant-leafminer systems and associated plant physiological alterations.

Methods: Using ELISA assays and colorimetric techniques the amount of phytohormones and nutrients in mined areas were recorded. Isopentenyl transferase gene expression (key enzyme of the cytokinin biosynthetic pathway) was investigated by RT-PCR. Using the Wolbachia specific *wsp* and *ftsz* genes and the 'green-island' phenotype we investigated the simultaneous presence of *Wolbachia* and visible altered host-plant physiology.

Results: Our results clearly show that leafminer insects trigger host plant physiology modification through an unexpected association with cytokinin-producing endosymbiotic bacteria. This plant physiology manipulation induced by a large accumulation of cytokinins in the mined tissues is responsible for the preservation of functional nutrient-rich green tissues at a time when leaves are otherwise turning yellow.

Conclusions: The primary role played by *Wolbachia* in the synthesis of cytokinins and in the induction of nutrient-rich tissues is of considerable ecological value to the development of the leafminer larvae as it allows the insect to maintain a favourable nutritional environment in an otherwise degenerating context.

POSTER PRESENTATION

Isolation and characterization of circadian clock genes *period* and *timeless* in Mediterranean flour moth, *Ephestia kuehniella*

Alena Kobelková[1], David Doležel[3], Radka Závodská[2], Ivo Šauman[3]

[1]*Faculty of Science, University of South Bohemia, Ceske Budejovice, Czech Republic,*
[2]*Pedagogical Faculty, University of South Bohemia, Ceske Budejovice, Czech Republic,*
[3]*Biology Center ASCR, Institute of Entomology, Ceske Budejovice, Czech Republic*

Introduction: Although homologous circadian genes are found in insect clocks, their contribution to circadian timing system may be different. Striking differences in the clock gene regulation were found between master clocks of the fruitly, *Drosophila melanogaster* (Diptera) and the silkmoth, *Antheraea pernyi* (Lepidoptera) (Sauman and Hashimi, 1999). Therefore we have extended our research to relatively primitive lepidopteran species, the Mediterranean flour moth (*Ephestia kuehniella*), in order to explore how well the *Antheraea* model is conserved within Lepidoptera.

Methods: Gene walking strategy supplemented with 3´and 5´ RACE were employed to clone full-length *per* and *tim* cDNA sequences. Northern and Southern analyses were used for further characterization of both genes. *per* and *tim* expressing neurons in *Ephestia* brain were localized using *in-situ* hybridization with digoxigenin-labeled RNA probes.

Results: *Ephestia kuehniella* has been used for the first time as a model organism for circadian rhythm studies. Full-length cDNA sequences encoding the circadian clock genes *period* and *timeless* in *E. kuehniella* were cloned. Southern analyses confirm one copy of *per* and *tim* gene, respectively, within both sexes. *In situ* hybridization revealed expression of *per* and *tim* RNAs in nuclei of most neurons throughout the brain and optic lobes. Strong cytoplasmic signal with antisense probe to *tim* RNA was detected in four neurons in the *pars intercerebralis* of each hemisphere. In addition, characterization of circadian controlled egg hatching behavior and locomotor activity of *E. kuehniella* adults is presented.

Conclusions: *Ephestia kuehniella* was established as a convenient non-drosophilid species for circadian rhytm studies.

POSTER PRESENTATION

A local outbreak of the northern pine processionary moth *Thaumetopoea pinivora* on Gotland, south Sweden

Stig Larsson[1], Cecilia Ronnås[1], Andrea Battisti[2]

[1]Swedish University of Agricultural Sciences, Uppsala, Sweden, [2]University of Padova, Padova, Italy

An outbreak of the northern pine processionary moth *Thaumetopoea pinivora* is currently occurring on *Pinus sylvestris* in an area of about 3,000 ha at the northern limit of its distribution on the Baltic island of Gotland, south Sweden. It is not clear how long the population has been present on Gotland, but from observations made by the local residents it appears that it has been present at least since the 1930s. *Thaumetopoea pinivora* has a two-year development cycle on Gotland, with discrete year classes; high larval densities occur in even years and much lower densities in odd years. The larvae feed between April and July on mature pine needles, and release microscopic hairs that can cause severe allergic reactions in humans. Presumably, the population escaped from controlling factors, but no strong control agent has been identified. A tachinid fly (*Blondelia nigripes*) is present in the population, but no precise data on degree of parasitism are available. Present research aims at understanding the local nature of the outbreak.

POSTER PRESENTATION

Influence of climate factors on biology and behavior of vine moth (*Lobesia botrana* Den & Schiff) in the "dealu bujorului" vineyards of Romania

Tabaranu Gabriel, Enache Viorica, Simion Cristina, Donici Alina

Research and development center for viticulture and wine –Bujoru, Targu Bujor Galati, Romania

The paper presents the researches carried out at the Research and development center for viticulture and wine –Bujoru (SCDVV) in the period 1996-2006 highlighting some climate factors (temperature, precipitation) which influence the biology and virulent behavior (F,I and G A%) of the vine moth -Lobesia botrana-Den &Schiff) in the South Moldavian vineyards In the past few years it has been noted a change in the average climate factors (high temperatures, more frequent droughts , aridity) which may induce changers of both biology and behavior of the major vine pest in the vineyard Dealu Bujorului (vine moth or eudemis) with consequences difficult to evaluate for the integrity of the entire vine eco-system.

POSTER PRESENTATION

Monitoring obscure mealybug, *Pseudococcus viburni* (Signoret), in pome fruit orchards in the Western Cape Province, South Africa

Pride Mudavanhu, Pia Addison

Stellenbosch University, Stellenbosch, South Africa

Morphological identification of various mealybug species infesting pome fruits is difficult; therefore mealybugs are still phytosanitary pests. This has led to rejections of export fruit to various markets. Chemical control options are becoming increasingly limited. Little is known about the efficacy of naturally occurring biological control agents and this was therefore investigated between December 2006 and March 2007. The seasonal movement of *P. viburni* was monitored in three pome fruit growing areas. A survey of the identity and incidence of natural enemies attacking mealybugs in pome fruits was conducted to determine the status of potential biocontrol agents. Natural enemies and male mealybugs were sampled on sticky bottoms of yellow delta traps. Correlations between percentage fruit infestation and mealybug trap counts were done. Preliminary results showed similar trends in mealybug populations on the two kinds of fruit, with much variation occurring on apples. Populations on pears remained more even and lower throughout the season. Most mealybugs were found on the main trunk and crutch, while few were found moving to other plant parts. 48% of parasitic wasps caught on yellow delta traps were identified as *Coccidoxenoides perminutus*, 12% were *Leptomastix* spp., 4% were *Anagyrus* spp., while 36% were unidentified. Some predatory beetles found could possibly belong to the genus *Cryptolaemus*. There was a positive relationship between average number of male mealybugs caught on pheromone traps and percentage fruit infestation but increasing male mealybug trap counts did not correlate well with increasing fruit infestation levels. The survey for biological control agents continues.

POSTER PRESENTATION

Metagenomic analysis of the microbiota hindgut of *Reticulitermes lucifugus* (Rossi) (Isoptera: Rhinotermitidae).

Paola Quatrini[1], Gabriella Butera[1], Giovanna Varrica[2], Giuseppe Alonzo[3], Stefano Colazza[2]

[1]Department of Cellular and Developmental Biology DBCS, University of Palermo, Palermo, Sicilia, Italy, [2]Department S.EN.FI.MI.ZO, Università di Palermo, Palermo, Sicilia, Italy, [3]Department ITAF, Università di Palermo, Palermo, Sicilia, Italy

Termites' hindguts host a microbial community consisting of anaerobic flagellates and bacteria. This gut microflora is responsible for the degradation of lignocellulosic material. Here we report the data concerning the analysis of the hindgut microbial community of *Reticulitermes lucifugus* (Rossi), a termite commonly present in Italy, based on a metagenomic approach. Metagenomic DNA was extracted from the gut content of termites and the SSU rDNA was polymerase chain reaction (PCR) - amplified using universal primers for prokaryotes and eukaryotes. Two clone libraries were constructed and clones were grouped into Operational Taxonomic Units (OTU) by RFLP analysis. One representative clone was sequenced for each OTU and sequences were compared to the database. In order to isolate the cellulolytic bacterial fraction from the gut of *R. lucifugus* enrichment cultures were set up on different substrates. The isolates obtained were characterized. A large and diverse population of microbial symbionts was found in the *R. lucifugus* hindgut. Comparisons with other termites communities are presented.

POSTER PRESENTATION

Evolutionary genetics of the invasive harlequin ladybird (*Harmonia axyridis*)

Cathleen Thomas[1], Lori Lawson Handley[1], Michael Majerus[2], Remy Ware[2]

[1]University of Hull, Hull, United Kingdom, [2]University of Cambridge, Cambridge, United Kingdom

Introduction: Biological invasions are currently the second largest cause of biodiversity loss after habitat destruction, and have important economical and ecological consequences. It is still not fully understood why certain species become invasive, what factors determine their success, and what impacts they have on the native species with which they interact.

The genetic composition of the founding population is crucial in determining how a species will adapt to a novel environment and its capacity for range expansion. Genetic data are therefore essential to develop our understanding of the evolutionary processes underlying species invasions, and to determine how genetic factors contribute to invasion success. However, to date, only a few studies have addressed the evolutionary genetics of invasive species. Knowledge of source populations could also be advantageous when developing methods of biological control for invasive species.

The initial aim of this project is to investigate the genetic structure of harlequin ladybird populations in the UK, where the species is invasive and spreading rapidly. Comparing this with native Asian populations and other invasive populations in Europe and North America should then allow identification of source populations and quantification of the number of founders of invasive UK populations. Further work to assess whether the genetic composition of the source population has influenced invasion success can then be done by comparing levels of genetic diversity within native and invasive populations.

Methods: Harlequin ladybirds were sampled from the species' native range in Asia, and invasive ranges in the UK, continental Europe and North America. Selected regions of mitochondrial and nuclear DNA are currently being amplified by polymerase chain reaction and then sequenced to create a phylogeny, and individuals are being genotyped at microsatellite loci.

Results: This work is ongoing, and we therefore present our preliminary results.

POSTER PRESENTATION

Evolutionary genetics of the invasive harlequin ladybird (*Harmonia axyridis*)

Cathleen Thomas[1], Lori Lawson Handley[1], Michael Majerus[2], Remy Ware[2]

[1]University of Hull, Hull, United Kingdom, [2]University of Cambridge, Cambridge, United Kingdom

Introduction: Biological invasions are currently the second largest cause of biodiversity loss after habitat destruction, and have important economical and ecological consequences. It is still not fully understood why certain species become invasive, what factors determine their success, and what impacts they have on the native species with which they interact.

The genetic composition of the founding population is crucial in determining how a species will adapt to a novel environment and its capacity for range expansion. Genetic data are therefore essential to develop our understanding of the evolutionary processes underlying species invasions, and to determine how genetic factors contribute to invasion success. However, to date, only a few studies have addressed the evolutionary genetics of invasive species. Knowledge of source populations could also be advantageous when developing methods of biological control for invasive species.

The initial aim of this project is to investigate the genetic structure of harlequin ladybird populations in the UK, where the species is invasive and spreading rapidly. Comparing this with native Asian populations and other invasive populations in Europe and North America should then allow identification of source populations and quantification of the number of founders of invasive UK populations. Further work to assess whether the genetic composition of the source population has influenced invasion success can then be done by comparing levels of genetic diversity within native and invasive populations.

Methods: Harlequin ladybirds were sampled from the species' native range in Asia, and invasive ranges in the UK, continental Europe and North America. Selected regions of mitochondrial and nuclear DNA are currently being amplified by polymerase chain reaction and then sequenced to create a phylogeny, and individuals are being genotyped at microsatellite loci.

Results: This work is ongoing, and we therefore present our preliminary results.

POSTER PRESENTATION

Potential for natural regulation of codling moth populations by natural enemies

Benoit Sauphanor, Emmanuel Cuenot, Jean François Toubon, Sylvaine Simon

INRA, Avignon, France

Introduction: The control of codling moth, *Cydia pomonella*, using chemical or microbiological insecticides was made difficult in southern Europe by the widespread of resistance phenomena. Environmental parameters which could affect the presence and distribution of *C. pomonella* predators and parasitoids were analyzed in two insecticide free experimental orchards.

Results: The field exposure of egg batches revealed a low egg parasitism by two *Trichogramma* species, similar in apple and pear orchards and increasing in late season. The egg predation was significant, and reduced from 30% to 7% and from 41% to 10% in pear and apple orchard, respectively, when the eggs batches were protected using exclusion cages giving only access to micro-predators. The use of tanglefoot rings designed to prevent the access of ants, earwigs or running spiders did not reduce the rate of egg predation, which was not affected by the distance to the hedgerow. The parasitism of late instar larvae and pupae of the first generation collected in corrugated band traps reached 12.9% and 3.4% in apple and pear orchards, respectively. The ovo-larval parasitoid *Ascogaster quadridentata,* and later in the season the larval parasitoid *Pristomerus vulnerator,* were the most frequent species. Their prevalence was not related to the distance to the hedgerow nor to the density of their host inside the orchard.

Conclusion: The addition of these predation and parasitism-based mortalities at different stages in the life cycle of the pest may reduce the intrinsic rate of increase of codling moth populations in environmentally friendly production systems.

POSTER PRESENTATION

Parasitoids' efficiency in controlling the population size of *Ceutorhynchus assimilis* (Payk.) (Coleoptera: Curculionidae) on winter oilseed rape

Eve Veromann, Anne Luik

Estonian University of Life Sciences, Tartu, Estonia

Introduction: *Ceutorhynchus assimilis* (Paykull) (Coleoptera: Curculionidae) (cabbage seed weevil) is widely distributed and major pest of oilseed rape in Europe. In Estonia, they are generally more abundant on winter oilseed rape and little is known about the occurrence, importance and efficiency of their parasitoids as biocontrol agents.

Methods: In this four year study, the damage of *C. assimilis* and their larval parasitization rates were assessed in winter oilseed rape. Pod samples were collected from oilseed rape plants in 2004–2007 from three commercially grown unsprayed winter oilseed rape crops at the pods maturing stage (BBCH 81–83) and incubated in emergence traps. Thereafter emerged larvae, their exit holes and parasitoids were counted, identified and the percentage of damaged pods and parasitism rate were calculated.

Results: Although, the number of damaged pods by larvae of *C. assimilis* was quite low it increased continuously during study years. The parasitization level showed generally a strong linear increase over the four years and reached noticeable 96% in 2007. The number of parasitizised larvae was the lowest in 2005 and this was the only year when parasitism rate decreased compared to the previous year. The most abundant parasitoid was *Trichomalus perfectus* (Walker) (Hymenoptera: Pteromalidae).

Conclusions: This study showed that parasitoids of *C. assimilis* were establishing a viable population during four years in suitable conditions. We conclude, therefore, that parasitoids of *C. assimilis* can efficiently control the population size of their host and that these natural enemies have a significant value for environmentally friendly crop protection.

POSTER PRESENTATION

Peach-*Myzus persicae* interactions as controlled by winter pruning and nitrogen fertilization: From experimental analysis to modeling.

Isabelle Grechi, Benoit Sauphanor, Marie Hélène Sauge, Jean-Philippe Lacroze, Nadine Hilgert, Françoise Lescourret

[1]INRA, Avignon, France, [2]INRA, Montpellier, France

Introduction: The research purpose is the management of the peach–*Myzus persicae* system, by integration of chemical, biological and cultural pest control methods. We used a modeling approach to address it. To assist model development, we first aim to experimentally characterize peach–aphid interactions driven by winter pruning and nitrogen (N) fertilization, proposed as potential cultural control methods.

Methods: We artificially infested peach trees with aphids and applied various levels of pruning intensity (from 0 to 80%) and N treatments (from shortage to overdose). Aphid dynamics, foliar growth, fruit yield and quality were monitored.

Results: Aphid infestation of peach trees increased with increasing pruning intensity because of an exponential increase of the proportion of growing shoots at the expense of short shoots, aphids having developed better on growing shoots. According to the N gradient, plant vigor increased then leveled off while aphid abundance increased then decreased. Plant vigor partially explained aphid performance that exhibited a significant nonlinear response to leaf N content. Preliminary analyses of foliar chemistry (free amino-acids, phenolic and cyanogenic compounds) gave elements to explain this response at N shortage but not at N overdose. Aphids induced premature defoliation on growing shoots and reduced their growth. Following infestation, trees had compensatory growth. Aphids did not significantly reduce fruit mass and refractometric index.

Conclusions: Winter pruning and N fertilization can be used to control aphids; application in production orchards is discussed. We illustrate the potential of a simulation model, incorporating these results, to investigate alternative strategies for crop-pest management.

POSTER PRESENTATION

Phylogenetic analysis of the tribe Pyrophorini (Coleoptera: Elateridae: Agrypninae)

Simone Policena Rosa

Museu de Zoologia da Universidade de São Paulo, São Paulo, SP, Brazil

Introduction: Pyrophorini comprises 144 species and 20 genera which occur in Southern Neartic, Neotropical and Australian Regions. They have been traditionally recognized as a monophyletic group, sharing as presumed synapomorphy the bioluminescent organs. A cladistic analysis of the tribe was conducted to test its monophyly and investigate the evolution of bioluminescence.

Methods: 140 species were examined and included in 36 in-group clades, representing all Pyrophorini species groups and genera. One species of Pityobiinae and 17 of several Agrypninae tribes, including the supposed sister-group Heligmini, were included as out-groups. Maximum parsimony analysis of 77 adult morphological characters was conducted on TNT traditional search.

Results: The eighteen most parsimonious cladograms show Pyrophorini as paraphyletic because it includes three Heligmini genera. Presence of bioluminescence is corroborated as synapomorphy, but this condition was lost in at least 4 clades. Several genera resulted as polyphyletic. The consensus cladogram shows the following relationships for Pyrophorini: (*Pyrearinus basalis* ((*Agnostelater* + *Coctilelater* + *Pyrearinus lampyris group*) (Pyrophorus + Genus A) (*Pyrearinus cinnameus* ((*Phanophorus* + *Hypsiophthalmus*) (*Noxlumenes* (*Nyctophyxis* + *Cryptolampros*) (*Pyrearinus major part*)) (*Meroplinthus* + *Hapsodrilus* + *Ptesimopsia* major part + *Ptesimopsia paralella* (*Pyroptesis* + *Sooporanga*) (*Fulgeochlizus*) (*Hifo* (*Opselater melanurus* group (*Lygelater bifossulatus* (*Deilelater physoderus* group (*Lygelater* major part (*Photophorus* + *Ignelater*) (*Deilelater sirius* group (*Vesperelater gemmiferus* + *Vesperelater* major part) (*Deilelater atlanticus* group).

Conclusion: Pyrophorini and several genera of this tribe are not monophyletic and their classification should be revised. The bioluminescent pronotal and abdominal organs are independant synapomorphies which were lost at least 4 times independently.

POSTER PRESENTATION

Host-preference of the parasitoid wasp *Sinarachna pallipes* (Holmgren, 1860) (Hymenoptera: Ichneumonidae: Pimplinae) in apple orchards

Stanislav Korenko, Stano Pekar, Veronika Michalkova

Masaryk University, Brno, Czech Republic

Introduction: The population of ectoparasitoid ichneumonid wasp *Sinarachna pallipes* (Holmgren, 1860) that was observed to attack araneid and linyphiid spiders (Gauld, Dubois 2006) was investigated in a commercial apple orchard in the central Europe. Aim of the study was to assess the host-preference and the rate of parasitation.

Methods: Arboreal spider population was observed by beating technique and incidence of parasitized spiders was recorded. Parasitized spiders were reared in laboratory conditions until hatching of the parasitoids.

Results: *S. pallipes* attacked 5 species of theridiid spiders: *Theridion varians* Hahn 1833, *Theridion pinastri* L. K. 1872, *Theridion impressum* L. K. 1881, *Neottiura bimaculata* (L. 1767), and *Paidiscura pallens* (Bl. 1834); and one species of araneid spiders: *Araniella* sp. Theridiid spiders were markedly preferred to araneid spiders. In total, about 2.75 % of theridiid spider population was parasitized. The highest incidence of parasitism was observed among medium sized spiders (prosoma length = 0.7 mm).

Conclusions: Contrary to expectation, *S. pallipes* was found to attack theridiid spiders.

POSTER PRESENTATION

Spatial distribution of aphid and scale populations

Isabel Borges[1], António O. Soares[1], Jean-Louis Hemptinne[2]

[1]University of the Azores, Ponta Delgada, Azores, Portugal, [2]École Nationale de Formation Agronomique, Castanet-Tolosan, France

Introduction: Spatial distribution of aphid and scale populations was assessed in July 2004 and in May, June, July and August of 2006 and 2007 using three distinct methods: Taylor's power law, Iwao's patchiness regression and Spatial Analysis by Distance IndicEs (SADIE).

Methods: Spatial distribution was assessed by three different approaches. Both Taylor's and Iwao's models use a regression to determine the spatial distribution. In the former the sample mean is regressed against the sample variance while in the latter the mean density and Lloyd's mean crowding are the parameters regressed. SADIE, on the other hand, uses the distance to regularity and compares the value observed with the value expected by random assignment of counts.

Results: For every sampling Taylor's power law indicated that both aphid and scale populations were aggregated. Iwao's patchiness regression indicated that aphids and scales formed colonies but differently distributed in space: aphids predominantly presented random colonies while scales' colonies were aggregated in space. According to SADIE, aphid spatial distribution varied between aggregated and random with significant aggregation in some samplings while scales' spatial distribution varied between aggregated and regular but never at a significant level. Additional information on clustering was provided by SADIE with significant patches and gaps identified only for aphids.

Conclusions: Aphid and scale populations seem to occupy differently the habitat. The method that provided the most consistent results was Iwao's patchiness regression. It is noteworthy that, in general, the methods did not provide conflicting results.

POSTER PRESENTATION

Time course of colonization of the glassy-winged sharpshooter precibarium by *Xylella fastidiosa* suggests two types of egestion during inoculation

Elaine Backus[1], David Morgan[2]

[1]USDA Agricultural Research Service, Parlier, CA, United States, [2]California Dept. of Food & Agriculture, Riverside, CA, United States

Introduction: Establishment of the invasive glassy-winged sharpshooter (GWSS), *Homalodisca vitripennis,* in California has caused an increase in incidence of Pierce's Disease bacterium, *Xylella fastidiosa* (*Xf*), in grape-growing regions. Although host plant resistance to the pathogen and its vector is being sought, research is hampered by lack of understanding of acquisition and inoculation mechanisms.

Methods: The anatomical location of acquisition (from which inoculation occurs) was studied using a confocal microscopy method to visualize *in situ* green fluorescent protein (GFP)-transformed *Xf* within the undissected precibarium and cibarium of the vector. We performed a time course study of GFP-*Xf* acquisition by GWSS, across acquisition access periods (AAP) ranging from 1 to 14 days.

Results: Bacterial colonies form in the cibarium within the first 24 hr AAP; at the same time, they begin to move forward from this cibarial reservoir into the precibarium. By AAP day 3, bacteria line the length of the precibarium except the area of the D-sensilla field (below the precibarial valve), which is almost nearly always free of bacteria. By AAP day 5, this large accumulation of bacteria has disappeared, and evidence suggests that the precibarium was physically swept clear of biofilm. After day 5, this cycle of loading above the valve then discharging starts again.

Conclusions: We hypothesize that there are two types of egestion (injection of material from the anterior foregut back into the plant): rinsing egestion (continuously occurring from below the precibarial valve) and discharging egestion (sporadically [every 3 to 5 days] occurring from above the precibarial valve).

POSTER PRESENTATION

The effects of two different biotypes (SA-1 and SA-2) of Russian wheat aphid, *Diuraphis noxia* (Kurdjumov) (Homoptera: Aphididae) on non-resistant and resistant wheat cultivars Tugela and Tugela-Dn (*Triticum aestivum*)

Shaun Walton, Ted Botha

Rhodes University, Grahamstown, South Africa

Introduction: The negative effect aphids such as the Russian Wheat Aphid (RWA) *Diurpahis noxia* have on commercially important crops such as wheat, *Triticum aestivum*, has in recent years received increasing attention due to the suspected evolution of aphid biotypes that are capable of inducing severe crop yield loss in modern day resistant wheat cultivars.

Methods: The effects of two different biotypes (SA-1 and SA-2) of Russian wheat aphid on non-resistant and resistant wheat cultivars, Tugela and Tugela-Dn *Triticum aestivum,* was investigated using both fluorescence microscopy and population studies.

Results: The new biotype Russian Wheat Aphid SA-2 (RWA SA-2) was found to be more damaging to both the non-resistant and resistant cultivars of wheat in both short term and long term feeding experiments. The results of the population experiment showed that the new biotype RWA SA-2 also has a significantly faster breeding rate than the old biotype RWA SA-1 on both the non-resistant and resistant cultivars ($P = 0.013$).

Conclusions: The suspected evolution of a new resistant and more virulent biotype of RWA is in fact true and that this new biotype poses a severe threat to the commercial wheat industry of South Africa.

POSTER PRESENTATION

The molecular phylogeny of oestroid Diptera, with special emphasis on the taxonomic position of the genus *Bengalia* (Robineau-Desvoidy, 1830)

Shaun Walton, Doug Downie, Martin Villet, Ashley Kirk-Spriggs

Rhodes University, Grahamstown, South Africa

Introduction: The taxonomic placement of the genus *Bengalia* has recently come under scrutiny. To resolve the current disparity, the taxonomic placement of *Bengalia* and phylogenetic relationships of the oestroid Diptera were investigated using molecular methods.

Methods: To test the hypothesis, 43 species of calyptrate fly including two *Bengalia* specimens; representative members of six of the currently recognized calliphorid subfamilies (Bengaliinae, Auchmeromyiinae, Rhiniinae, Luciliinae, Calliphorinae, Chrysomyiinae); and a range of suitable out-group taxa representing three families within the Oestroidea (Sarcophagidae, Oestridae, Tachinidae); and two other superfamilies (Muscoidea and Tephritoidea) were used. Phylogenies were constructed using sequences derived primarily from published data in combination with sequences obtained from seven additional species. Portions of both the large ribosomal subunit RNA gene (28S rDNA) and mitochondrial cytochrome oxidase subunit I were used. Analysis used Parsimony and Bayesian Inference methods.

Results: *Bengalia* placed well within the main calliphorid clade, however the placement was weakly supported.

Conclusions: Support for the placement of *Bengalia* within the Calliphoridae was obtained from three sources: 1) previous morphological studies; 2) similar biology and common termite mound association amongst closely related taxa; and 3) common taxonomic placement of the group well within the main calliphorid clade. The well supported placement of the Rhiniinae as well as the strange placement of a number of other out-group taxa within the main calliphorid clade [Calliphoridae (Tachinidae (Oestridae (Muscidae))) Calliphoridae]; suggest that the Calliphoridae, as it is currently recognized, does not appear to be a monophyletic group or that the genes are saturated.

POSTER PRESENTATION

The sharpshooter X-wave: Correlation of xylem penetration by *Homalodisca* spp. with an Electrical Penetration Graph (EPG) waveform

Elaine Backus[1], Wendy Holmes[2], Brendon Reardon[3], Fred Schreiber[2], Gregory Walker[3]

[1]USDA Agricultural Research Service, Parlier, CA, United States, [2]California State Univ., Fresno, Fresno, CA, United States, [3]Univ. of California, Riverside, Riverside, CA, United States

Introduction: Electrical penetration graph (EPG) monitoring is a rigorous means of observing and quantifying the feeding of piercing-sucking insects. Previous studies with aphids and leafhoppers have demonstrated the value of what is termed the X wave, i.e. the waveform that represents first penetration of the insect's piercing-sucking mouth parts, the stylets, into a preferred vascular tissue for ingestion, usually a phloem sieve element or xylem tracheary element.

Methods: Salivary sheath termini of smoke tree sharpshooters, *Homalodisca liturata*, were correlated with successive events of X wave components.

Results: We observed the consistent association of the X wave with salivary sheath termini in a xylem cell, especially mature (lignified), secondary xylem cells. The sharpshooter X wave is a complex, multi-component waveform family that is composed of waveform types B1s (previously shown to represent precibarial valve movement and possible egestion), B1w (salivation), proto-C (possible micro-ingestion) and C (macro-ingestion/ cibarial pumping). The X wave is a pathway- and interruption-phase waveform that is best visualized using the AC-DC EPG monitor, with input impedance set at 10E7 Ohms, to balance emf and R components.

Conclusions: The sharpshooter X wave is correlated with first penetration of xylem, and represents a suite of behaviors that we propose function to: 1) physically seal stylet tips into the cell via sheath salivation, 2) taste constituents of the cell to determine acceptability, and 3) mechanically test strength of the stylet seal via trial cibarial pumping. We hypothesize that the X wave is associated with behaviors that control inoculation of *Xylella fastidiosa*.

POSTER PRESENTATION

Calesidae, a potential new family of Hymenoptera

Jason Mottern, John Heraty, Emily Hartop

University of California, Riverside, Riverside, CA, United States

Although the monophyly of some groups of Chalcidoidea is strongly supported by morphological and/or molecular synapomorphies, higher-level relationships within the superfamily remain uncertain. Several families are regarded as either paraphyletic or even polyphyletic. This uncertainty regarding sister-group relationships, combined with hyperdiversity of form and function, has left some chalcid groups unplaced into higher taxonomic categories Establishing relationships within Chalcidoidea is further hindered by a dearth of comprehensive morphological studies, either across character systems or across taxa. Calesinae (Howard) is a small group of Australian and Neotropical parasitoids of whiteflies, comprising a single genus, *Cales*. Historically, the Calesinae have been included within the Trichogrammatidae and Mymaridae, though they are most often associated with the Aphelinidae. In addition, they share some features with the Eulophidae. The subfamily is currently unplaced within the superfamily Chalcidoidea. Here we present a detailed morphological examination of the three described species in addition to a newly discovered species from New Zealand. The apparently apomorphic characteristics of the head, mouthparts, antennae, wings, mesosoma and genitalia, are weighed against characteristics suggesting affinities with established chalcidoid families. We suggest that the Calesinae are sufficiently unique to warrant family-level status, the Calesidae.

POSTER PRESENTATION

Thoracic vibrations in stingless bees: is body size important for an efficient buzz pollination?

Patrícia Nunes-Silva, Michael Hncir, Vera Lucia Imperatriz-Fonseca

Faculty of Philosophy, Science and Letters of Ribeirão Preto, University of Sao Paulo, Ribeirão Preto/São Paulo, Brazil

Various morphological and behavioral characters determine the efficiency of an animal as pollinator. Many bee species vibrate their thorax when in contact with poricid anthers, thereby inducing a rapid pollen release. This so called buzz pollination occurs in many angiosperms. Here, the most important physical aspects for an efficient pollen release are the vibrations' velocity and acceleration. These two parameters putatively depend on the size of the bees' thorax, since this character correlates with the mass of the flight muscles, which, further, determines the strength of the vibration. The annoyance buzzing, which is similar to the vibrations produced during buzz pollination, of seven stingless bee species (*Melipona scutellaris*, *M. seminigra*, *M. quadrifasciata anthidioides*, *M. rufiventris*, *Schwarziana bipunctata*, *Scaptotrigona* aff. *depilis* and *Nannotrigona testaceicornis*) was measured using a laser vibrometer. The thorax size was described by the area of the scutellum. This measure was used as an estimate for the bees' size and the mass of their flight muscles. The seven analyzed bee species differed significantly in their size. Moreover, the thoracic displacement amplitude during annoyance buzzing strongly depended on the thorax size of the respective species. However, there was no significant difference between the fundamental frequencies and the velocity amplitudes among most species. Therefore, since the vibration velocity does not necessarily depend of the bees' size, small bees might be as efficient as big ones during buzz pollen collection. Thus, the behavior of stingless bees while collecting pollen might be the main determinant of their efficiency as buzz pollinators.

POSTER PRESENTATION

Geographical distribution of mutant carboxylesterase gene involved with insecticide resistance in New World screwworm fly (NSW) *Cochliomyia hominivorax* (Diptera: Calliphoridae).

Renato Assis Carvalho, Norma Machado Silva, Ana Maria Lima Azeredo-Espin

[1]Centro de Biologia Molecular e Engenharia Genética. Instituto de Biologia. Universidade Estadual de Campinas, Campinas, São Paulo, Brazil, [2]Centro de Biologia Molecular e Engenharia Genética. Instituto de Biologia.Universidade Estadual de Campinas, Campinas, São Paulo, Brazil, [3]Centro de Biologia Molecular e Engenharia Genética. Depto. Genética e Evolução. Instituo de Biologia. Universidade Estadual de Campinas, Campinas, São Paulo, Brazil

Introduction: The New World screwworm (NWS) *Cochliomyia hominivorax* Coquerel is one of the most important myiasis-causing flies in Central and South America. It is responsible for severe economic losses in livestock. The improper and continuous use of insecticides can lead to the selection of resistant strains. Mutations in carboxylesterase E3 gene associated with organophosphate and pyrethroids resistance (Gly137/Asp and Trp251/Ser) have been recently characterized in this species.

Methods: Part of the *C. hominivorax* E3 gene was sequenced, by direct sequencing of PCR products, from several localities of Central and South America. The mutations were analyzed and their frequencies were recorded.

Results: The sequences were analyzed in a total of 10 individuals for each of 8 populations. Three possible genotypes were found: mutant Gly137/Asp, mutant Trp251/Ser and wild types. The mutation Gly137/Asp (a general form of OP resistance) was mainly found at the regions with intense use of OP insecticide in Brazil (33-55%). The mutation Trp251/Ser (dimethil OP and pyrethroid resistance) was found in high frequency in regions with intense use of OP (Brazil) and pyrethroids insecticides for *C. hominivorax* control (Uruguay: 80% and Venezuela: 100%). However, in Cuba, where another class of insecticide (a GABA inhibitor) was used for long time, no mutant individuals were found.

Conclusions: The data obtained indicates a correlation between the mutations in the *C. hominivorax* carboxylesterase and the class of insecticide used throughout its current geographic distribution. This characterization will provide information for the selection and for the implementation of more effective pest management programs.

POSTER PRESENTATION

New, Universal AC-DC Electrical Penetration Graph (EPG) monitor reveals detailed R- and emf-component waveforms for any piercing-sucking insect

Elaine Backus[1], Murugesan Rangasamy[2], Heather McAuslane[2], Margaret Redinbaugh[3], Astri Wayadande[4], William Bennett[5]

[1]USDA Agricultural Research Service, Parlier, CA, United States, [2]Univ. of Florida, Gainesville, FL, United States, [3]USDA Agricultural Research Service, Wooster, OH, United States, [4]Oklahoma State Univ., Stillwater, OK, United States, [5] private consultant, Otterville, MO, United States

Introduction: Electrical Penetration Graph (EPG) monitoring is the most rigorous means of observing and quantifying the feeding of any piercing-sucking arthropod. However, until now, most studies have emphasized relatively few insects, mostly small-bodied hemipterans such as aphids (Aphididae) and leafhoppers (Cicadellidae). Virtually no heteropterans or blood-sucking arthropods have been studied.

Methods: A recently designed Universal AC-DC EPG monitor provides updated, high-quality amplifiers with a wider range of user-selectable adjustments, to tailor the monitor to each new species.

Results: The instrument is briefly described. Then, examples are provided of representative waveforms from the following insects: cotton aphid, *Aphis gossypii* (Aphididae), smoke tree sharpshooter, *Homalodisca liturata* (Cicadellidae: Cicadellinae), black-faced leafhopper, *Graminella nigrifrons* (Cicadellidae: Deltocephalinae), chinch bug, *Blissus insularis* (Heteroptera: Lygaeidae), and squash bug, *Anasa tristis* (Heteroptera: Coreidae). These insects range in size from 0.3 mm to 18 mm in length, a wider array of insect sizes than has been recordable in the past. For aphids and leafhoppers, comparisons are made with the same species' waveforms from older monitors, to show that waveform detail and resolution are highly improved with the new monitor. In addition, examples from chinch bug waveforms demonstrate how simple switches of input resistor values can distinguish between emf-component and R-component waveforms.

Conclusions: EPG holds the potential to significantly improve research on a wide array of species, such as heteropterans and blood-sucking vectors of medical/veterinary pathogens. The key to broadening the applicability of EPG has been improving the electronic design and flexibility of the instrument.

POSTER PRESENTATION

Temporal dynamics of insecticide aerosols in a small experimental store

Jan Plachy, Vladimir Kocourek, Vaclav Stejskal, Radek Aulicky, Jana Hajslova

DDD servis sro, Prague, Czech Republic

Introduction: In mill industry there is an urgent need for replacement toxic fumigants. One viable option is the use of insecticide aerosols. The prerequisite for their efficient use is the knowledge of their temporal dynamic in the air. The objective of the presented study was to assess the dynamics of insecticides when applied as aerosols in an experimental store (simulated by a small experimental room) under two different regimes of sealing using plastic sheets and strips.

Methods: In the experiments, aerosol sm.oke generator (Ultimate super SG, TransChem s.r.o) was employed. The tested pesticide preparation contained two types of active ingredients: pirimiphos-methyl (71, 3g/1 kg) and cypermethrin (13, 1 g/kg). Air sampling was carried out by the Escort Elf sampler (Mine Safety Appliances Co., Pittsburg, PA, USA) 3, 6 and 12 hours after application. The temporal dynamics was estimated on the basis of data obtained by gas chromatographic analysis (GC) of trapping filters; conventional (EGO or NPO) and mass spectrometric (MSO) detectors were used for detection of target compounds. Blattella germanica was used as a model insect to evaluate biological efficacy of insecticide aerosols.

Results and Conclusions: The obtained data document distinct effect of sealing quality on the temporal dynamics of air residues in both types of insecticides. The full biological activity was achieved in the sealed room only where losses of active ingredients due to air circulation were avoided. This study was supported by the MSMT (project NVP2-CHEMKONTAM-2B06099) and partly by MZe (project Vyzkumny zamer 0002700603).

POSTER PRESENTATION

Complex food web created by a biological control agent – the case of *Dasineura dielsi* on *Acacia cyclops*

Carien Kleinjan

University of Cape Town, Cape Town, South Africa

The Australian midge, *Dasineura dielsi* (Cecidomyiidae) induces gall formation within the flowers of *Acacia cyclops* thereby preventing pod formation. Following its introduction into South Africa for biological control of *A. cyclops, D. dielsi* dispersed rapidly and occurred throughout the range of the weed within four years. The incidence of galling everywhere is consistently high and most flower-heads now develop into complex, convoluted gall clusters rather than seed pods. Details of the organisms associated with the galls induced by *D. dielsi* were obtained by observation, dissection of gall material and by rearing immature stages in galls through to adulthood. Parasitoids developing within afflicted hosts were reared, where possible, to determine host associations. The study has revealed that galls created by *D. dielsi* are utilized, either as a resource or as a refuge, by a variety of other organisms. In conjunction with *D. dielsi,* they support a complex web of predators and parasitoids.

POSTER PRESENTATION

Oviposition site selection in natural populations of *Ramosiana insignis* and *Vulcirea violaceae* (Hemiptera: Pentatomidae) involve a trade-off in the survival of progeny.

Maurilio López[1], Francisco Díaz-Fleischer[1], Trevor Williams[2]

[1]Laboratorio de Biotecnología y Ecología Aplicada, Universidad Veracruzana, Xalapa, Veracruz, Mexico, [2]Instituto de Ecología A.C.,, Xalapa, Veracruz, Mexico

Introduction: The selection of oviposition sites of natural populations of two species of pentatomid bugs *Ramosiana insignis* and *Vulcirea violaceae* (Hemiptera: Pentatomidae) were studied on and around focal trees of *Schoepfia schreberi* J.F. Gmel (Olacaceae) in Veracruz State, Mexico.

Methods: Observations were performed at approximately weekly intervals at Tejerias and natural area Ejido Monte Blanco from Teocelo, Veracruz Mexico, from September to April, 2005-2007. The numbers of eggs laid by each species, percentage of parasitism, type of vegetation and distance from the focal host tree were noted.

Results: One species, *V. violaceae* reproduced and fed exclusively on the fruits of *S. schreberi* during the entire lifecycle. In contrast, *R. insignis* was found in association with *S. schreberi* and on 40 other species from 23 families of plants that surrounded focal trees. These plants were used as oviposition sites and appeared to represent natural enemy free space around each focal tree. Two species of egg parasitoids, *Telenomus* spp. (Hymenoptera: Scelionidae), an unidentified parasitoid and two species of tachinids, one of which was *Trichopoda pennipes* F. (Diptera: Tachinidae) attacked pentatomid egg masses and nymphs on *S. schreberi.* Predators included ants, salticid spiders and *Eutyrhinchus floridanus* (L.) (Hemiptera: Asopinae). Maternal care was observed in both species from oviposition to the first nymphal instar. The mean (±S.D.) number of eggs laid per female on *S. schreberi* was 343.8 ± 91.1, of which 28.4% were parasitized. In contrast, the mean number of eggs laid per female on the vegetation surrounding focal trees was 400.3 ± 69.6 (*R. insignis*) of which 15.2% suffered parasitism. The average distance between the focal tree and egg masses laid on surrounding vegetation was 3.1 ± 1.8 m. Nymphs of *R. insignis* had to migrate this distance to locate the fruits of *S. schreberi*, with associated risks of predation.

Conclusions: The two species adopt differing oviposition site selection that appears to represent a trade-off between the higher prevalence of parasitism of their progeny on *S. schreberi* and the risks associated with migration from surrounding vegetation to the focal host tree for feeding.

POSTER PRESENTATION

Assessment of containerized insecticide baits for the control of ants (Hymenoptera: Formicidae) in South African vineyards

Casper Nyamukondiwa, Pia Addison

Stellenbosch University, Stellenbosch, South Africa

Ant infestations comprising the Argentine ant, *Linepithema humile* (Mayr); common pugnacious ant, *Anoplolepis custodiens* (Smith); and cocktail ant, *Crematogaster peringueyi* (Emery) are a widespread pest problem in South African vineyards. Integrated Pest management (IPM) programmes aimed at suppressing problematic honeydew excreting mealybug pests on grapes must include ant control in order to optimize the effectiveness and efficacy of mealybug natural enemies. If ants are eliminated, natural enemies are capable of keeping these Homopteran pests below the Economic Threshold Level (ETL). Current strategies for ant control are limited and generally include the application of long term residual insecticides that are detrimental to the environment, labour intensive to apply and can disrupt natural biological control. A more practical method of ant control using low toxic baits was therefore investigated. Bait preference assessments and bait acceptance assessments were carried out in three different vineyards during the 2007/08 season. Five low toxic insecticide baits comprising 0.5% Gourmet ant bait, 0.5% boric acid, 0.0001% fipronil, 0.001% fenoxycarb and 0.5% spinosad were tested against a 25% sucrose solution control. Preliminary results showed that low toxic ant baits were equally preferred and accepted by the three ant species compared to the 25% sucrose solution control. Thus, use of low toxic baits can offer producers with a more practical, economical and environmentally friendly method of ant control which is compatible with vineyard IPM programmes.

POSTER PRESENTATION

Gene expression pattern of caste and life-stage specific EST libraries in the termite, *Reticulitermes flavipes*, utilizing bioinformatic tools

Matthew Steller, Srini Kambhampati

Kansas State University, Manhattan, KS, United States

Introduction: Termites (Isoptera) are separated into morphologically and behaviorally distinct castes of sterile workers and soldiers, and reproductive alates. Previous research has implicated that caste differentiation is controlled genetically. We compared the gene expression patterns of each caste and two larval life stages of *R. flavipes* in an attempt to better understand caste-specific gene expression.

Methods: Five caste- and life stage-specific cDNA libraries were constructed , cloned, and sequenced to generate an EST library of almost thirteen thousand sequences. All sequences were trimmed and arranged into contiguous sequences using Sequencher 4.7. Putative gene functions were assigned based on a tblastx swissprot search. Expressed gene patterns for each library were compared using Blast2GO.

Results: Seventy to ninety percent of sequences had no significant (e-value<1E-10) homology to sequences in existing databases. ESTs of workers and soldiers were from the widest array of functional classes. All libraries showed sequences with putative functions assigned to reproduction, which is unexpected in the non-reproductive soldier and worker castes. The biological process ontology was most variable for the worker caste with three unique terms (reproductive process, biological adhesion, and growth), however soldiers did have 10% of the ontology terms represented as sequences that made up less than 1% of the total, while workers consisted of 8% indicating increased functional variability in the soldier ESTs.

Conclusions: As expected, each caste appears to have unique expression patterns; of special interest are genes associated with transcriptional control and reproduction. We plan on performing fine-scale analysis of caste-specific expression patterns using a microarray of over 2,000 ESTs.

POSTER PRESENTATION

Efficacy of five selected acaricides against *Tetranychus urticae* (Acari: Tetranychidae) and their side-effects on relevant natural enemies occurring in citrus orchards

Alberto Urbaneja[1], Sara Pascual-Ruiz[1], Tatiana Pina[1], Raquel Abad-Moyano[1], Pilar Vanaclocha[1], Helga Montón[1], Pedro Castañera[3], Josep A. Jacas[2]

[1]Centro de Protección Vegetal y Biotecnología. Instituto Valenciano de Investigaciones Agrarias (IVIA), E-46113-Moncada. Valencia, Spain, [2]Departament de Ciències Agràries i del Medi Natural. Universitat Jaume I (UJI); Campus del Riu Sec, E-12071-Castelló de la Plana, Spain, [3]Departamento Biología de Plantas. Centro de Investigaciones Biológicas CIB, Consejo Superior de Investigaciones Científicas (CSIC), C/ Ramiro de Maetzu, 9, E-28040. Madrid, Spain

Introduction: Three groups of natural enemies are fundamental in citrus IPM in Spain: coccinellid and phytoseiid predators and hymenopteran parasitoids. *Tetranychus urticae* is an important pest affecting citrus, for which biological control has not yet been achieved; therefore, acaricides are commonly used to control it.

Methods. The aims of this study were to assess the efficacy of five acaricides widely used in citrus against *T. urticae,* and their acute side-effects on the adult stage of three selected natural enemies present in Spanish citrus orchards, which represent the key groups mentioned: the coccinelid *Cryptolaemus montrouzieri* Mulsant, a mealybug predator, the phytoseiid *Neoseiulus californicus* McGregor, a spider mite predator, and the braconid *Aphidius colemani* Viereck, an aphid parasitoid. Furthermore, sublethal effects were also considered for *C. montrouzieri* adults and immature stages.

Results: Some products proved highly effective against *T. urticae* and harmless to *A. colemani* (mineral oil, tebufenpyrad, clofentezin and fenazaquin). However, almost all products tested were slightly harmful for both predators considered. Fenazaquin was even moderately harmful for *N. californicus*.

Conclusions: Further studies, like the one presented here, are necessary to gain a better understanding of integrating biological and chemical controls. When considering both efficacy and side-effects on beneficial arthropods, the best options would seem to be mineral oil, tebufenpyrad and clofentezin. However, it is urgent to complete testing the side-effects of the acaricides used in citrus. This question is crucial if we consider that two recently introduced Tetranychidae are being controlled in citrus by chemical means exclusively.

POSTER PRESENTATION

Reparation of heat and cold injury in the bug *Pyrrhocoris apterus*: Does it require the expression of inducible *hsp70* gene?

Michaela Tollarová[1], Alena Kobelková[1], Vladimír Košťál[2]

[1]*Faculty of Science, University of South Bohemia, Ceske Budejovice, Czech Republic,* [2]*Biology Center ASCR, Institute of Entomology, Ceske Budejovice, Czech Republic*

Introduction: The expression of Heat Shock Proteins (Hsps) is known to be induced by diverse stresses, including heat and cold shocks, desiccation, anoxia, and exposure to a wide range of chemicals. Hsps function as molecular chaperones binding to partially denatured proteins and promoting their return to native conformation. Although it has been well established that Hsps are developmentally up-regulated in various diapausing insects, their exact physiological roles during diapause are not completely clear (Rinehart et al., 2007: PNAS USA 104, 11130-11137).

Methods: We have cloned structural homologs of inducible *hsp70* and cognate *hsc70* genes in the heteropteran *Pyrrhocoris apterus*, and quantified the abundance of their mRNA transcripts after the exposures to high (+45ºC) and low (-5ºC) temperature shocks using qRT-PCR technique.

Results: While the levels of *hsp70* mRNA increased by about three orders (1 000 – 4 000-fold) after the shocks, the levels of *hsc70* mRNA remained constant. After the injection of synthetic *hsp70* dsRNA (RNAi technique), we managed to diminish the shock-induced *hsp70* response to approximately 30 – 60-fold increase. Such a suppression of *hsp70* expression was sufficient to completely prevent the recovery from heat-injury. While more than 95 % of the control bugs (treated by injection buffer only) recovered and were fit 3d after the exposure, none of the *hsp70* dsRNA-treated bugs survived after the exposure to +45/5h.

Conclusion: The results of ongoing experiments will be presented, in which we asked whether the recovery of *P. apterus* bugs after cold shock also requires the up-regulated expression of inducible *hsp70* gene.

POSTER PRESENTATION

Suitability of the tomato borer *Tuta absoluta* as prey for *Macrolophus caliginosus* and *Nesidiocoris tenuis*

Alberto Urbaneja[1], Helga Montón[1], Óscar Mollá[1], Josep Anton Jacas[2]

[1]Centro de Protección Vegetal y Biotecnología. Instituto Valenciano de Investigaciones Agrarias (IVIA), E-46113 Moncada/Valencia, Spain, [2]Departament de Ciències Agràries i del Medi Natural. Universitat Jaume I (UJI); Campus del Riu Sec;, E-12071-Castelló de la Plana, Spain

Introduction: The tomato borer, *Tuta absoluta* (Meyrick) (Lepidoptera: Gelechiidae) is an important tomato pest native to South America which appeared in eastern Spain at the end of 2006. As a first step to discovering the extent to which two indigenous predators, *Macrolophus caliginosus* Wagner and *Nesidiocoris tenuis* Reuter (Hemiptera: Miridae) can adapt to this invasive pest, the prey suitability of eggs and larval instars of *T. absoluta* was evaluated.

Methods: Both predators and both sexes were exposed separately to different *T. absoluta* egg densities (10, 20, 40 and 60) whereas the capacity of both predators to feed on *T. absoluta* larval instars was evaluated in a no-choice experiment.

Results: Both predators preyed actively on *T. absoluta* eggs. Females of both species consumed more *T. absoluta* eggs than males. Both mirid predators were able to prey on the four *T. absoluta* larval instars. However, the number of preyed larvae varied significantly with prey instar for both mirid predators. The first larval instar was the most frequently preyed followed by the second instar larvae, for *M. caliginosus* and *N. tenuis*, respectively.

Conclusions: Our results again demonstrate the adaptability of both mirids to different environmental conditions, in this case an invasive pest, which contributes to their value as a biological control agent in tomato crops. A challenge for future studies will be to clarify how both predators can be used in the biological control of *T. absoluta*.

POSTER PRESENTATION

A comparison of decomposition and succession process on pig carcass: preliminary study of forensic entomology in the Western São Paulo State, Brazil

Juliana Alves Neves, Patricia Jacqueline Thyssen, Helton Otsuka, Carolina G. P. Lima, Wesley A. C. Godoy

UNESP, BOTUCATU, SP, Brazil

Introduction: This is the first report of an ongoing study of insect succession on carrion carried out in the Western of São Paulo State, Brazil, using pigs (*Sus scrofa* L.) as a model to determine the insect sequence over 14 days. The main objective was setting up a preliminary data-base for medicolegal purposes in this region.

Methods: Invertebrates were collected daily in a field investigation and identified in laboratory.

Results: During this period, 16,493 insects belonging to the following orders and families were collected: Diptera: Calliphoridae, Muscidae, Piophilidae, Sarcophagidae, Syrphidae, Otitidae; Micropezidae; Tachinidae; Asilidae; Faniidae; Tephritidae; Richardidae; Lauxaniidae; Hymenoptera: Formicidae, Vespidae; Coleoptera: Histeridae, Scarabaeidae, Dermestidae; Lepidoptera and Hemiptera. Four decomposition stages were observed (fresh, bloated, active decay and dry remains) and four insect ecological categories (necrophagous, predators, omnivorous and incidental). The first insects that appeared and oviposited were flies of the family Calliphoridae, *Lucilia eximia* (Wiedemann), but the predominant species were *Chrysomya albiceps* (Wiedemann) during almost all decomposition process. During the second and third stages, the most abundant families were Calliphoridae and Sarcophagidae. During the last stage, the dominant family was Formicidae followed by Histeridae with a large number of immature insects.

Conclusions: The fauna collected in the course of this work contained fewer species than were previously recorded as occurring in corpses in other regions from Brazil, due to the strong competition and predation by *C. albiceps* on other species. We understand that these community level approaches must be considered of potential forensic interest for estimating the post-mortem interval.

POSTER PRESENTATION

Prevalence of microsporidian infection of the European corn borer, *Ostrinia nubilalis* Hbn. (Lepidoptera: Pyralidae) at the Krasnodar Territory

Yury Tokarev, Julia Malysh, Dmitry Serapionov, Andrei Frolov

All-Russian Institute for Plant Protection, St. Petersburg, Russian Federation

Introduction: Incidence of microsporidia infecting of the European corn borer (ECB), *Ostrinia nubilalis* in Eurasia has been studied not enough. Only few reports are known from Italy, France, Poland, Czech Republic and Slovakia. In present work we compare prevalence rates of different geographic insect populations inhabiting different host-plants at the Krasnodar Territory.

Methods: Microscopic analysis of larvae, collected in field and perished under lab conditions was carried out with the use of fluorescent microscopy. Preparations of spores fixed by absolute methanol were stained with DAPI. Spore sizes were evaluated using Carl Zeiss Axiovision 4.6.

Results: Microsporidian infection of ECB in Russia was revealed for the first time. DAPI staining confirmed presence of *Nosema*-like spores with markedly stained diplocarya and weakly stained cytoplasm and exospore, as well as unstained zone of endospore. Prevalence rates of last instar larvae varied from 4.8 to 12.5%. We have compared prevalence rates for larvae collected i) near west vs east borders of the Krasnodar Territory, ii) during 2005 vs 2006, iii) from dicotyledonous (cocklebur, mugwort) vs monocotyledonous (maize) hosts. Microsporidia prevalence rates failed to differ significantly in all cases compared.

Conclusions: Microsporidia are widespread parasites in ECB populations inhabiting the south of Russia. Since *Nosema pyrausta* shows high efficiency as controlling ECB in North America, further research of microsporidia of ECB in Russia should be of importance. Supported by RFBR grants 06-04-48265, 07-04-92170, and a grant of the President of Russian Federation MK-653.2007.4.

POSTER PRESENTATION

Outbreak dynamics and natural enemies of the pine bark beetle *Ips acuminatus*

Fernanda Colombari, Massimo Faccoli, Andrea Battisti

University of Padova Dep. Environmental Agronomy, Padova, Italy

Introduction: Since 2004, many Scots pine (*Pinus sylvestris*) stands growing in the South-Eastern Italian Alps are severely attacked by the bark beetle *Ips acuminatus*. The investigated forests show dozens of infestation spots having size ranging from about 20-30 trees (small spots) up to 300 trees (large spots). The spots show up and extinguish quickly, while new ones appear within a radius of hundreds of meters. We hypothesize that natural enemies may drive the spot dynamics.

Methods: During 2007 we sampled branches from small and large spots and lodged them into emergence cages. Adults of *I. acuminatus* as well as natural enemies were collected weekly, identified and counted. At the same time, a monitoring of the examined pine stands was carried out to check the enlargement of old spots and the appearance of new ones. Voltinism and phenology of *I. acuminatus* were investigated by pheromone traps.

Results: In the surveyed areas *I. acuminatus* is bivoltine, with the first generation showing the highest density. Twentythree species of natural enemies (7 predators and 16 parasitoids) emerged from the branches, with *Metacolus unifasciatus* (Pteromalidae), *Dendrosoter hartigii* and *D. middendorfi* (Braconidae) being the most common.

Conclusions: The parasitism may have a role in outbreak dynamics as it was significantly higher (about 75%) during the second host generation, in both small and large spots. The number of both *I. acuminatus* and its natural enemies was not affected by spot size.

POSTER PRESENTATION

Expression and localization of cadherins in the honey bees (*Apis mellifera* L.) ovary

Mônica Florecki, Klaus Hartfelder

University of São Paulo, Ribeirão Preto, São Paulo, Brazil

Background: Cadherins constitute a superfamily of transmembrane glycoproteins involved in intercellular adhesion and signaling pathways. Classical cadherins (e.g. E-cadherin and N-cadherin) are the best studied members of this family. The role of cadherins in insect oogenesis has been investigated in *Drosophila* showing the importance of E-cadherin in (i) anchoring germline stem cells to their niche at the top of the germarium and (ii) in organizing follicles. The differences in ovary function between the female castes stimulated us to study the expression and localization of cadherins in honey bee oogenesis.

Materials and Methods: Indirect immunofluorescence analyses were performed with a polyclonal primary antibody against pan-cadherin. Nuclear DNA was labeled with Hoechst 33252. The expression of classical cadherins and of some protocadherins in honey bee ovaries was investigated by RT-PCR.

Results: Cadherins were visualized in the cytoplasm of trophocytes, oocytes and follicle cells and concentrated in focal points inside the nuclei of trophocytes and follicle cells. The immunolabeling results indicate additional functions for cadherins in somatic and germline cells, besides intercellular adhesion, such as a possible role in a signaling pathway between the plasma membrane and the nucleus. The expression of honey bee orthologs for E-cadherin and N-cadherin and of the protocadherins Fat, Fat-like and Starry Night was confirmed by RT-PCR and verified by sequencing of the amplification products. To our knowledge, this is the first report on a nuclear localization of classical cadherins in insects and of the expression of protocadherins in the context of gametogenesis.

Financial support: FAPESP and CAPES

POSTER PRESENTATION

Biology and determination of temperature requirements in *Tamarixia radiata* (Hymenoptera: Eulophidae)

José Roberto Parra, Mariuxi Torres

University of Sao Paulo, ESALQ, Piracicaba, Brazil

Introduction: The objective of this study was to determine ideal conditions for *T. radiata* development under laboratory conditions, allowing its effectiveness to be evaluated in the citrus-growing regions of the State of São Paulo.

Methods: Fifth-instar *D. citri* nymphs were offered for parasitism by *T. radiata* during a 24-hour period at 25 ± 1°C. After that period, the nymphs were transferred to incubators adjusted to 18, 20, 22, 25, 28, 30, and 32°C, RH: 70 ± 10%, and a 14-hour photophase. Three hundred nymphs were observed at each temperature, divided into 10 replicates containing 30 nymphs per plant.

Results: Parasitism by *T. radiata* had values ranging between 56.6 and 90%. In the various treatments, emergence remained between 55.6 and 80.2%; temperature did not have a significant effect on sex ratio, with values of 0.8±0.10. Based on development velocity at the temperatures studied for the egg-adult period of the parasitoid, the lower temperature development threshold (Tb) and thermal constant (K) were determined, with values of 7.13°C and 188.7GDD, respectively, and a coefficient of determination (R^2) of 94.7, which attests to the reliability of the results obtained.

Conclusions: By observing aspects of the interaction between *T. radiata* and *D. citri*, the data obtained can be useful to support mass production and estimate the number of generations of the parasitoid in order to implement a biological control program within *D. citri* management in ecologically distinct regions under our conditions.

POSTER PRESENTATION

Field validation of a temperature requirements model obtained in the laboratory for *Diaphorina citri* Kuwayama (Hemiptera: Psyllidae).

José Roberto Parra[1], Dori Nava[2], Mariuxi Torres[1]

[1]University of Sao Paulo, ESALQ, Piracicaba-SP, Brazil, [2]Embrapa Clima Temperado, Pelotas-RS, Brazil

Introduction: The confirmation that *Diaphorina citri* transmits the bacterium that causes greening has been a reason for concern among professionals involved in the citrus production chain in Brazil, since this is considered one of the most important citrus diseases worldwide. The objective of this study was to validate a laboratory temperature requirements model under field conditions.

Methods: Air temperature was used in the growing degree-day linear model determined for the insect under laboratory conditions. The number of growing degree-days accumulated for *D. citri* development was determined by the daily sum of thermal units above the base temperature (13.5ºC), using *Citrus limonia* (rangpur lime) and *Murraya paniculata* (orange jessamine) plantlets as food. The thermal constant value (K) was used to predict the occurrence of the insect, based on the mean air temperature values recorded during the experimental period. The data were compared by the overlapping confidence intervals technique at 0.05 probability.

Results: The sum of growing degree-days (GDD) obtained in the field from the mean daily temperature for the biological cycle (egg-adult) of *D. citri* was lower than the quantity of degree-days determined in the laboratory. The degree-day totals obtained in the field for *D. citri* reared on *C. limonia* (rangpur lime) and *M. paniculata* (orange jessamine) were 167.8 and 171.1, amounting to differences of 43.2 GDD (20.5%) and 39.8 GDD (18.9%), respectively, in relation to the laboratory-estimated value of 210.9 GDD. In both citrus and orange jessamine, the confidence intervals calculated for the field model did not overlap the laboratory model, indicating an apparent inadequacy.

Conclusions: The temperature requirements model obtained in the laboratory using constant temperatures (linear model $y = 0.004741x - 0.064134$) was not adequate to predict the occurrence of *D. citri* in the field.

POSTER PRESENTATION

Climate change alters phenology and abundance in butterflies and dragonflies

Luc De Bruyn, Geert De Knijf, Dirk Maes

Research Institute for Nature and Forest, Brussels, Belgium

Phenology refers to the study of seasonal appearances and timing of life-cycle events. Phenological activities of ectotherm animals are influenced by environmental temperatures. It is hypothesised that, due to increasing temperatures, spring activities will shift forward in time while autumn activities will occur later in the year. In the scope of the Flemish Nature Report, we analyse flight periods of butterflies and dragonflies. To assess flight periods, we used the data collected between 1980 and 2006 by volunteers of the Flemish butterfly and Flemish dragonfly working groups. These data were related to temperature data collected over the same period by the Belgian Royal Meteorological Institute. Overall, the flight period in most butterfly species changed over 26 years. Early generations generally shifted forward in spring; late generations occur later. Some species did not change. In dragonflies, the flight period did not change over time for most species. Annual flight period is correlated with temperature in 20 of the 23 species tested in butterflies and in 18 of the 22 tested dragonflies. Species where the flight period extended also showed an increased abundance over the same time span.

POSTER PRESENTATION

Activity of *Cordulegaster erronea* (Odonata: Cordulegastridae) studied using Radio-Tracking and Mark-Resighting techniques

David Moskowitz, Michael May

Rutgers University, New Brunswick, New Jersey, United States

Cordulegaster erronea is a large dragonfly confined to small forested streams in temperate eastern North America. Males patrol along the streams, apparently seeking females, while females fly in briefly to oviposit. We placed miniature radio-transmitters on 5 males and 1 female during July and August 2006 and relocated them 2-4 times per day for up to 15 days. Individuals apparently spent the great majority of their time in the tree canopy within an area of about 75 Ha centered on the study stream. During these intermittent observations, only one radio-tagged male was observed to return to the stream. During July and August of 2007, we and several assistants individually marked males using a coded pattern of paint dots on the wings. Up to 17 separate individuals per hour were resighted from a single station during peak activity. Despite frequent but very brief aggressive interactions, males gave no indication of territoriality. The apparent tenure of individual males was commonly less than ½ hour, at any given stream reach that we monitored, although some males did reappear at different reaches or even on another small stream about 800 m away. Females were observed very rarely and successful tandem formation only once on the stream in 2007. Given the brief tenure of both males and females at the stream and the long periods spent in the canopy, we consider the existence of alternate mating strategies by both sexes deserves investigation.

POSTER PRESENTATION

Predators associated with citrus blackfly *Aleurocanthus woglumi* Ashby (Hemiptera: Aleyrodidae), in the area of Manaus, Am

Maiara Gonçalves, Márcia Pena, Neliton Marques

Universidade Federal do Amazonas, Manaus, Brazil

Introduction: The citrus blackfly (*Aleurocanthus woglumi* Ashby) is an important citrus plague of Asian origin. Recently introduced in Brazil, was detected for the first time in Belem/PA in 2001. In Manaus this plague was detected in 2004. In various parts of the world biological control has been most efficient than chemical control; with the use of parasitoids, predators and entomopathogenic fungus.

Methods: The collects were realized fortnightly. Were sampled 20 plants of citrus (4 quadrants per plant). For the survey of parasitoids, were collected citrus leaves infested with blackflies. These were conditioned in Petri dishes, covered with pierced plastic and conditioned in B.O.D. (26±2℃; 80% UR) until the emergency of adults. The predators were collected manually.

Results: Were registered 11 specimens of predators from the Neuroptera order associated to nymphs colonies of citrus blackfly. The species identified were: *Ceraeochrysa ubana, Ceraeochrysa cincta, Ceraeochrysa claveri, Ceraeochrysa sanchezi, Leucochrysa (Nodita) sp,* mainly during the raining season, and two specimens of parasitoids from the Hymenoptera order, Signiphoridae family.

Conclusions: It is possible that the low rates of natural enemies are due to the relationship, not established yet, between the blackfly and its predators and parasitoids.

POSTER PRESENTATION

Ficus trees and shrubs under attack – thrips, scales, and whiteflies

Catharine Mannion

University of Florida, Homestead, Florida, United States

The genus, *Ficus*, consists of over 800 species, several of which are desirable interior foliage plants. Although most ornamental figs are trees, a few are shrubs or vines. Ficus are native throughout the tropics with a few species extending into the warm temperate zone. The ornamental industry in Florida produces numerous species and cultivars of ficus which are sold in a wide range of sizes. Ficus trees and shrubs are also a common landscape plant in south Florida. In Florida, insect pest problems on ficus have been relatively few, however, recent pest introductions and outbreaks of previously introduced pests are causing much concern to the industry. Most recently a whitefly, *Singhiella simplex*, was identified attacking many of the ficus species in south Florida, causing massive defoliation and branch dieback. This whitefly in conjunction with other introduced pests such as *Gynaikothrips uzeli*, *Ceroplastes rusci* (ficus wax scale), *Pulvinaria psidii* (green shield scale) and most recently, *Horidiplosis ficifolii* (gall midge), are causing severe damage and potential plant loss in the landscape as well as to the nursery industry. Investigations on the presence and impact of natural enemies have been conducted for the whitefly and thrips. The distribution, biology and management of these pests in Florida will be presented.

POSTER PRESENTATION

Oviposition sites of three generalist predators in non-crop vegetation adjacent to cotton fields

Ingrid Rencken[1], Letitia Silberbauer[2]

Department of Primary Industries & Fisheries, Toowoomba, Queensland, Australia

Introduction: Non-crop vegetation which provides oviposition sites for generalist predators is an important resource, particularly in ephemeral cropping systems. The oviposition sites of three generalist predators were identified through sampling the non-crop vegetation surrounding cotton fields.

Method: Dry-land pastures, a travelling stock route, dry-land lucerne and a planted native windbreak were sampled using a suction sampler. The presence of immature and larval stages of generalist predators was used as indication of oviposition sites.

Results: Larval stages of generalist predators were collected in the non-crop vegetation during winter and early spring before planting of the cotton crop. There appeared to be a correlation between plant species and capture of different species of juvenile generalist predators.

Conclusion: Non-crop vegetation adjacent to crops is an important resource providing oviposition sites for generalist predators, particularly in ephemeral cropping systems. A range of vegetation types is needed to support a suite of generalist predator species.

POSTER PRESENTATION

Using differential responses to light spectra as a push-pull control strategy for wood borers and bark beetles

Stephen Pawson, Michael Watt

Scion, Christchurch, New Zealand

Wood borers and bark beetles are globally significant quarantine pests of export timber. Insect are known to have strong responses to ultra-violet light and weak responses to other regions of the visible spectra. In a two part experiment we ascertained the least attractive light spectra to wood borers and then tested a push-pull strategy that takes advantage of these differential spectral responses to control unwanted insect species at wood processing or transfer facilities.

Yellow light was the least attractive spectrum to wood borers with more than an order of magnitude fewer individuals caught than ultra-violet light. The push-pull strategy was implemented to test the effect of commercially available lamps and was simulated in recent clearfells rather than manipulating light at processing facilities. Metal halide (white light) and both high and low-pressure sodium (two yellow lamps) were tested to determine which attracted the fewest individuals thus representing a 'push' component and ultra-violet lamps were used to attract unwanted insects to kill traps. Both high and low-pressure sodium lamps attracted fewer individuals than the metal halide lamps for the *Prionoplus reticularis* (Cerambycidae), however the results for *Arhopalus ferus* were less clear and we propose a behavioural interaction between the two species as the cause. Ultra-violet pull traps were successful in reducing the catch of beetles in adjacent non-illuminated control traps.

The results show that visual cues can be used successfully in a push-pull strategy for controlling insect populations; additional trials are required on a greater range of quarantine insects.

POSTER PRESENTATION

Insecticidal activities of basil oil, *trans*-anethole, estragole, and linalool to adults of *Ceratitis capitata*, *Bactrocera dorsalis*, and *B. cucurbitae*

Chiou Ling Chang[1], Il Kyu Cho[2], Qing Xiao Li[2]

[1]USDA-ARS, Honolulu, Hawaii, United States, [2]Department of Molecular Biosciences and Bioengineering, University of Hawaii, Honolulu, Hawaii, United States

Basil oil, *Ocimum basilicum* Linn, and its three major active constituents, trans-anethole, estragole, and linalool, were tested on three tephritid fruit fly species for insecticidal activities. The insecticidal action of basil oil, linalool, *trans*-anethole, and estragole is very fast and follows a very steep dose-response relation. The 90% lethal times (LT_{90}) of the three tephritid fruit fly species under 10% of these test chemicals were 8-38 min. The action of basil oil is faster to *C. capitata* than to *B. dorsalis* and *B. cucurbitae;* estragole is faster to *B. dorsalis* than to *C. capitata* and *B. cucurbitae;* linalool is faster to *B. dorsalis* and *C. capitata* than to *B. cucurbitae;* and *trans*-anethole is similar to all three species. When linalool was mixed with cuelure (attractant to *B. cucurbitae* male), its potency to the three fly species decreased as the concentration of cuelure increased, which was confirmed by chemical analysis, due to linalool hydrolysis catalyzed by acetic acid from cuelure degradation. When methyl eugenol (*B. dorsalis* male attractant) was mixed with basil oil, *trans*-anethole, estragole or linalool, it did not apparently reduce the mortality of *B. dorsalis* from both basil oil and linalool, but did significantly decrease the mortality from *trans*-anethole and estragole. Structural similarity between methyl eugenol and *trans*-anethole and estragole suggests that methyl eugenol might compete with *trans*-anethole and estragole at the same action site and serve as an antagonist if a distinct action site would exist. Methyl eugenol may also play a significant physiological role on the toxicity reduction.

POSTER PRESENTATION

Santocellus, a new genus of green lacewings (Neuroptera: Chrysopidae: Leucochrysini) from South America

Catherine Tauber[1], Maurice Tauber[1], Gilberto Albuquerque[2]

[1]Cornell University, Ithaca, NY, United States, [2]Universidade Estadual do Norte Fluminense, Campos dos Goytacazes, RJ, Brazil

Introduction: Among the six previously recognized genera of Leucochrysini, five are very small and well defined. However, the sixth, *Leucochrysa*, encompasses a large array of species (approx. 200 described and several more undescribed) that are united only by the lack of features that distinguish the other genera. As an initial step towards revising and subdividing *Leucochrysa*, here we used a broad approach, including characters from both the adult and larval stages, to describe a new genus with three species.

Results: *Santocellus atlanticis* gen. et sp. nov. and *Santocellus riodoce* (Tauber) comb. nov. are from the Atlantic Forest of Brazil; *Santocellus bullata* (Tauber) comb. nov. is from Peru. The adults of the three species, as well as the larvae of the first two (the third is unknown), share a distinguishing suite of features: wings with dark (sometimes pustulate) markings; males with an elongate, cylindrical mediuncus and stiff membrane below; females with round, doughnut-shaped spermatheca having a shallow invagination and a sail-shaped velum that extends anteriorly; larvae with discrete, longitudinal head markings, short mandibles, broad labial palpi, and short, stubby, ventrally projecting terminal palpomeres.

Conclusion: recent descriptions of the larvae of several genera of Leucochrysini have demonstrated the value of larval characteristics in deciphering generic relationships within this tribe. Without such knowledge, the three species that now comprise the new genus *Santocellus* would have fallen within *Gonzaga* Navás or *Leucochrysa* (subgenus *Leucochrysa*) McLachlan.

POSTER PRESENTATION

Influence of ants on arthropod communities in vineyard

Chee Seng Chong, Linda J. Thomson, Ary A. Hoffmann

Centre for Environmental Stress and Adaptation Research, Department of Zoology, University of Melbourne, Parkville 3010, Australia

Introduction: Ants are highly dominant and have a significant role in structuring arthropod communities in many agroecosystems. They are often implicated in interfering in control of pests by natural enemies. Manipulative experiments were conducted to determine the impact of ants on arthropod diversity in canopy and ground within a vineyard.

Methods: Ants were excluded from vine canopy in randomly assigned row sections with Tacgel. Arthropods were sampled in treatment (ant-excluded) and control vines with beat-and-collect method, yellow sticky and pitfall traps over several occasions. Egg cards of light brown apple moth, the dominant insect pest in vineyards in southeastern Australia, were also placed to determine that effect of ants on egg parasitism and mortality.

Results: A higher ground ant foraging activity was present in ant-excluded vines. There were more spiders in ant-excluded vines. Differences were also detected for other groups but these were complex and depended on the month of sampling.

Conclusions: Preliminary findings indicate ant effects on other arthropods but these are complex and change over time.

POSTER PRESENTATION

Vegetation effect on spatial distribution of ants in vineyards

Chee Seng Chong, Linda J. Thomson, Ary A. Hoffmann

Centre for Environmental Stress and Adaptation Research, Department of Zoology, University of Melbourne, Parkville 3010, Australia

Introduction: The spatial distribution of ants within a landscape is influenced by interplay of many factors including competition, habitat preferences, environment heterogeneity and stochastic processes. Here, we investigate the influence of adjacent vegetation on the spatial distribution of ground-dwelling ants within vineyards.

Methods: Ants were sampled with pitfall trappings that were placed in either random or systematic arrangements in several vineyards that had adjacent vegetation (remnant forest patches or complex shelterbelts). The x- and y-coordinates at each sampling point, ant species and their abundance were recorded. Data were analysed using Spatial Analysis by Distances IndicEs (SADIE) to determine dispersal or aggregation of ant species and spatial maps were generated.

Results: Ant richness was relatively high (30-50 species within a hectare) in vineyards surveyed with several species only found close to adjacent vegetation. Spatial maps showed that the distribution of ant genera and species were significantly aggregated and ants occupied spatially-exclusive patches with dominant *Iridomyrmex* ants being negatively associated with other ant genera. In particular, *Rhytidoponera* species were found to be closely associated with adjacent vegetation suggesting the role of adjacent vegetation in modifying habitats that are suitable for particular ant species and thus modifying competitiveness.

Conclusions: The presence of significant patches and gaps demonstrated the role of interspecific competition in structuring ants' spatial distribution. However, the distribution of some ants especially *Rhytidoponera* species close to vegetation clearly suggested the importance of adjacent vegetation in enhancing a species advantage over another.

POSTER PRESENTATION

Analysis of the sex pheromone composition of the variegated cutworm (*Peridroma saucia*) in Korea

Kyung San Choi, Jum Rae Cho, Jeong Heub Song, Doon Soon Kim, Kyung Saeng Boo

National Institute of Subtropical Agriculture, Jeju, Republic of Korea

Introduction: In Korea, the variegated cutworm, classified as a quarantine pest insect by Korean National Plant Quarantine Service, was first discovered at Mudeung Mountain and in Jeju Island in 1996. Since then, the damage by *P. saucia* was found in carrot, corn, cabbage, and citrus in Jeju. The goal of this study was identifying the sex pheromone composition and applying it to monitor the population fluctuation of *P. saucia* in Korea.

Method: Calling and mating behavior of female *P.saucia* was investigated during scotophase under 16L:8D photoperiod and 25□±1 temperature. The extract of female sex pheromone glands was analyzed with GC-MS and then GC-EAD test was conducted. EAG test of male antennae was investigated on sex pheromone analogues and a series of dose of their own sex pheromone components. Changes of amount of sex pheromone components biosynthesized in a sex pheromone gland were analyzed with GC. Field attraction test was conducted with a series of sex pheromone blend at Milyang and Snaggui.

POSTER PRESENTATION

Isolations of new *Bacillus thuringiensis* strains with high toxicity to *Spodoptera litura* (Lepidoptera: Noctuidae)

Da-A Kim, Mi-Ra Kil, Seung-Kyoung Baik, Jin-Su Kim, Su-Yeon Choi, Da-Yong Jin, Jang Hyun Hur, Yong-Man Yu

[1]Chungnam National. Uni., Daejon, [2]Kangwon Nat'l Univ., Chuncheon, Republic of Korea

New strains of *Bacillus thuringiensis* with high toxicities against the tobacco cutworm, *Spodoptera litura* (Lepidoptera: Noctuidae), were isolated and selected from several kinds of domestic soils. Sixteen *B. thuringiensis* strains were isolated from 12 among 142 soil samples. Among 16 *B. thuringiensis* isolated strains, 11 strains have toxical activities against *Plutella xylostella* (Lepidoptera: Yponomeutidae), 7 strains on *Spodoptera litura* (Lepidoptera: Noctuidae), 5 strains on *Spodoptera exigua* (Lepidoptera: Noctuidae), 5 strains on *Arcte coerulea* (Lepidoptera: Noctuidae), and 5 strains on *Culex pipiens pallens* (Diptera: Culicidae). When being examined with a phase-contrast microscope, the insecticidal crystal proteins were observed. These crystal proteins were produced from selected strains; 13 strains showed bipyramidal crystal protein shapes and other 3 strains showed spherical shapes. As results of identifying by H serotype, 13 strains separated among 16 strains, 1 strain was showed *ostriniae* (8ac), 8 strains were *kurstaki* (3abc), 3 strains were *aizawai* (7) and 1 strain was *colmeri* (21). On the other hands, insecticidal activities were examined against 3rd larva of *S. litura* with new strains and existing ready-made products. CAB109 strain of *B. thuringiensis aizawai* showed 100% mortality with 1.3×10^7 spore concentration (cfu/ml). LC_{50} values of CAB109 strain of *B. t. aizawai* were 9.78×10^5, 6.87×10^6 and 1.83×10^7 spore concentration (cfu/ml) against 2nd, 3rd and 4th larva of *S. litura*, respectively. It was a very high insecticidal activity compared with existing ready-made *B. thuringiensis* products. Unlike *P. xylostella, S. litura* was slowly died up to 7 days after application at same concentration.

POSTER PRESENTATION

Electronic noses for the detection of flystrike in sheep

Andrew Cramp[1], Jae Ho Sohn[2], Peter James[1]

[1]Animal Research Institute, Department of Primary Industries and Fisheries, Yeerongpilly, Queensland, Australia, [2]Sustainable Intensive Systems, Department of Primary Industries and Fisheries, Toowoomba, Queensland, Australia

Introduction: Cutaneous myiasis (flystrike) is a debilitating, painful and potentially lethal disease of sheep. In Australia, South Africa and New Zealand the principal agent of myiasis is *Lucilia cuprina* (Wiedemann). Early detection of flystrike is difficult and continual flock surveillance is required to enable timely treatment of struck sheep. Electronic nose technology offers the potential for the early and remote detection of flystrike.

Methods: Two electronic noses were evaluated, one an array with six metal oxide semiconductor sensors chosen on the basis of GC-MS flystrike odour profiles and the other, a non-specific gas sensor array of 24 metal oxide semiconductor sensors. Odour samples were collected by dynamic headspace sampling from the sheep's back before and during flystrike development and from urine- and faeces-stained fleece. Conventional statistical analyses and chemometrics were used for data pre-processing and model development to discriminate strike and excrement odours from dry fleece.

Results: Both electronic noses accurately discriminated the odours of day 1, 2 and 3 flystrike from that of dry wool. Both successfully distinguished urine staining from dry wool and strike and faeces staining from strike, but not dry wool. The accuracy of prediction of the best sensor array was 96.8%, 100%, 98.3%, and 98.4%, for strike on days 0 (day of implant), 1, 2 and 3 respectively.

Conclusion: This study provides proof of concept for the detection of flystrike using electronic nose technology. Suitable detection algorithms and methods for collection of odour in the field will be required for development to practical application.

POSTER PRESENTATION

Pathogenicity of entomopathogenic nematodes to sheep lice (*Bovicola ovis* Schrank)

Peter James, Stacey Hook, Andrew Cramp

Animal Research Institute, Department of Primary Industries and Fisheries, Yeeronpilly, Queensland, Australia

Introduction: Alternatives to chemical methods for controlling sheep lice are required to address resistance in sheep louse populations and increasing 'eco-consciousness' amongst consumers and sheep producers worldwide. Entomopathogenic nematodes (ENs) have been referred to as 'pesticides with the power of search' and have particular advantages against pests in cryptic habitats, such as the fleeces of sheep, where it is difficult to directly contact the target pest with conventional pesticides.

Methods: Laboratory assays were conducted with *Steinernema carpocapsae* (ALL strain), *S. feltiae* (NJ), *Heterorhabditis bacteriophora* (Otio) and *S. riobrave* to test their pathogenicity to lice at different temperatures and confirm their ability to infect *B. ovis* when applied to wool. Preliminary studies with *S. carpocapsae* applied to sheep were carried out to test their longevity in the fleece and effectiveness in reducing louse numbers.

Results: Infective juvenile nematodes of all species were able to move along wool fibres to infect and kill lice when applied to wool in solution with Tween80 at 25°C. At temperatures above 30°C only *S. carpocapsae* and *S. riobrave* caused significant mortality. Treatment of louse-infested sheep with *S. carpocapsae* reduced louse numbers by 89.8% at 11 days after treatment. Live nematodes were recovered from the fleeces of treated sheep for up to 20 days, but baiting studies suggested significant infectivity for only 6 days.

Conclusion: To our knowledge this is the first report of the use of direct animal application of ENs to control ectoparasites and the first report of pathogenicity of ENs to chewing lice.

POSTER PRESENTATION

The arthropod fauna of Bt corn, hybrid corn, and sweet corn

Bonifacio Cayabyab[1], Wilma Cuaterno[2], Edwin Alcantara[3], Pablito Gonzales[1], Josemari Belen[1]

[1]National Crop Protection Center-Crop Protection Cluster, Los Baños, College, Laguna, Philippines, [2]Crop Protection Division, Bureau of Plant Industry, San Andres, Manila, Philippines, [3]Institute of Biotechnology, UP Los Baños, Los Baños, College, Laguna, Philippines

The information on the arthropods fauna of Bt corn and other varieties of corn in the Philippines is not updated. There are very few studies conducted on this subject matter recently. This study was conducted at Lubao, Pampanga, Philippines from February 2008 – May 2008. The study aims to generate data on the arthropods fauna on the three most common varieties planted in the locality and these are Bt corn (Pioneer 30b80YG), sweet corn (SG 75) and hybrid corn (Bioseed 900). It will elucidate the pest and natural enemies and damages on these varieties during the various growth stages.

A randomized complete block design on a one thousand two hundred square meters field was used. Each variety was planted on a 120 sq m area replicated three times. Standard agronomic practices were done. Monitoring of arthropods was thru sticky traps, pitfall traps and sweep net. Damages were recorded on plants within the 50 sq m plot located at the middle of its replicate. There were very few arthropods at three leaves stage and no damages were recorded. The study is on-going and the results with statistical analysis will be presented.

POSTER PRESENTATION

Climate change and its effect on the migratory locust, *Locusta migratroria manilensis* Meyen (Orthptera: Acrididae), population in the Philippines

Bonifacio Cayabyab, Pablito Gonzales, Melvin Ebuenga

Plant and Environmental Health Division Crop Protection Cluster, UP Los Baños, College, Laguna, Philippines

Climate change particularly elevated temperature or increased warming due to El Niño can greatly affect the population of the migratory locust, *Locusta migratoria manilensis* Meyen in the Philippines. This phenomenon causes prolonged dry spell and widespread drought resulting to the formation of patches of green vegetation in certain areas wherein the migratory locust congregate and multiply. Gregarization follows that eventually lead to migration.

Migratory locusts devastated rice, corn and sugarcane in Central Luzon (1996-2000), it threatened the sugarcane growing areas of Negros Island (2000-2002) while population build-up in various islands of the archipelago were observed from 2003-2006. Just recently, a prolonged dried spell in the Fuga Island, the located at the tip of Northern Luzon from October 2006 resulted to the population build-up and destruction of rice crops in the island in December 2006 – January 2007. It is now imperative to do a risk assessment of the various islands by using climate change models. The temperatures during the last 50-100 years could be used in developing population simulation models. The result can be used to issue early warning pest advisories. Technicians and farmers must be trained to monitor population build-up and massive information campaign for community efforts to control outbreaks should be done. The government must allocate funds for information campaign and community based locust management. ASEAN member countries should be forewarned since the *Locusta migratoria manilensis* has the ability to fly long distances.

POSTER PRESENTATION

Impact of glyphosate-resistant soybean weed management on abundance and taxonomic composition of arthropods in Missouri soybeans

Clinton Meinhardt[1], Wayne Bailey[1], Thomas Clark[2]

[1]University of Missouri, Columbia, Missouri, United States, [2]Monsanto Corporation, St. Louis, Missouri, United States

Introduction: Glyphosate-resistant soybeans, *Glycine max* (L.) Merr., enables flexibility in the timing of weed removal from the soybean agroecosystem. The wide adoption of this weed management technology in the USA has the potential to alter the occurrence and timing of winter annual and spring germinating weeds. Changes in weed dynamics may result in changes in the abundance and taxonomic composition of arthropods in the soybean agroecosystem

Methods: Field studies were conducted in Missouri to investigate how arthropods are affected by glyphosate-resistant soybean weed management when exposed to four different weed removal times and four weed species compositions. Sweep net and pitfall collection methods were used to estimate numbers of foliar and soil surface dwelling arthropods, respectively.

Results: Sixty percent of arthropod groups investigated were affected by weed management. Arthropods were most influenced by weed removal timing and exhibited preferences for either weedy soybean habitats with delayed weed removal or soybean habitats with reduced weed density from early weed removal. Ground-dwelling arthropod populations, were supported by increased weediness. Carabidae were 1.5 – 2 times more abundant in the weediest treatment (season-long mixed grass and broadleaf weeds) than in the weed-free control treatment. Soybean habitats with prolonged weediness supported 10 of the 15 foliage-dwelling arthropod groups with significant weed removal timing effect results, including the total natural enemy and phytophagous arthropod groups.

Conclusion: Glyphosate-resistant soybean weed management impacts the taxonomic composition and abundance of arthropods in soybean agroecosystems; however yield disadvantages associated with increase arthropod numbers have yet to be elucidated.

POSTER PRESENTATION

Effects of sugar availability on the mating behaviour of *Anopheles gambiae* (Diptera: Culicidae)

Chris Stone, Robin Taylor, Woodbridge Foster

The Ohio State University, Columbus, Ohio, United States

Sugar is the only source of energy for adult male mosquitoes, but the extent to which the lack of opportunities to sugar feed impacts a cohort of males' ability to inseminate female mosquitoes is unknown. We report here on an investigation on the impact of sugar availability on the mating performance of male *Anopheles gambiae* in both mesocosms and in cages.

Over a ten day period, each day twenty male and female mosquitoes were allowed to emerge into mesocosms; enclosures with simulated natural conditions, and cages. Sugar was either absent or present in the form of 10% sucrose solutions. Every night female mosquitoes were given the chance to blood feed. After 10 days all surviving mosquitoes were inspected for insemination.

In the mesocosms 10.9% of the females were inseminated when sugar was not available, against 49.7% when sugar was present. Enclosure size also influenced insemination rates; in the cages 23.5% of the females were inseminated in the absence of sugar, whereas 76% were inseminated in the presence of sugar. No significant differences in biting activity were discovered. Survival of females after ten days was 51.6% with sugar, and 25.6% with water only in the mesocosms. In the cages female survival was 95% with sugar and 73% without.

We conclude that insemination capability of males in the absence of sugar sources is greatly diminished but not completely absent under semi-field conditions, and stress the importance of using an appropriately scaled experimental system for behavioural studies of this medically important species

POSTER PRESENTATION

Phylogeny analysis of Thripidae based on 28S rDNA

Wen-Bin Yeh, Mei-Rong Tseng

National Chung Hsing University, Taichung, Taiwan, Taiwan

The nuclear 28S rDNA sequence has been widely used in higher phylogenetics of Insecta, but has seldom been applied to thrips. In this study, ~3000 bp of 28S rDNA sequences from 45 Thripinae and three Panchaetothripinae were used to probe the essence of this gene and its applicability to the delineation of phylogenetic relationship of these species. Sequences of 28S rDNA across thrips, though with variable region, were not randomly distributed, with the expansion segments being more variable than the core regions and with an increasing sequence divergence with taxonomic distances. Scatter plots of total substitutions (Tvs) against transversions (Tv) or transitions (Ts) in 28S region revealed similar and linear evolving processes for both Tv and Ts. Sequence divergence of the 28S rDNA region of 30 species among 48 individuals was less than 1.2% within species, and that among species in a given genus was 0.7-15 %, that among genera in the same subfamily was 5-20 %, and that between subfamilies was 14-20%. Phylogenetic inferences from both parsimony and clustering methods suggested members of the same subfamily and genus were grouped together except *Thrips* genus. Analyses of the nearly complete sequences of thrips 28S rDNA have shown that its expansion region may be more useful in the resolution of lower taxonomic relationship, and its core region may be more reliable for that of higher category.

POSTER PRESENTATION

Indo-Australian Aleyrodidae (Whiteflies): A molecular analysis of phylogenetic relationships

Paul DeBarro[1], Rosemarie C. Rosell[2], Heather S. Costa[2], Donald R. Frohlich[3]

[1]CSIRO, Brisbane, Queensland, Australia, [2]University of St. Thomas, Houston, Texas, United States, [3]University of California, Riverside, California, United States

Two nuclear DNA sequences (D2 and 18S) were used to reconstruct the phylogeny of 89 species of whiteflies in over 40 Indo-Australian Aleyrodid genera. Four methods were applied: distance, parsimony, maximum likelihood, and a bayesian technique. Herein we discuss relationships between the genera and compare the utility and differences of the four analytic approaches with relationships based on morphological characteristics of puparia.

POSTER PRESENTATION

Nutritional factors influencing whitefly development in a hydroponic system

Jacquelyn Blackmer, Lynn Forlow Jech

US ALARC-ARS-USDA, Maricopa, Arizona, United States

Introduction: Whiteflies are phloem feeders and encounter some of the lowest levels of N found; however, they manage to excel due to behavioral and physiological modifications. Understanding how fluctuations in their diet influence their life-history traits could provide us with novel means of controlling this major pest.

Methods: We used hydroponic units to deliver known quantities of macronutrients or macro- and micronutrients at three concentrations. Bollguard II® cotton was grown in rockwool media, and nutrients were supplied via a drip system. The influence of different nutrient regimes on plant attributes (height, basal diameter, and petiole NPK) and whitefly life-history traits (oviposition preference, developmental time, emergence rates, and adult weights) were measured. Whiteflies were placed on the 3rd (vegetative), 6th (pinhead square) and 9th (flowering) true leaf and allowed to oviposit for 48-h. Subsequent development was monitored.

Results: Plants provided with macronutrients were taller and had larger basal circumferences under the medium and high nutrient regimes, but when macro- and micronutrients were supplied, no differences relative to nutrient levels were observed. Petiole analysis indicated fluctuations in NPK were correlated with plant phenology and nutrient levels. Whiteflies deposited twice as many eggs on plants that were supplied with both macro- and micronutrients, and female weights decreased with leaf age; however, few other parameters showed a response to nutrient regime or nutrient levels.

Conclusions: Plant attributes and whitefly oviposition were influenced by nutrient regimes and levels, but few other whitefly life-history parameters showed a clear response. Additional studies are underway to better define these relationships.

POSTER PRESENTATION

Superoxide dismutase activity in temperature stressed viruliferous whiteflies (Hemiptera: Aleyrodidae)

Rosemarie C. Rosell[1], Arsalan Shah[1], Mudasser Khan[1], Niloufar Aghakasiri[1], Robert S. Jr. Shatters[2], Cindy L. McKenzie[1]

[1]University of St. Thomas, Houston, Texas, United States, [2]USDA, ARS, Horticultural Research Laboratory, Ft. Pierce, Florida, United States

Whiteflies' remarkable ability to transmit and spread begomovirus diseases has had an immense impact on global food production and thus they have become one of the most serious crop pests throughout much of the world. Our hypothesis is that the ability of the whitefly to survive under extreme temperature conditions is related to the regulation of the enzyme, superoxide dismutase (SOD). The purpose of our study is to determine the relationship between stress, virus infection and SOD activity. SOD functions in the conversion of O_2^- free radicals to less toxic products. Superoxide free radicals bind to macromolecules in cells and may lead to breakdown of cellular membranes. Previously, we have shown under normal metabolic conditions the presence of superoxide dismutase in *Bemisia tabaci* whole body extracts. In this study, we determined the effects of temperature stress on whiteflies fed on either begomovirus-infected tomato or healthy tomato plants. Two begomoviruses, tomato mottle virus (ToMoV) and tomato yellow leaf curl virus (TYLCV) were used in the study. We characterized and quantified SOD activity using an electrophoretic assay combined with. a commercially available spectrophotometric assay. Our data showed that SOD activity was directly proportional to an increase in temperature in non-viruliferous whiteflies. However, the SOD activity in whiteflies reared on virus-infected plants was varied. These data were supported by the SOD isozymes observed in the electrophoretic assay. The roles of SOD activity and temperature stress in relation to whitefly interactions with begomovirus in whitefly are discussed.

POSTER PRESENTATION

Dynamic population density of the coconut hispine beetle, *Brontispa longissima* Gestro (Coleoptera: Chrysomelidae)

Sopon Uraichuen, Kittiya Suksen, Wiwat Suasa-ard

National Biological Control Research Center, Central Regional Center, Nakhon Pathom, Thailand

Introduction: The coconut hispine beetle, *Brontispa longissima* Gestro was accidentally introduced into continental Southeast Asian countries, presumably in the early 2000's, with ornamental palms. Since then it become one of the most serious insect pest of coconut in Thailand.

Methods: Dynamic population density study of *B. longissima* was taken place by using 3 coconut fields at Kamphaeng Saen, Nakhon Pathom province in the Central Region of Thailand. Data collection was done twice a month. The sampling program was set by using 5 leaves as a sample unit and 16 samples per location. The number of eggs, larvae, pupae and adults of the beetle were recorded from August 2006 to December 2007. All data were subsequently analyzed and considered with density independent (DI) factors.

Results: Analysis results of the combinative DI factors affected to dynamic population of *B. longissima* indicated that rain volume, temperature and relative humidity caused change of the beetle population. The result revealed that the more rain volume and the less relative humidity, the greater number of egg pest. Meanwhile, temperature was a negative additional effect to the survival beetle larvae. Regard to adult population, the DI factors did not directly make a change in its population. Nevertheless, they could substantially give the lower egg laying rate of the female adult as well as the lesser hatch percentage.

Conclusions: The DI factors, rain volume, temperature and relative humidity which seasonal alter through the year round were the combinative effect to the dynamic change of *B. longissima* population.

POSTER PRESENTATION

Malaria transmission risk and the potential role of microbial larviciding in irrigated rice agroecosystems

Simon Muriu[1], Josephat Shililu[1], John Githure[1], Robert Novak[2]

[1]I.C.I.P.E., Nairobi, Kenya, [2]UAB, Birmingham, AL, United States

Introduction: Irrigated rice agro-ecosystems are associated with high densities of malaria vectors due to expansive open water surfaces conducive for *Anopheles* mosquito breeding. These habitats are amenable to larval control. The use of biological control agents in malaria vector control is becoming popular in Africa with use of two microbial larvicides, *Bacillus thuringiensis* var *israelensis* (Bti) and *B. sphaericus* (Bs). The study evaluated the potential of a new combined Bti/ Bsph microbicide formulation for larval control in rice agroecosystems in Mwea, Kenya.

Methods: Data on *Anopheles* mosquito breeding habitat types and their productivity in space and time in Mwea irrigated rice scheme was collected. Anopheline species abundance and diversity was evaluated based on larval and adult collections. The effect of Bti/ Bs on vector populations was evaluated at village level.

Results: Eleven habitat types were identified with differential mosquito productivity potential during the year. Rice paddies and drainage canals were the most productive especially during the early vegetative stages of rice growth while the other habitats provided ideal breeding areas during rainy seasons. The peak adult vector density expressed as the human biting rates (10.4 bites per person per night) occurred shortly after rice planting. The application of the microbial larvicides significantly reduced larval densities in the study sites confirming its potential for control of the immature stages of anopheline mosquitoes.

Conclusions: *Anopheles* habitats in irrigated systems are differentially productive and application of larval interventions using microbial insecticides has to be time and habitat specific. The new combined Bti/Bsph formulation has shown a potential in reducing malaria vector populations and transmission risk in the irrigated rice agroecosystems.

POSTER PRESENTATION

Insecticide resistance in a major malaria vector from South Africa, *Anopheles arabiensis*

Lizette Koekemoer[1], Joel Mouatcho[1], Basil Brooke[1], Givemore Munhenga[2], Ron Masendu[2], Keith Hargreaves[3], Richard Hunt[4], Maureen Coetzee[1]

[1]NICD, Johannesburg, South Africa, [2]University of Zimbabwe, Harare, Zimbabwe, [3]Malaria Control Programme, KwaZulu/Natal, South Africa, [4]University of the Witwatersrand, Johannesburg, South Africa

Introduction: *Anopheles arabiensis* is a major vector of malaria in South Africa in addition to *An. funestus* and is responsible for seasonal malaria transmission. DDT resistance in a population of *An. arabiensis* in the Mamfene region of Kwazulu/Natal was recorded in 2003. There was no pyrethroid resistance observed in this population at that time.

Methods: *Anopheles arabiensis* originating from Mamfene in 2003 was colonized and a DDT resistant line selected. Wild females were collected during 2005 using exit traps in sprayed houses. Two-day-old adult progeny obtained from these wild females and from the colony were exposed to permethrin, bendiocarb and deltamethrin according to the standard WHO bioassay procedures followed by biochemical and target site analysis.

Results: The DDT resistant strain of *An. arabiensis* showed 25% mortality after 1 hr exposure to DDT. Susceptibility assays on field collected material revealed 63-73% mortality against permethrin. All F1 families tested showed full susceptibility to bendiocarb and deltamethrin. Biochemical analysis showed elevated levels of monooxygenase correlating with the permethrin bioassay data. Although elevated levels of non specific esterases were found in some families, these did not show any correlation to the permethrin bioassay data. F1 progeny were also used to select a pyrethroid resistant laboratory strain in order to characterize the pyrethroid resistance mechanism. Parallel to these studies a bendiocarb resistant line was selected in order to characterize the bendiocarb resistance observed in the *An. arabiensis* strain colonised in 2003. Both these selected lines were analysed using biochemical assays as well as synergists. Molecular analysis revealed no mutations associated with target site insensitivity to insecticide.

Conclusions: Biochemical analyses suggest that the insecticide resistance found in *An. arabiensis* from South Africa is most likely metabolic and does not involve target site insensitivity mutations.

POSTER PRESENTATION

Insecticidal properties of bistrifluron against sycamore lace bug, *Corythucha ciliata* (Hemiptera: Tingidae)

Changmann Yoon, Jeong-Oh Yang, Shin-Ho Kang, Gil-Hah Kim

Chungbuk National University, Cheongju, Chungbuk, Republic of Korea

Bistrifluron, a member of the benzoylphenylurea (BPU) class, was developed in the Republic of Korea as an inhibitor of chitin synthesis. This study examined the effect of bistrifluron on insecticidal activity, adult longevity, fecundity and ovarian development in the sycamore lace bug, *Corythucha ciliata*. The results showed that bistrifluron had no direct effect on the egg, but produced 100% mortality in larvae hatched within 24 hr with a similar effect regardless of the instars of the larvae (LC50_0.01–0.06 ppm). When the final instar was treated with bistrifluron, the emergence rate, adult longevity and reproduction decreased with increasing concentration (up to 100 ppm). With the passage of time after the final larvae had emerged, chemical treatment delayed the preoviposition period of the adults at high concentrations, and decreased adult longevity, fecundity and the hatching rate. Ovarian development of the adult was also inhibited.

POSTER PRESENTATION

On the interactions of whitefly, *Bemisia tabaci* and its natural enemies on different chilli cultivars

Khalid Saeed Aqlan Naser[1], Idris Ghani[2], Mohamad Roff Mohd Noor[3]

[1]Sana'a University, Sana'a, Yemen, [2]Universiti Kebangsaan Malaysia, Bangi, Selangor, Malaysia, [3]Malaysian Agricultural Research and Development Institute, Serdang, Selangor, Malaysia

Introduction: Whitefly (WF) is causing a significant damage to chilli crops in Malaysia. Nevertheless, presence of natural enemies are expected to control their populations but their interactions are yet to be resolved. Temporal and vertical distributions of WF and its natural enemies were assessed on four cultivars of chillies.

Methods: Yellow sticky traps on poles were placed in plots of chilli cultivars in a randomized block design. Trapped WF adults were counted weekly and infested leaves were examined for WF of other life stages and natural enemies.

Results: Infestation rates among cultivars varied periodically with plant maturity causing adult population to tremendously increased through time. Concentration of eggs and larvae were obviously varied, being higher at 63 DAT, whilst lower at 35 DAT. Differences were also observed amongst chilli plant strata of cultivars with upper stratum more infested than the lower stratum. A strong correlation was found between plant height and the WF population. In terms of natural enemies, number of predatory coccinellid viz. *Menochilus sexmaculatus* Fabricius, was significantly higher on infested cultivars. However, the other important coccinellids, *Coccinella transversalis* F. and *Coelophora inaequialis* F. per plant remain lower. The percentage of lacewing and of *Encarsia* sp. were also significantly higher among infested plants. Strong correlations were evident between different life stages of WF and its natural enemies with multilevel interactions.

Conclusion: The study provides a base line data for the interactions of WF with their natural enemies which can be useful in developing the IPM strategies for chilli crops.

POSTER PRESENTATION

Relationship between dehydration rate and success of anhydrobiosis in the sleeping chironomid, *Polypedilum vanderplanki*

Yuichi Nakahara, Gusev Oleg, Masahiko Watanabe, Daisuke Tanaka, Ken-ichi Iwata, Yasushi Kanamori, Cornette Richard, Takahiro Kikawada, Takashi Okuda

National Institute of Agrobiological Sciences, Tsukuba, Ibaraki, Japan

Introduction: Aquatic larvae of the sleeping chironomid, *Polypedilum vanderplanki*, can enter anhydrobiosis, a latent life (ametabolism) without free water. In general, for successful anhydrobiosis, slow dehydration is required to form biological glasses which can provide effective protections against threats such as oxidative stress. It is assumed that degree of damages sustained during desiccation affects survivorship of the larvae.

Methods: *P. vanderplanki* larvae were desiccated by exposing them to different drying regimes, each progressing from high to low relative humidity, and we examined the cell damage and survival rate after rehydration. DNA damages were detected by comet assay.

Results: Without preconditioning at high relative humidities, rapid desiccation caused an immediate death. Exposure to RH 100% for at least 12 h assured to revive after rehydration. Even after the preconditioning, if dehydration rate exceeded 0.7 mg water/day, most of the rehydrated larvae died before reaching the adult form. However, differential scanning calorimetry showed that such larvae formed glasses during desiccation, indicating that vitrification is insufficient for successful anhydrobiosis. To our surprise, considerable DNA-damages occurred even in the larvae dehydrated by an adequate regime. However, number of cells with broken DNA decreased with the course of time after rehydration. Gene expression analysis showed upregulation of proteins involved in reducing oxidative stress and enzymes involved in DNA damage repair.

Conclusion: *P. vanderplanki* larvae suppress accumulation of damages during desiccation to a repairable level for entering successful anhydrobiosis. Unrepairable damages probably cause delayed death.

POSTER PRESENTATION

Susceptibility of ussur brown katydid, *Paratlanticus ussuriensis* (Orthoptera: Tettigoniidae) to commercially registered insecticides

Doo-Jin Noh, Jeong-Oh Yang, Changmann Yoon, Gil-Hah Kim

Chungbuk National University, Cheongju, Chungbuk, Republic of Korea

Insecticidal activity of 33 registered insecticides was tested against last nymphal instars and adults of ussur brown katydid, *Paratlanticus ussuriensis*. All experiments were tested at the recommended concentration of each insecticides by producer. Acephate, chlorpyrifos, diazinon, EPN and fenitrothion which were organophosphates, and a mixture combined with chlorpyrifos+α-cypermethrin showed 100% mortality of *P. ussuriensis*. But fipronil showed only 100% mortality in leaf-dipping method. Carbamates insecticidal groups, benfuracarb and furathiocarb were showed over 80% and phenthoate was 60~80% in mortality of *P. ussuriensis*. Among the mixture, etofenprox+diazinon and esfenvalerate+fenitrothion were showed 60~80% against last nymphal instars of *P. ussuriensis*. Otherwise, acephate, chlorphyrifos, diazinon, EPN and fenitrothion were showed 100% mortality of *P. ussuriensis* within only 24 hours after treatment, but there was no effective after then in residual tests with leaves.

POSTER PRESENTATION

Pathogenicity of the entomopathogenic fungi *Paecilomyces fumosoroseus* and *Lecanicillium* (= *Verticillium lecanii*) against *Trialeurodes vaporariorum*

Samuel Pineda, Marcela-Inés Schneider, Ana-Mabel Martínez

[1]Instituto de Investigaciones Agropecuarias y Forestales. Universidad Michoacana de San Nicolás de Hidalgo., Tarímbaro, Michoacán., Mexico, [2]Centro de Estudios Parasitológicos y de Vectores CEPAVE, La Plata, Buenos Aires., Argentina

Introduction: Entomopatogenic fungi are a promising alternative for the control of agricultural pests. We evaluated the pathogenicity of three isolates of *Paecilomyces fumosoroseus* (Pf_1, Pf_2, and Pf_3) and six isolates of *Lecanicillium* (= *Verticillium lecanii*) (Vl_1, Vl_2, Vl_3, Vl_4, Vl_5, and Vl_{10}) on eggs, second, third, and fourth nymphal instars of the greenhouse whitefly, *Trialeurodes vaporariorum*.

Methods: Pathogenicity tests were performed in the laboratory. For this, fungal applications were made on tomato leaves infested with *T. vaporariorum.* After three days post-treatment, eggs and nymphs were observed daily for eight days to register and confirm mortality caused by fungi. Two field trials were conducted independently with the most infective isolate (Pf_2) on zucchini squash plants. Five fully expanded middle leaves were randomly selected at different times from each replicate and were transported to the laboratory to count all living *T. vaporariorum* nymphs.

Results: Three of the nine isolates (Pf_1, Vl_3, and Vl_5) produced 11-26% infections on eggs, while the remaining isolates had no significant effect. All three *P. fumosoroseus* isolates caused homogeneous pathogenicity in all nymphal instars, while *L. lecanii* isolates showed high variability. In field conditions, survival of whitefly nymphs decreased by 19 and 28% after the first and second fugal applications, respectively, in one trial, and by 62 and 71% in the another trial.

Conclusions: We concluded that the use of fungal preparations based on the Pf_2 isolate could be feasible for controlling *T. vaporariorum*.

This work was supported by the Coordinación de la Investigación Científica, Universidad Michoacana de San Nicolás de Hidalgo and the Programa de Mejoramiento al Profesorado (PTC-110).

POSTER PRESENTATION

Expressed Sequence Tags from cDNA library of the sleeping chironomid (*Polypedilum vanderplanki*) and analysis of mRNAs expression patterns during the induction of anhydrobiosis.

Richard Cornette, Yasushi Kanamori, Kanako Mitsumasu, Oleg Gusev, Takahiro Kikawada, Takashi Okuda

National Institute of Agrobiological Sciences, Tsukuba, Ibaraki, Japan

In the semiarid regions of central Africa, larvae of the sleeping chironomid (*Polypedilum vanderplanki*) are able to survive in a completely desiccated state without any metabolic activity throughout the dry season, which may last for 8 months. This phenomenon is known as anhydrobiosis or cryptobiosis. During anhydrobiosis, trehalose represents ca. 20% of the dry mass of the larva. Loss of free water, accumulation of trehalose and the subsequent vitrification phenomenon are thought to play an important role in the protection and stabilization of cells in anhydrobiotic individuals.

In the laboratory, induction of anhydrobiosis was triggered artificially by slow desiccation for 48 hours and individuals dehydrated in such conditions successfully recovered normal activity after immersion into water.

In order to identify genes involved in the anhydrobiosis of *P. vanderplanki*, cDNA libraries were constructed from normally active larvae (0h of desiccation), larvae during early stage of anhydrobiosis induction (desiccation for 12h) and advanced induction of anhydrobiosis (desiccation for 36h). After sequencing, a total of 15,054 clones were incorporated into an anhydrobiosis-related EST database. Analysis of this EST database allowed the identification of genes up- or down-regulated during the induction of anhydrobiosis. General expression patterns were inferred for important functions such as signal transduction, ion transport or regulation of transcription.

Actual expression patterns were investigated by real-time quantitative PCR for some genes involved in anhydrobiosis such as enzymes from the trehalose synthesis pathway, Late Embryogenesis Abundant (LEA) proteins and aquaporins. The general mechanism of successful induction of anhydrobiosis was finally discussed, on the basis of these data.

POSTER PRESENTATION

Comparison of feeding behavior of biotype B and Q of *Bemisia tabaci* (Homoptera: Aleyrodidae) against red pepper and tomato varieties

Jeong-Oh Yang, Eun-Hee Kim, Changmann Yoon, Gil-Hah Kim

Chungbuk National University, Cheongju, Chungbuk, Republic of Korea

This study was performed to investigate the feeding behavior of *Bemisia tabaci* B- and Q-biotypes using EPG technique against nine red peppers and seven tomatoes commercial varieties. EPG waveforms was recorded during three hours compare to the characteristic patterns of feeding behaviors between two biotypes such as total non penetration times, the time taken until stylet activities changed after reaction, frequencies of stylet pathway pattern, and total duration of phloem feeding. In comparing the effect of the pepper varieties between the two biotypes, biotype Q showed the feeding behavior against all pepper varieties in the total duration of phloem feeding. Daeshin variety has the longest feeding time. However in total duration of phloem feeding, biotype B was observed in hanyeoreumbigarim and Daeshin varieties, but feeding time was very short. Biotype B was longer time in non-probing pattern, and showed lower frequencies of stylet pathway pattern, and probing time. However biotype Q was shorter time in non-probing time than biotype B, but showed more aggressive probing and stylet pathway pattern. These results suggest that biotype Q are more preferred the pepper host than biotype B. However, tomato varieties between the two biotypes did not show the difference.

POSTER PRESENTATION

Novel alpha-amylase inhibitor mutant genes and their potential use for insect-pests control

Maria Fatima Grossi de Sa, Rafael P. Del Sarto, Cesar C. Cruz, Osmundo B. Oliveira Neto, Marise V. Coutinho, Thales L. Rocha, Maria Cristina M. Silva

Embrapa Recursos Genéticos e Biotecnologia, Brasília -DF, Brazil

The cotton boll weevil *Anthonomus grandis* is an important insect-pest in South America. It causes severe damage in cotton floral buds and fruits. The *A. grandis* larvae development is difficult to control because it occurs inside the floral structures. Starch granules from cotton structure are digested by α-amylases in the intestinal lumen. Alpha-amylase inhibitors (α-AIs) are attractive candidates to control seed weevils. However *A. grandis* α-amylases (AGA) showed no significant inhibition by α-AI-1 and α-AI-2, two α-AIs isoforms isolated from common and wild bean, respectively.

In this work, a large combinatorial library of 10^7 inhibitor variants, obtained by DNA shuffling of *αAI-1* and *αAI-2* genes, was used to select α-amylase inhibitor mutant genes for novel α-AIs with potential to inhibit cotton boll weevil α-amylases. Twenty-six αAIs mutants were selected by Phage display technique showing different mutation patterns. Five of these mutants were expressed in *Arabidopsis thaliana* and their α-amylase inhibitory activity assayed. Two of these AI mutants, denominated C3 and A11 were active against AGA *in vitro* assay at nM range. Molecular modeling studies of the C3 and A11 inhibitors in complex with AGA revealed residues probably involved in the stabilization of the enzyme-inhibitor complex. Our results demonstrate the potential of α-AI mutants in controlling cotton boll weevil, which put them as candidates to generate insect-pest resistant cotton transgenic plants.

Supported by EMBRAPA, CAPES, CNPq, FACUAL, FIALGO, FUNDEAGRO.

POSTER PRESENTATION

Contribution to the knowledge of predatory mites and insects associated with brown mite in Hamedan, Iran

Mohammad Khanjani, Amir Hosein Eeghbalian

Bu Ali Sina University, Hamedan, Islamic Republic of Iran

Introduction: Brown mite *Bryobia rubrioculus* (Scheuten) is one of the most important pests of cherry and plum trees in west of Iran. This pest was found abundantly on fruit trees in Hamedan (west of Iran). It causes considerable damage in some orchards of this area. Some predatory of insects and mites were found to the associated with this pest.

Methods: The collecting of natural enemies which are associated with brown mite was carried out during 2005 – 2006. In this study infested leaves were transferred to laboratory and have been shaken on white tray then brushes into Petri dish The Petri dish which containing the samples were examined by stereomicroscope. Also some specimens were mounted as slides microscope.

Results: In this study were collected and identified 11 species associated with brown mite. Their scientific name as follows: O*rius niger* Wolff., *Coccinella septempunctata* L., *Adalia bipunctatus* G., *Stethorus gilviferons* (M.). C*hrysoperla carnea* (S.), *Scolothrips longicornis* (P) *Deraeocoris* sp., *Anystis baccarum* (L.) *Zetzellia pourmirzai* Khanjani & Ueckermann, *Amblyseius iraniensis* Daneshvar & Danmark and *Eupalopsellus hamedaniensis* Khanjani, *et al*. were found from this pest. They feed on different stages of brown mite and causing considerable decease its population.

Conclusion: Among the mutual enemies *O. niger, S. longicorni* and *A. baccarum* were high level of population and abundant.

POSTER PRESENTATION

Transgenic Bt-potato in South Africa: Effect on non-target organisms

Thembisa Majola, Diedrich Visser, David Sehlola, Sakhi Sambo

ARC-Vegetable and Ornamental Plant Institute, Pretoria, South Africa

Introduction: A genetically modified potato containing the *Bacillus thuringiensis* gene (*Bt-Cry1Ia1*) to control potato tuber moth (*Phthorimaea operculella*) (PTM) was evaluated for six consecutive years in South Africa. The first three years comprised of efficacy studies and the last three years were environmental impact studies relating to the effect on non-target organisms.

Methods: Field trials comprising randomized block designs were conducted in three provinces, namely, Gauteng (Pretoria), Free State (Petrus Steyn) and the Western Cape (Ceres). Non-target arthropods and nematodes were monitored regularly during the growing season using various techniques and traps, e.g. soil samples, pitfall traps, sticky traps, sweep net catches and monitoring of natural enemies and non-target pests. All arthropods were divided into orders or lower guilds for comparisons between the GMO potato and non-GMO potato lines. Nematodes were divided into plant parasitic and free-living guilds.

Results: The results showed no differences between the GMO potato and non-GMO potato lines except that no PTM or PTM damage was observed on the GMO potato compared to the non-GMO potato lines where PTM and damage was found. All micro- and macro arthropods, nematodes, natural enemies and other non-target pests were equally represented in all treatments.

Conclusion: Bt-potato containing the *Bacillus thuringiensis* gene (*Bt-Cry1Ia1*) provided complete control of PTM and had no effect on non-target organisms under field conditions in South Africa.

POSTER PRESENTATION

The role of litter decomposition, fertility, and litter-dwelling animals in the carbon cycle of a tropical rain forest

Evan Poirson, Terry McGlynn

[1]Occidental College, Los Angeles, CA, United States, [2]California State University - Dominguez Hills, Carson, CA, United States

Understanding the global carbon cycle is a crucial step in confronting one of the foremost concerns of our era: the unprecedented rate of worldwide climate change. Tropical rainforests, which process more carbon than any other terrestrial ecosystem, are an unparalleled research location in the effort to comprehend the implications of environmental variation on the cycling of carbon in food webs. As the continuation of a larger study begun in 2007, this research project completed measurements of decomposition and animal density across a fertility gradient. Our results show that decomposition rate was independent of nutrients, but that detritivore communities responded to decomposition rate and a nutrient gradient.

POSTER PRESENTATION

Investigation of the effects of different doses of chloropryfos-methyl against *Phyllocnistis citrella* Stainton (Lepidptera: Gracillariidae)

Behnam Amiri-Besheli

University of Mazandaran, Sari/Mazandaran, Islamic Republic of Iran

The object of this experiment was to determine the potential poison of the five doses (1, 0.5, 0.1, 0.05 & 0.01 ml per liters) of chemical insecticidal Chloropryfos methyl which is used Emulcifiable furmolation on after 24, 48, 72 and 96 hours post treatments against *phylocnistis citrella* Stainton in laboratory. In all experiments, leaves of citrus with second and third instars of leafminer larvae were used and the mortality was monitored. The analysis of variance has shown that there were significantly difference between treatments and control ($p<0.01$) and also significant differences were found among treatments and among days. The mortality of the leafminer with Chloropryfos-methyl was dose dependent. The analysis of variance has shown that there were significantly different among post test periods. LSD & Tukey-Test with different dose of the Chloropryfos methyl have shown that 1 & 0.5 ml per liters of Chloropryfos methyl with 80.62% and 62.33% mortality were more effective than the other doses ($p<0.01$). LSD & Tukey-Test among post test period has shown that 72 and 96 h post treatments with 52.6±7.7 and 47±7.4 percentage mortality are more effective than 24 and 48 h post treatments with 21±5.6 and 40.9±7.2 percentage mortality respectively. Based on the composite response of this assay with the probit analysis, the predicted LC_{50} of toxin was 0.10 ml per liters with confident interval 0.04-4.17 ml per liters respectively. The results showed that Chloropryfos methyl provided very good control of CLM larvae and would greatly reduce adult emergence.

POSTER PRESENTATION

The potential use of plant extracts as control option for Russian wheat aphid

J.M. Richter[1], G.J. Prinsloo[2], T.C. van der Linde[3]

[1]Department of Agriculture, Glen Research Institute, Bloemfontein, South Africa, [2]ARC Small Grain Institute, Bethlehem, South Africa, [3]Department of Zoology & Entomolgy, University of the Free State, Bloemfontein, South Africa

Introduction: Traditional, subsistence and resource-limited farmers remain poorly served by the top-down-transfer of technologies. In these low input agriculture systems where financing, necessary equipment, and know-how is not readily available, the use of insecticides are very limited. The presence of Russian wheat aphid in some of these production areas therefore causes severe yield loss. Plants are known to have insect repellent properties and extracts of such plants are used to control insects. The purpose of this study was to test repelling properties of three plants commonly found in the area where subsistence farmers grow wheat.

Methods: Water and light mineral oil extracts were made from three different plants, *Tagetes minuta*, *Artemisia afra* and *Tulbachia violaceae*. The behavioural response of alate Russian wheat aphid to these abstracts was tested with a four-arm olfactometer in the laboratory.

Results: The results of the different tests will be discussed.

Conclusion: Extracts from plants with aphid repellent properties may be a more user-friendly method of pest control for subsistence and resource limited-farmers, which can save them costs and is easy to use.

POSTER PRESENTATION

Fungal biopesticides for sheep lice (*Bovicola ovis*) control?

Diana Leemon, Peter James, Jacinta McMahon

Animal Research Institute, Department of Primary Industries and Fisheries, Yeerongpilly, Queensland, Australia

Introduction: Biological control of sheep lice (*Bovicola ovis* Schrank) is an attractive option to address concerns associated with the use of chemicals and the development of resistance to some currently available products.

Methods: Isolates of the fungi *Metarhizium anisopliae* and *Beauveria bassiana* collected in Queensland Australia were screened for ability to grow and infect *B. ovis* at high temperatures, a high sporulation rate suitable for mass production and virulence to different stages of *B. ovis* in wool-based assays. The best strains from the laboratory investigations were selected and tested in live animal studies.

Results: *S*everal isolates caused 100% mortality to all stages of lice within 7 days in wool based bioassays. Scanning electron and light microscope examination showed a large number of spores in the gut within 48 hours of exposure and extensive hyphal growth in louse tissues within 72 hours, suggesting ingestion as the main route of infection. The lipophilic spores adhered well to wool grease and were still viable and highly virulent to lice in laboratory tests after 14 weeks. Formulated *Metarhizium* spores applied to the fleece of lousy sheep by immersion dipping caused a 98% reduction in louse numbers in comparison to controls at 14 weeks post treatment.

Conclusions: This research demonstrates the potential for the use of appropriate strains of *Metarhizium* in the control of sheep lice. Further trials towards the registration of a commercial product are currently in progress.

POSTER PRESENTATION

Differentiation between forensic important Central South African Calliphoridae and Sarcophagidae puparia, using puparium specific characteristics

Sonja Brink, Theuns Van der Linde, Linda Basson, Pieter Van Wyk

University of the Free State, Bloemfontein, South Africa

Introduction: Viable puparia or empty puparial cases can be utilised as forensic evidence from after a week up to years post-mortem. The correct identification of puparia is crucial if it is to be used as forensic entomological evidence.

Methods: Dehydration and critical point drying was not required as the puparium was cut in half to remove the soft, hydrated inner pupa in preparation to examine the hardened, dehydrated puparium with a JSM 6400 WINSEM at 5 kV.

Results: The bubble membrane, present in early puparia, was investigated for the number of bubbles, the shape and size of the bubbles as well as the arrangement. Consideration was given to the general shape of the puparia, examining specifically the angle of its anterior end. Furthermore, the prominence of the lateral ridge varied and was therefore also of diagnostic use. Due to pupariation, the surface characteristics of puparia, namely reflectivity and striations, varied and had diagnostic value. The caudal segment was assessed for (i) being flat, bulging or recessed and (ii) the prominence of the perispiracular tubercles. However, the newly introduced diagnostic characteristic of the frontal field yielded the most significant puparium characteristic. The retraction of the head capsule during pupariation caused unique folding patterns in each of the species.

Conclusion: Puparia of forensic important Calliphoridae and Sarcophagidae can be identified, using only the frontal field characteristic. Identification can be backed-up using a range of other puparium specific characteristics as well as third instar characteristics.

POSTER PRESENTATION

Comparisons of the toxicity of different doses of methoxyfenozide against *Phyllocnistis citrella* Stainton (Lepidptera: Gracillariidae)

Behnam Amiri-Besheli

Faculty of Agricultural Science, Sari/ Mazandaran, Islamic Republic of Iran

The purpose of this study was to determine the toxicity of chemical insecticidal Methoxyfenozide which is apply on the control of *Phyllocnistis citrella* Stainton in lab conditions. In this experiment five dose of Methoxyfenozide (1, 0.5, 0.1, 0.05 & 0.01 ml per liter) have been tested. Leaves of citrus with second and third instar of citrus leafminer (CLM) larvae were used in all tests. The mortality was monitored after 24, 48, 72 and 96 hours post treatments. The analysis of variance (ANOVA) has shown that there were significantly different between treatments and control ($p<0.01$) but ANOVA has shown that there were not significant differences among post treatment periods. The mortality of the leafminer with Methoxyfenozide was dose dependent. LSD and Tukey-Test with different dose of the Methoxyfenozide have shown that 1 & 0.5 ml per liter of Methoxyfenozide with 85.10% and 77.97 % mortality were more effective than the other doses ($p<0.01$). LSD & Tukey-Test among post test period has shown that after 72 and 96 hours post treatments with 52.1±7.2and 59±6.9 percentage mortality are more effective than 24 and 48 hours post treatments with 44.1±6.9and 49.1±7 percentage mortality respectively. Based on the composite response of this assay with the probit analysis, the predicted LC_{50} of the Methoxyfenozide was 0.04 ml per liter with confident interval 0.08-2.57 ml per liter respectively. The results showed that Methoxyfenozide provided good control of CLM larvae and would greatly reduce adult emergence.

POSTER PRESENTATION

Comparisons of the toxicity of different doses of methoxyfenozide against *Phyllocnistis citrella* Stainton (Lepidptera: Gracillariidae)

Behnam Amiri-Besheli

Faculty of Agricultural Science, Sari/ Mazandaran, Islamic Republic of Iran

The purpose of this study was to determine the toxicity of chemical insecticidal Methoxyfenozide which is apply on the control of *Phylocnistis citrella* Stainton in lab conditions. In this experiment five dose of Methoxyfenozide (1, 0.5, 0.1, 0.05 & 0.01 ml per liter) have been tested. Leaves of citrus with second and third instar of citrus leafminer (CLM) larvae were used in all tests. The mortality was monitored after 24, 48, 72 and 96 hours post treatments. The analysis of variance (ANOVA) has shown that there were significantly different between treatments and control ($p<0.01$) but ANOVA has shown that there were not significant differences among post treatment periods. The mortality of the leafminer with Methoxyfenozide was dose dependent. LSD and Tukey-Test with different dose of the Methoxyfenozide have shown that 1 & 0.5 ml per liter of Methoxyfenozide with 85.10% and 77.97 % mortality were more effective than the other doses ($p<0.01$). LSD & Tukey-Test among post test period has shown that after 72 and 96 hours post treatments with 52.1±7.2and 59±6.9 percentage mortality are more effective than 24 and 48 hours post treatments with 44.1±6.9and 49.1±7 percentage mortality respectively. Based on the composite response of this assay with the probit analysis, the predicted LC_{50} of the Methoxyfenozide was 0.04 ml per liter with confident interval 0.08-2.57 ml per liter respectively. The results showed that Methoxyfenozide provided good control of CLM larvae and would greatly reduce adult emergence.

POSTER PRESENTATION

Egg parasitism rates of the invasive Australian eucalyptus weevil, *Gonipterus sp.*, in its home range

Jane Elek[1], Nita Ramsden[1], Vinu Patel[2], Geoff Allen[2]

[1]Forestry Tasmania, Hobart, Tasmania, Australia, [2]CRC for Forestry, Hobart, Tasmania, Australia

Gonipterus scutellatus (Coleoptera: Curculionidae) is native to Tasmania, Australia, as are the plantation tree species, *Eucalyptus globulus*. This weevil has invaded and become a serious pests of eucalypt plantations around the world. In the past, the weevils were not considered a pest in their home range because their populations were generally well controlled by egg parasitism. However, they have become serious pests that require management in *E. globulus* plantations in Western Australia. More recently, they also appear to be achieving pest status in Tasmanian *E. globulus* plantations.

Field surveys were conducted over two consecutive egg-laying seasons to collect weevil egg pods that were held in the laboratory until they hatched. Fresh pods were collected fortnightly in early spring, during October and November, from adult-phase foliage three 4-year-old (in 2004) and three 2-year-old (in 2005) *E. globulus* plantations in southern Tasmania that had had notable weevil populations in the previous year. In 2004, up to 50 egg pods were collected from 20 random plots per site per collection date. One collection was made in early November at six other sites around Tasmania. At each collection date in 2005, 4 egg pods were collected at 25 m intervals along four transects from the edge of the plantation bordering native eucalypt forest, for 100 m towards the centre (a total of 80 pods). Pods were held in the laboratory at 20^0 C, and all emerged larvae and parasitoid wasps counted. After three weeks all pods were dissected and unhatched larvae and wasps scored. The numbers of eggs per pod averaged seven.

In 2004, the percentage of pods parasitised ranged from zero early in October to 86%, and the percentage of eggs parasitised increased from zero to 72% by the end of November. In 2005, the levels of parasitism fell from a high of 46% in early October to a low of 5% at the end of November. The levels of parasitism remained relatively constant from the plantation edge for 100 m into the plantation for the first three sample dates, but declined sharply away from the edge for the last sample date, when the parasitism rates were lowest.

The parasitoid wasps most likely comprise a species complex of *Anaphes nitens* and its hyperparasitoids that are native to the area.

POSTER PRESENTATION

Resistance mechanism and inheritance of two-spotted spider mite, *Tetranychus urticae* (Tetranychidae), to Chlorfenapyr

Choi Byeong-Ryeol, Lee Si-Woo, Park Hyung-Man, Kwon Deok-Ho, Lee Si-Hyeock

[1]National Institute of Agricultural Science and Technology, RDA, Suwon, Gyeonggi, [2]Entomology Program, School of Agricultural Biotechnology, Seoul National University, Seoul, Republic of Korea

Field populations of *T. urticae* collected from apple trees in 2002 and strawberries in 2003 appeared to be highly resistant to chlorfenapyr in spite of its short-term use. A strain of *T. urticae* collected from apple orchard was further selected with chlorfenapyr 10% SC for 27 times at a selection pressure of 30-50% mortality (CR-27 strain). Resistance and cross-resistance levels of the CR-27 strain to 16 acaricides were determined by spray method. The CR-27 strain was extremely resistant to chlorfenapyr (Resistance ratio (RR) was 2,600-fold). The strain exhibited high cross-resistance to chlorfenpyr. pyridaben(RR 56.1), fenpyroximate(RR 38.8). But, showed low cross-resistance to tebufenpyrad(RR 2.8), abamectin(RR 2.5), and nearly no cross-resistance to benfenthrin, bifenazote, etc. Synergist experiments with specific metabolic inhibitors revealed that piperonyl butoxide known as inhibitor of P450 oxidase, had synergistic effect of **164.4**-fold on the efficacy of chlorfenapyr. Iprobenfos rolling as inhibitor of carboxylesterase showed **41.1**-fold inhibition to CR-27 mite. It was proposed that metabolic detoxification by esterase and P450 oxidase might play an important role in resistance *T. urticae* to chlorfenapyr. Degrees of dominance were 0.48 and 0.34 in F_1 progenies of CR×S, S×CR, respectively. Inheritance of chlorfenapyr resistance was incomplete dominant in TSSM.

POSTER PRESENTATION

Ovary structure and development in *Stomaphis quercus* (Hemiptera, Aphidinea: Lachnidae)

Teresa Szklarzewicz, Grazyna Pyka-Fosciak

Jagiellonian University, Krakow, Poland

Introduction: The aphid, *Stomaphis quercus*, like other aphids, has a complex life cycle that includes four viviparous generations and one oviparous generation.

Methods: The ovaries of *Stomaphis quercus* were examined using light and electron microscopes.

Results: The ovaries of young embryos of *S. quercus* contain a limited number of oogonial cells. The last generation of oogonia (cystoblasts), enters the cycles of incomplete mitotic divisions that lead to the formation of clusters of interconnected cells (cystocytes). In the ovaries of viviparous generations arise 6-9 clusters, in the ovaries of oviparous generation - 5 clusters. Clusters of viviparous females consist of 32 cystocytes. In oviparous females the number of cystocytes is larger and variable (i.e. 45-60). Each rosette-shaped cluster is surrounded by a single layer of follicular cells. During further development, cystocytes differentiate into oocytes and trophocytes. Subsequently, rosettes of cystocytes transform into ovarioles. The anterior region of the ovariole enclosing trophocytes becomes the tropharium, whereas its posterior region containing oocytes becomes the vitellarium. In the vitellaria of viviparous generations two oocytes develop, while in oviparous females only one. The oocytes of viviparous females do not accumulate yolk and are not covered by eggshells. Immediately after previtellogenesis, the oocyte nuclei start to divide forming embryos. In oviparous females, the only oocyte develops through three stages: previtellogenesis, vitellogenesis and choriogenesis.

Conclusions: There are significant differences between viviparous and oviparous females regarding: (1) the number of germ cell clusters per ovary, (2) the number of germ cells per cluster, (3) the course of oogenesis.

POSTER PRESENTATION

A comparison of the toxicity of different doses of Spinosad against *Phyllocnistis citrella* Stainton (Lepidoptera: Gracillariidae)

Behnam Amiri-Besheli

Faculty of Agric. Univ. of Mazandaran, Sari/ Mazandaran, Islamic Republic of Iran

The purpose of this experiment was to examine the efficacy of Spinosyn that is used on the control of *phylocnistis citrella* Stainton (Lepidoptera: Gracillariidae) in lab condition. In this experiment five doses of Spinosyn (1, 0.5, 0.1, 0.05 & 0.01 ml per liter) have been tested. Leaves of Citrus with the second and third instar larvae of the citrus leaf miner (CLM) larvae were used in all tests. The mortality was monitored after 24, 48, 72 and 96 hours post treatments. The analysis of variance (ANOVA) has shown that there were significantly different between treatments and control ($p<0.01$) and also the ANOVA has shown that there were significantly different among post treatment periods. The mortality of the leafminer with Spinosyn was dose dependent. LSD and Tukey-Test with different dose of the Spinosyn have shown that 1 & 0.5 ml per liter of the Spinosyn with 100% and 98.95% mortality were more effective than the other doses ($p<0.01$). LSD & Tukay-Test among post test period has shown that after 72 and 96 hours post treatments with 58.2±8.4 and 63.8±7.9 total percentage mortality are more effective than 24 and 48 hours post treatments with 41.2±8.9 and 52.7±8.6 total percentage mortality respectively. Based on the composite response of this assay with the probit analysis, the predicted LC_{50} of the Spinosad was 0.05 ml per liter with confident interval 0.01-0.17_ml per litre respectively. The results showed that Spinosad provided good control of CLM larvae and would greatly reduce adult emergence.

POSTER PRESENTATION

Systematics and evolution of weevils of the genus *Wagnerinus* Korotyaev (Coleoptera: Curculionidae)

Hiraku Yoshitake, Toshihide Kato, Utsugi Jinbo, Nozomu Utsuki, Motomi Ito

University of Tokyo, Tokyo, Japan

The weevil genus *Wagnerinus* Korotyaev in the tribe Ceutorhynchini, subfamily Ceutorhynchinae is revised systematically. A phylogenetic study combined with ecological field surveys is conducted to elucidate the evolution of host plant utilization pattern within this genus.

Presently, *Wagnerinus* comprises four species from Northeast Asia, but species identification is often very difficult in this genus due to the presence of morphologically similar undescribed species. Ecological information on *Wagnerinus* weevils is extremely limited, except that *W. costatus* (Hustache) is known to be associated exclusively with galls on the axillary buds of *Weigela hortensis* (Caprifoliaceae) induced by the gall midge *Asphondylia baca* Monzen (Diptera).

As the result of our systematic revision of *Wagnerinus*, this genus is classified into two species groups and 16 species from the Russian Far East, Northeast China, Korea, and Japan, including twelve undescribed species. Our field surveys revealed that *Wagnerinus* weevils are associated with *Weigela* or *Abelia* species (Caprifoliaceae) and their host plant utilization can be divided into four types: 1) flower-bud feeding, 2) facultative cecidophagy (gall and flower-bud feeding), 3) obligatory cecidophagy (obligate gall-feeding), and 4) seed-capsule feeding.

Results of molecular phylogenetic analyses based on sequences of the mitochondrial COI and 16S rRNA genes agree well with classification based on morphological traits. The ancestral state reconstruction of host plant utilization on the molecular phylogeny suggests that the ancestral state for *Wagnerinus* was flower-bud feeding and that cecidophagy occurred once within one of the species groups, with subsequent diversification in the host plant utilization.

POSTER PRESENTATION

Reference and image databases TABR and TAB based on tropical Asian bees

Osamu Tadauchi, Katsushi Mitai, Ryuki Murao, Hitoshi Inoue

Kyushu University, Fukuoka, Japan

Since Fabricius (1775) described some bees, including *Apis cerana* and *Apis dorsata* from tropical Asia, many investigators have reported bees from this area. The most comprehensive works of bees in tropical Asia were published as the Fauna of British India including Ceylon and Burma by Bingham (1897). Europeans were the main researchers who then studied tropical Asian bees in the first half of the 20th century. But on the whole it may be said that studies of bees in this area are inadequate at the present time, compared with those of Africa and South America. Michener (1965) presented a monograph of bees in the neighboring areas of Australia and the Pacific Islands. But a comprehensive work on bees in tropical Asia absent. It is, therefore, necessary for investigators in this area to search sporadic references. Furthermore, it is important to construct a database of bees in tropical Asia for future studies. We have constructed two files, representing image and reference databases of tropical Asian bees. One of the files, reference database TABR is based on main articles related to tropical Asian bees and is open to the public via the Internet. The other is an image database TAB. The files are written in English and is administered by a SIGMA text database management system working at a workstation in the Entomological Laboratory at Kyushu University, Fukuoaka. A user can presently access the TAB database files by visiting the following URL: http://konchudb.agr.agr.kyushu-u.ac.jp/tabr/.

POSTER PRESENTATION

Trachelas L. Koch, 1872 (Araneae: Corinnidae), with emphasis on southern Africa

Robin Lyle, Charles Haddad

Department of Zoology & Entomology, University of the Free State, Bloemfontein, South Africa

The dark sac spider subfamily Trachelinae (Araneae: Corinnidae) is currently represented in the Afrotropical region by seven genera, *Austrachelas* Lawrence, 1938, *Cetonana* Strand 1929, *Paccius* Simon, 1898, *Pronophaea* Simon, 1897, *Spinotrachelas* Haddad, 2006, *Thysanina* Simon, 1910 and *Trachelas* L. Koch, 1872. The genus *Trachelas*, with a worldwide distribution in the tropical and temperate regions, is revised in the Afrotropical region. The species *T. chubbi* Lessert, 1921, *T. minor* O. P. –Cambridge, 1872, *T. punctatus* Simon, 1885, *T. pusillus* Lessert, 1923, *T. roeweri* Lawrence, 1938, *T. schenkeli* Lessert, 1923, *T. scopulifer* Simon, 1896 and *T. sylvae* Caporiacco, 1949 are redescribed. Based on its redescription, *T. scopulifer* is misplaced and is transferred to the genus *Thysanina*. Thus far more than 20 new species are described from the Afrotropical region, with the majority of these distributed in southern and eastern Africa.

POSTER PRESENTATION

Effect of sugarcane varieties on performance of *Telenomus busseolae* Gahan (Hymenoptera: Scelionidae) an egg parasitoid of sugarcane stem borers *Sesamia* spp. (Lepidoptera: Noctuidae) in Iran

Arsalan Jamshidnia[1], Aziz Kharrazi-Pakdel[1], Hossein Allahyari[1], Ebrahim Soleymannejadian[2]

[1]Tehran University, Karaj, Tehran, [2]Chamran university, Ahwaz, Khuzestan, Islamic Republic of Iran

Introduction: The sugarcane stem borers *Sesamia cretica* and *S. nonagrioides* are the most important pest of sugarcane in Iran. The egg clusters of *Sesamia* spp. are attacted by *T. busseolae*. A field experiment was conducted to evaluate the performance of T. busseolae on sugarcane commercial varieties in Khuzestan province (southwest of Iran).

Methods: This study evaluated in a split plot design on 4 sugarcane commercial varieties (CP69-1062, CP48-103, CP57-614 and SP70-1143) with 5 fields per variety in Khuzestan in 2007. Sampling of egg masses were carried out in tillering stage of sugarcane (5-15 June) and final stage of sugarcane growing (10-20 October). All percentage data were arcsine-transformed before being subjected to analysis of variance using the GLM procedure.

Results: Our results of a two-way ANOVA indicated both growth stage and variety of sugarcane had a significant effect on the egg batch density, discovery efficiency and percent parasitism. The interaction between growth stage and variety on percent parasitism and discovery efficiency were statistically significant. There was no effect on parasitism efficiency, adult emergence and F1 progeny sex ratio of growth stage , variety, or any interaction between them. The highest egg batch density, discovery efficiency and percent parasitism was observed in CP48-103 variety.

Conclusion: *T. busseolae* in CP48-103 variety is more efficient than the other sugarcane commercial varieties.

POSTER PRESENTATION

Repellency effect of cyphenothrin against *Aedes aegypti* in field tests in Thailand

Piti Mongkalangoon, John P. Grieco, Nicole L. Achee, Wannapa Suwonkerd, Theeraphap Chareonviriyaphap

[1]Department of Entomology, Kasetsart University, Bangkok, 10900, Thailand, [2]Department of Preventive Medicine and Biometrics, Uniformed Services University of the Health Sciences, Bethesda, MD. 20891, United States, [3]Office of Disease Prevention and Control No.10, Ministry of Public Health, Chaing Mai, 50200, Thailand, [4]Corresponding Author, Department of Entomology, Kasetsart University, Bangkok, 10900, Thailand

The main objective of this study was to find the optimal dosage of cyphenothrin to use for field collected *Aedes aegypti*. Such dosage was further utilized in the experimental hut study for testing the excito-repellency effect. All of dosages were first tested in the excito-repellency system. It was found that cyphenothrin had both repellency effect and contact irritancy effect. The LC50 was selected as the appropriate dosage for testing in the field. Two identical experimental huts were used for evaluation the efficacy of cyphenothrin to *Ae. aegypti*. The results indicated that cyphenothrin at LC50 level could protect the mosquitoes to fly into the treatment hut and chase the mosquitoes out of the treatment hut as compared to the controls.

POSTER PRESENTATION

Repellency effect of cyphenothrin against *Aedes aegypti* in field tests in Thailand

Piti Mongkalangoon, John P. Grieco, Nicole L. Achee, Wannapa Suwonkerd, Theeraphap Chareonviriyaphap

[1]Department of Entomology, Kasetsart University, Bangkok, 10900, Thailand, [2]Department of Preventive Medicine and Biometrics, Uniformed Services University of the Health Sciences, Bethesda, MD. 20891, United States, [3]Office of Disease Prevention and Control No.10, Ministry of Public Health, Chaing Mai, 50200, Thailand, [4]Corresponding Author, Department of Entomology, Kasetsart University, Bangkok, 10900, Thailand

The main objective of this study was to find the optimal dosage of cyphenothrin to use for field collected Aedes aegypti. Such dosage was further utilized in the experimental hut study for testing the excito-repellency effect. All of dosages were first tested in the excito-repellency system. It was found that cyphenothrin had both repellency effect and contact irritancy effect. The LC50 was selected as the appropriate dosage for testing in the field. Two identical experimental huts were used for evaluation the efficacy of cyphenothrin to Ae. aegypti. The results indicated that cyphenothrin at LC50 level could protect the mosquitoes to fly into the treatment hut and chase the mosquitoes out of the treatment hut as compared to the controls.

POSTER PRESENTATION

Culturally Significant Insects in Blouberg, Limpopo Province, South Africa

Bronwyn Egan[1], Rob Toms[2], Piet Olivier[1], Dr Abe Addo-Bediako[1]

[1]University of Limpopo, Polokwane, South Africa, [2]Transvaal Museum, Pretoria, South Africa

Introduction: Blouberg has a rich culture of entomophagy, resulting in a valuable body of indigenous knowledge around edible insects and their associated food plants. To date, this data has been available only to the local inhabitants through the oral traditions of the area. Younger generations do not have the time for and/or interest in sustaining this culture. This study documents the use of the insects and the attitudes of the inhabitants of the area to entomophagy.

Methods: Fieldworkers from nine villages collected specimens of and information on the insects eaten. Structured questionnaire surveys were conducted amongst households and competition questionnaires were conducted amongst school going youth. Data were also collected during harvesting trips.

Results: There is a strong culture of entomophagy across the Blouberg, with more than 23 different insect species eaten. They are considered a delicacy and eaten in large numbers during the harvesting season, although most are unavailable in winter despite effective preservation methods. Certain insects are sold but most are collected for own consumption. The older generation has a deeper understanding of the insects than the younger generation and collect and utilise them more frequently than the youth. Most residents feel that edible insect numbers have declined over the years due to a lack of rain. There is concern amongst older people at the loss of this culture of entomophagy and of the decline of the insects themselves.

Conclusions: Linking available indigenous knowledge around these insects, to ecological data collected through conventional scientific methods and simultaneously involving the local community in the process, will give valuable insights into insect conservation management and into that of the associated plant species.

POSTER PRESENTATION

New and rare Hemigasterini and Euryproctini (Hymenoptera: Ichneumonidae) for the Romanian fauna in protected areae

Irinel Constantineanu, Raoul Constantineanu, Camil Stefan Lungu-Constantineanu

Biological Research Institute, Iasi, Romania

Introduction: The authors did their researches in the following protected areae in Romania: Retezat National Park, natural reservations “Slatioara Secular Forest” and ”Todirescu Alpine Clearing”, situated in the Carpathians mountains, with a rich and varied biodiversity. In the first two protected areae there are a mixture of beech with coniferous forests and many clearings with a rich herbaceous vegetation and ”Todirescu Alpine Clearing” only with alpine lawn.

Methods: The ichneumonids were collected in June and July during the period 2001 – 2007 with entomological net, many of them in clearings upon some species of Apiaceae, especially *Angelica archangelica, Laserpitium latifolium* and *Angelica sylvestris*. For the identification of the ichneumonid species we used the Olympus stereomicroscope.

Results: The authors present 14 species of Ichneumonidae. Of these, 4 species belong to three genera of the tribe Euryproctini (subfamily Ctenopelmatinae) and 10 species belong to 7 genera of the tribe Hemigasterini (subfamily Cryptinae). The following 3 species: *Euryproctus plantator* Thunb., *Mesoleptidea hohenwartensis* Schm. and *Hadrodactylus rectinervis* (Rom.) are new for the Romanian fauna and the other ones are rare for the Romanian fauna and for the European fauna, too. About geographycal distribution, *Parmortha parvula* (Grav.) and *P. pleuralis* Thoms. are holarctic species and the others are palaearctic, majority of them being European species.

POSTER PRESENTATION

Leaf insect *Galerucella nipponensis* as a useful bioindicator for heavy metal pollution

Heungtae Kim, Jihyun Yoon, Jae Geun Kim

Seoul National University, Seoul, Republic of Korea

Introduction: Heavy metals flowed into a wetland ecosystem threaten organisms in higher trophic level through biomagnification. *Galerucella nipponensis* (Coleoptera: Chrysomelidae) feeds on mainly *Trapa japonica* in wetland. They might be a prey to predators such as spiders. The purpose of this study was to identify the transfer of heavy metals through the beetle-centered food chain and to certify the potential of the beetle as bioindicator for heavy metal pollution.

Methods: The heavy metals (Cd, Cr, Cu, Mn, Pb, Zn) in the beetle, spiders, the aquatic plant leaf, and sediments were analyzed with ICP-MS. Stable isotope was also analyzed for trophic level analysis. The superficial sediments were characterized for physico-chemical properties.

Results: The heavy metals excluding Pb and Mn showed higher contents in the beetle than in the plant. Although higher contents of most heavy metal were found in the spiders, Cr and Pb showed a decreasing phase through the beetle-centered food chain. The beetle-centered food chain reflected the difference of Cd, Cu and Pb contents in the study sites. The beetle showed marked differences of Cd, Cu and Pb contents among the sites, while the spiders indicated the difference of Cd and Cu; the plant for Cu, Pb and Zn.

Conclusions: *G. nipponensis* as an herbivorous insect and a prey for predator might play an important role in the transfer of heavy metals (Cd, Cu, Mn, Zn) through the food chain. The beetle can be a useful bioindicator for heavy metal pollution.

POSTER PRESENTATION

Field monitoring of Mediterranean fruit fly (C*eratitis capitata*) (Diptera: Tephritidae) populations on cherry peppers (C*apsicum baccatum*) (Solanaceae) in the Belmont Valley, Eastern Cape

Jessica Cockburn, Colleen Hepburn, Martin Hill

Rhodes University, Grahamstown, South Africa

Introduction: The cherry pepper, *Capsicum baccatum*, is an export crop new to the Eastern Cape. Little is known about pest insects associated with the crop in this region. The Mediterranean fruit fly, *Ceratitis capitata*, has been identified as a potential key pest of the crop.

Methods: *C. capitata* field populations were monitored in a crop of *C. baccatum* over a 20-week period in the Eastern Cape. Adult *C. capitata* numbers were measured weekly using pheromone traps. Larvae and pupae were collected from pod and soil samples respectively on a fortnightly basis. An analysis of edge effects and a vegetation survey of alternate hosts in natural vegetation adjacent to the crop were carried out to determine the effect of these on movements of *C. capitata* populations.

Results: Populations fluctuated during the growing season, starting out low, reaching a number of peaks and tailing off at the end of the season. The highest peaks occurred during periods of higher temperatures and low rainfall and when the pepper crop was at its ripest, reaching a maximum of over 2000 individuals per plot. Edge effect analyses indicated that edge vegetation had an effect on *C. capitata* movements into the pepper plots. The vegetation survey revealed numerous alternate hosts in close proximity to the crop.

Conclusions: Temperature, rainfall, edge vegetation and availability of alternate hosts affect movements of *C. capitata* populations in the *C. baccatum* crop in the Eastern Cape. These factors have important implications for IPM-based control measures including population monitoring and cultural control.

POSTER PRESENTATION

Wireworms (Coleoptera: Elateridae) faunal-structure evaluation on Romanian sugar-beet crops

Maria Iamandei[1], Grigore Margarit[1], Gheorghe Solcan[2], Gheorghe Ciubuc[2]

[1]Department of Entomology, Research-Development Institute for Plant Protection, Bucharest, Romania, [2]Department of Plant Protection, S.C. AdminDate & Inf S.R.L., Bucharest, Romania

Introduction: Between the sowing time and the appearance of the first real leaves, the sugar beet crop might be attacked by a group of insects generically named “soil pests”, among which the most important are the species of the *Bothynoderes, Tanymecus* (Coleoptera: Curculionidae) and *Agriotes* (Coleoptera: Elateridae) genera. This research aims to also evaluate the presence in the sugar beet crops and other three crops recommended in the crop rotation of the wireworms species collected all over Romania, in over 25 years.

Methods: The material analyzed was obtained by two methods: (I)Surveys on soils with areas of 25/25/25 cm (3 for each crop) were used for collecting the larvae; (II)The adults were collected either by threading or by direct collecting from the plants.

Results: The analyzed material includes a number of 2904 specimens belonging to 7 sub-families, 8 genera, 19 species and one variety. Two species were exclusively found in the sugar beet crop, while the species of the *Agriotes* genus were frequently found in all four crops. The wireworms are practically represented in all soils, but the specific composition changes, as each type of soil is characterized by a faunal complex that is in close connection with the ecological elements.

Conclusions: The results will be the starting point for realizing a data base concerning the sugar beet pests and they will be useful for developing experimental models for the remote detection of the sugar beet pest agents, which will constitute a support for the management decision.

POSTER PRESENTATION

Development of group-specific primers for prey DNA detection in the predator gut

Anna-Karin Kuusk[1], Nuria Agustí[2]

[1]Department of Ecology, Swedish University of Agricultural Sciences, 750 07 Uppsala, Sweden, [2]IRTA, Plant Protection, E-08348 Cabrils (Barcelona), Spain

Introduction: The development of molecular techniques to analyze the gut content of polyphagous predators allows understanding how the diversity and the availability of alternative preys (non-pest) contribute to the maintenance of the predator populations in the crops. The Order of the springtails (Hexapoda: Collembola), covers a whole range of species present in the soil of agricultural ecosystems, and represents one of the most abundant alternative preys. Some arthropod species have been described as major predators of springtails in unfavorable periods (no pest species present). In these periods the springtails represent in many cases the alternative prey numerically dominant.

Methods: Group-specific primers were designed for the first time in order to detect springtails within predator gut contents. Degenerate primers were developed based on the sequences of 17 species of springtails collected in agricultural ecosystems. 18S rDNA was the region used to be a multi-copy and semi-conserved genomic region.

Results: Primers designed amplified DNA fragments of 272 and 177 bp. Specificity analysis demonstrated that these markers were not detecting DNA of 41 other species of arthropods. The use of these group-specific primers is advantageous when trying to study a broad spectrum of species close phylogenetically and/or potentially ingested by a polyphagous predator.

Conclusions: These group-specific markers can greatly facilitate the study of trophic relationships between springtails and generalists predators.

POSTER PRESENTATION

Proteomic analysis of the parasitized host (*Plutella xylostella*) fat body

Min Kyo Jung, Kyung Han Song, Sung Sik Han

School of Life Sciences and Biotechnology, Seoul, Republic of Korea

Introduction: Insect fat body has been considered as a principal organ that performs with multiple and diverse metabolic functions. In the parasitized Diamondback moth (*Plutella xylostella*) by *Cotesia Plutellae* showed hypertrophied structures in fat body compared with non-parasitized larvae.

Methods: To investigation, we used a proteomic approach to obtain the proteomic profiles of the parasitized larva fat body. We used a total of 300 μg of protein of fat bodies and detected about 100 protein spots on specially chosen area by 2-DE.

Results: Amount of the parasitized *P. xylostella* fat body was decreased in posterior part and the residual lipid droplets in the parasitized host fat cells were smaller than non-parasitized host fat cell. Total 4 proteins were identified as a TIM (Triose-phosphate isomerase), FKBP (FK506-binding protein), TCTP (Translationally-controlled tumor protein homolog) and Hypothetical protein (from *Cotesia plutellae* polydnavirus) by quadrupole time-of-flight tandem mass spectrometry (QTOF-MS/MS) analysis.

Discussion: Hypothetical protein was newly synthesized in parasitized host and came from *Cotesia plutellae* polydnavirus. Probably up-regulation of Tim is involved in gluconeogenesis of lipid. Down-regulated FKBP and TCTP might be involved in immune response by parasitism.

POSTER PRESENTATION

Long-term aphid monitoring in seed potatoes in South Africa

Mark Robertson, Kerstin Kruger, Lezel Muller, Michelle Fourie

Department of Zoology & Entomology, University of Pretoria, Pretoria, South Africa

Introduction: Accurate prediction of the spread of aphid-transmitted viruses and the risk they pose depends amongst others on reliable estimation of aphid numbers. Several aphid species are known to transmit viruses that reduce the profitability of seed potato production. Populations have to be monitored to determine overall vector pressure and manage virus vectors. Monitoring is usually done using a combination of yellow bucket traps and suction traps. The aim of this study is to correlate yellow bucket and suction trap counts to assess the efficiency of suction traps as a monitoring tool in a seed potato producing region in South Africa.

Methods: Long-term monitoring trials were conducted in the Christiana region (Free State). For each trial, six yellow bucket traps were placed evenly around a circular potato field at each of six sites. A 12 m high suction trap was placed north of the potato fields, the furthest from the fields distance being 25 km. Yellow bucket and suction trap samples were collected weekly. Pearson correlations were calculated between the weekly aphid counts of yellow bucket and suction trap samples.

Results: Initial results suggest that total aphid abundance between the weekly yellow bucket and suction trap samples is poorly correlated.

Conclusions: Total aphid counts are of limited use. Although the correlation of aphid abundance between the two types of traps was poor, for some aphid species the suction trap may provide a good surrogate for the yellow bucket traps.

POSTER PRESENTATION

Species diversity of plants and insects in the Mokolodi Nature Reserve and Gaborone Game Reserve

Ntebaleng Makate, Moffat Setshogo

University of Botswana, Gaborone, Botswana

Two game reserves, Gaborone Game Reserve (GGR) and Mokolodi Nature Reserve (MNR) were used for the one-year study to compare plant and insect diversity during the dry and wet seasons. GGR is located within the city of Gaborone, i.e., in an urban setting, while MNR is about 15km to the south west out of the city. Vegetation composition and topography of the two reserves differ. The vegetation type for both is tree savanna but it is the species composition that varies. The vegetation in MNR was found to be predominantly of *Combretum* / *Acacia* association with hilly and undulating topography; while that of GGR was *Acacia* dominated with the topography being mainly flat. There was a significant difference in the insect species densities between the two reserves.

POSTER PRESENTATION

Possible function of the soybean stink bug, *Piezodorus hybneri* (Heteroptera: Pentatomidae) male pheromone

Nobuyuki Endo[1], Tetsuya Yasuda[2], Takashi Wada[1], Keiichiro Matsukura[1], Shin-etsu Muto[3], Rikiya Sasaki[3]

[1]National Agricultural Research Center for Kyushu Okinawa Region, Koshi, Japan, [2]National Agricultural Research Center, Tsukuba, Japan, [3]Fuji Flavor Co., Ltd., Hamura, Japan

Introduction: Male-produced pheromone system of *P. hybneri* has been reported to be a mixture of three components. However, the function or role of the pheromone still remains unknown. Thus, we investigated the relationship between sexual maturity and pheromone production in males of the bug. We also evaluated the attractiveness of the synthetic *P. hybneri* pheromone in soybean fields.

Methods: Copulation and the development of ectodermal accessory gland (EAG) were checked as an indicator of male sexual maturity. Males at particular ages were extracted individually with hexane to quantify each pheromone production. The hexane extracts were concentrated and further analyzed by GC-MS. Attractiveness of the synthetic pheromone was evaluated with water-pan traps baited with the synthetic pheromone (30 mg). The numbers of adults and nymphs of *P. hybneri* captured in the traps were counted everyday.

Results: The male pheromone was produced simultaneously with the beginning of mating behavior and EAG development. No pheromone components were detected in any of diapause males which were reared under short-day condition (12L:12D). Both sexes of adults were attracted to the synthetic pheromone, but the sex ratio was significantly female-biased particularly in non-diapaused period (summer). Nymphs and diapausing adults were also attracted to the synthetic pheromone in autumn.

Conclusions: The pheromone system of *P. hybneri* has a sex-related function but seems to play multifunctional roles.

POSTER PRESENTATION

Cabbage looper, *Trichoplusia ni* (Lepidpotera: Noctuidae) is now common pest in Japan

Masashi Nomura[1], Takako Itoh[1], Yutaka Minagawa[1], Jun-ya Yase[2]

[1]Chiba University, Chiba, Japan, [2]Hyogo Prefectural Agricultural Experiment Station, Hyogo, Japan

Introduction: Cabbage looper (CL), *Trichoplusia ni* (Lepidoptera: Noctuidae) is a notorious pest species of vegetables in North America. While CL was known to occur in Japan, the species was previously considered to be rare and not a pest species in Japan. However, in 2000, CL was observed in a cabbage field in Kagoshima and Hyogo Prefecture in western Japan, and then in the east of Japan shortly thereafter. The objectives of our study were thus to (1) clearly define the distribution of CL in Japan, especially in cabbage fields, and (2) determine the why the distribution of the species has extended into agricultural areas in Japan.

Materials and Methods: We determined the (1) distribution of CL in cabbage fields throughout Japan, (2) assessed the seasonal population dynamics of CL at several locations in Japan using sex pheromone traps, (3) examined resistance to insecticides, and (4) maximum and minimum temperature tolerance of the species. The data collected in each of the experiments was compared with those obtained for another plusiine moth, *Autographa nigrisigna*, a common cabbage pest species in Japan.

Results and Discussion: Our investigations showed that CL is widely distributed in western Japan, and that it has spread to the eastern and northern parts of the country. As CL populations increase with the approach of fall this species becomes the dominant pest in cabbage fields in western Japan. CL did not exhibit resistance to insecticides or extremes in temperature. However, recent increases in temperature due to global warming have facilitated the survival in Japan, where it is becoming a major pest on a variety of vegetables.

POSTER PRESENTATION

The characteristics of the populations of five *Agriotes* (Coleoptera: Elateridae) species in three regions in Croatia

Reneta Bažok, Antonela Kozina, Jasminka Igrc Barčić, Tomislav Kos

Faculty of Agriculture, Zagreb, Croatia

Introduction: The literature data reported that the most abundant species in eastern regions of Croatia are *A.ustulatus* and *A.sputator. A.lineatus* together with *A.obscurus* were reported as the most abundant species in western regions. *A.brevis* was not mentioned. Our investigations indicated the changes in the distribution and abundance of these species.

Methods: The abundance of the five species was examined on sex pheromone traps (Csalomon) in 15 fields (corn, soybean, barley and alfalfa) located in three different regions in Croatia in 2007. Pheromones were operated from April to September, checked weakly and changed every 6 weeks.

Results: The total number of collected beetles varied between 181 and 1482 per field. No significant differences between the total numbers of adults among different crops were registered. The average number of collected adults per field per region varied between 419 and 868 without any significant difference among the regions. The most abundant species in all regions was *A.ustulatus* with dominance index between 52 and 80%. *A.lineatus* had significantly higher dominance index in the west region (28.72%) while *A.obscurus* had significantly higher dominance index in east region than in other 2 regions. The abundances of *A.brevis* and *A sputator* were between 1.42 and 13.08% depending on the species and region without significant differences.

Conclusions: The most dangerous species *A.ustulatus* has been spread toward west and is eudominant species in all regions. *A.lineatus* is eudominant in the west region but *A.obscurus* is eudominant in east region and these species do not appear together.

POSTER PRESENTATION

The characteristics of the populations of five *Agriotes* (Coleoptera: Elateridae) species in three regions in Croatia

Reneta Bažok, Antonela Kozina, Jasminka Igrc Barčić, Tomislav Kos

Faculty of Agriculture, Zagreb, Croatia

Introduction: The literature data reported that the most abundant species in eastern regions of Croatia are *A.ustulatus* and *A.sputator. A.lineatus* together with *A.obscurus* were reported as the most abundant species in western regions. *A.brevis* was not mentioned. Our investigations indicated the changes in the distribution and abundance of these species.

Methods: The abundance of the five species was examined on sex pheromone traps (Csalomon) in 15 fields (corn, soybean, barley and alfalfa) located in three different regions in Croatia in 2007. Pheromones were operated from April to September, checked weakly and changed every 6 weeks.

Results: The total number of collected beetles varied between 181 and 1482 per field. No significant differences between the total numbers of adults among different crops were registered. The average number of collected adults per field per region varied between 419 and 868 without any significant difference among the regions. The most abundant species in all regions was *A.ustulatus* with dominance index between 52 and 80%. *A.lineatus* had significantly higher dominance index in the west region (28.72%) while *A.obscurus* had significantly higher dominance index in east region than in other 2 regions. The abundances of *A.brevis* and *A sputator* were between 1.42 and 13.08% depending on the species and region without significant differences.

Conclusions: The most dangerous species *A.ustulatus* has been spread toward west and is eudominant species in all regions. *A.lineatus* is eudominant in the west region but *A.obscurus* is eudominant in east region and these species do not appear together.

POSTER PRESENTATION

Ecological divergence within a population of the bladder grasshopper *Bullacris discolor*

Vanessa Couldridge

University of the Western Cape, Bellville, South Africa

Bullacris discolor (Orthoptera: Pneumoridae) is a species of bladder grasshopper endemic to South Africa. A single population of this species has been found to exhibit two distinct colour morphs, each of which feeds and lives on a different species of host plant. Morphological measurements and sound recordings of male advertisement calls were compared between the two types to determine to what extent they differ from each other. Morphology was found to be fairly similar for the two colour morphs, with pronotum length being the only characteristic that differed significantly between them. Male calls differed significantly in three of the seven characteristics measured, including carrier frequency, total length and length of the introductory syllables. These results suggest that ecological differentiation may be taking place within this population, which may be the first step towards speciation in sympatry. Host switching may provide the initial catalyst for population divergence that is then reinforced through natural or sexual selection.

POSTER PRESENTATION

Long-lasting repellents for treatment of mosquito nets against insecticide resistant and susceptible malaria vectors

Raphael N'Guessan, Carnevale Pierre, Bart GJ Knols, Pelagie Boko, Abibathou Odjo, Mark Rowland

[1]Centre de Recherche Entomologique de Cotonou (CREC), Cotonou, Benin, [2]Institut de Recherche pour le Developement (IRD), Montpellier, France, [3]University of Wageningen, The Netherlands, Wageningen, Netherlands

Owing to the development of pyrethroid resistance in malaria vectors, it is of paramount importance to identify chemical alternatives, which if necessary could be used to replace or supplement the pyrethroids for use on bed nets. Synthetic insect repellent are widely used for personal protection as skin or clothing applications. The efficacy of conventional repellent treated nets (RTNs) was evaluated in experimental huts against insecticide-resistant *Anopheles gambiae* and *Culex quinquefasciatus*. The repellents tested were DEET (N,N-diethyl-3-methylbenzamide) at 7.9g/m^2 and two formulations of ethyl butylacetylaminopropionate (IR3535) at 7.6 and 7.3 mg/m^2. Over 45 nights the RTNs reduced by 74-82% the number of *An. gambiae* entering the huts but had no impact on *Cx. quinquefasciatus* entry to huts.

There was a 62-64% reduction in the proportion of *An. gambiae* blood-feeding in huts with RTNs but no reduction in the proportion of *Cx. quinquefasciatus* blood-feeding. An unexpected result was a 69-76% mortality of *An. gambiae* and 58%-61% mortality of *Cx. quinquefasciatus* in huts containing RTNs. Tunnel tests conducted in the laboratory to assess the residual activity of RTNs indicated that mortality and bloodfeeding inhibition were still apparent 6 weeks after treatment though a rapid decline in residual activity over time was observed. A more rapid decline in toxicity was noticed with the IR3535 brands than with DEET. The conventional repellent being inherently volatile, further tests of a Microcapsule suspension of DEET on nets in which the active ingredient slowly diffuses from a capsule that binds the repellent, strongly enhanced the residual efficacy of the net. The formulation repelled, inhibited bloodfeeding and killed mosquitoes for a period of at least 6 months. The high mortality of wild mosquitoes bearing multiple insecticide resistance mechanisms indicates that application of repellent to nets might constitute a useful tool to overcome insecticide resistant mosquitoes and have potential for use on clothing, bedding materials distributed in disasters, emergencies and refugee camp settings.

POSTER PRESENTATION

Eusocial beetle revealed as diploid

Shannon Smith[1], Andrew Beattie[1], Adam Stow[1], Deborah Kent[2]

[1]Department of Biological Sciences, Macquarie University, New South Wales, Australia, [2]New South Wales Department of Primary Industries Science and Research, New South Wales, Australia

The ambrosia beetle, *Austroplatypus incompertus* (Schedl), is the only known Coleopteran that exhibits eusocial behaviour. It lives in a multi-branched gallery system excavated in living trees of the genus *Eucalyptus* and is distributed across the east coast of New South Wales, Australia. Gallery systems are initiated by solitary fertilised females. Mature colonies are composed of overlapping generations, with morphologically distinct females undertaking tunnel maintenance and predator control. Despite the economic importance and unique characteristics of *A. incompertus*, this study is the first to apply molecular techniques to investigate their demography and mating system.

We developed a highly polymorphic and informative microsatellite marker for *A. incompertus*, and used this marker to reveal their diplo-diploid nature. Our finding supports the notion that collateral kin selection as a result of genetic relatedness has not played a significant role in the evolution of eusocialty in the beetle. In this case, eusociality could be attributed to factors such as: relatively easily defended gallery systems, stability of their habitat and food source, and the risk and difficulty associated with new gallery establishment. Current research has been designed to consider this premise. Examination of spatio-temporal molecular variation within *A. incompertus* will reveal details of their mating system, colony composition and persistence, illuminating historical and current dispersal patterns. These specifics will also provide the basis of practical advice for hardwood forest management.

POSTER PRESENTATION

Side-effects of bait formulated insecticides with potential use against *Bactrocera oleae* on *Chrysoperla carnea*

Pilar Medina, Gladis Contreras, Angeles Adán, Flor Budia, Pedro Del Estal, Manuel González, Pedro Luis Aguado, Elisa Viñuela

[1]Technical University of Madrid (UPM), Madrid, Spain, [2]Dpto. Protección Vegetal, INIA, Madrid, Spain

Introduction: *Bactrocera oleae* (Gmelin) (Diptera: Tephritidae) is one of the key pests on olives in the Mediterranean area, representing 97% of world production. Olive fly larvae feed on olive fruits, causing premature drop of attacked fruits and direct pulp destruction as well as an increase on oil acidity, which renders the oil unmarketable.

Methods: The main method usually used to control this pest in Spain, is the application of aerial or terrestrial bait spraying of hydrolysate attactants with conventional insecticides (currently dimethoate) targeting adults. One disadvantage of these treatments is the negative impact on non-target insects such as *Chrysoperla carnea* (Stephens), the major oophagous predator of the olive moth *Prays oleae* (Bernard), the second pest on importance on Mediterranean basin on olive groves. In this work, some candidate insecticides for the control of the olive fruit fly were investigated: fipronil (Regente®), imidacloprid (Confidor®), natural pyrethrins+piperonyl butoxide (Pelitre Hort®) and spinosad (Spintor Cebo®) and compared with the standard dimethoate (Perfeckthion®). The maximum field recommended rate was tested on *C. carnea* larvae following the IOBC (International Organization of Biological Control) guidelines for extended laboratory and persistence tests.

Results: Fipronil was the most toxic insecticide on extended laboratory test, followed by dimethoate, imidacloprid, natural pyrethrins+piperonyl butoxide and, finally, spinosad, which was harmless. Regarding persistence, fipronil was the most persistant, followed by dimethoate and imidacloprid, whereas natural pyrethrins+piperonyl butoxide resulted innocuous.

Conclusions: Our results show that out of the studied pesticides, spinosad is compatible with the studied natural enemy while fipronil is clearly harmful.

POSTER PRESENTATION

Epicuticular lipids as caste-recognition cues in the termite *Prorhinotermes simplex* (Isoptera: Rhinotermitidae)

Robert Hanus, Rafal Piskorski, Jan Šobotník, Irena Valterová

Institute of Organic Chemistry and Biochemistry AS CR, v.v.i., Prague, Czech Republic, Prague, Czech Republic

Introduction: The recognition of nestmates in eusocial animals is a prerequisite for the maintenance of integrity of societies. It allows an exchange of altruistic behaviour with related individuals and reduces social parasitism. Another level of recognition in eusocial communities is the recognition of particular castes. In termites the epicuticular lipids are involved at both levels. We compare the chemical diversity of epicuticular lipids in imaginal and neotenic reproductives, soldiers, and pseudergates from related and unrelated populations of *Prorhinotermes simplex* from Cuba and Florida with emphasis on a) discrimination among castes and its dynamics, b) chemical phenotype distances between populations.

Methods: Individuals were removed from laboratory colonies, their body washes were analysed by means of gas chromatography with flame ionisation and mass spectrometric detection. Multivariate statistical comparison allowed us to compare the similarities between samples and draw conclusion about chemical diversity of epicuticular lipids.

Results: In each colony, a clear distinction could be made among castes, often based not only on quantitative but also on qualitative differences. However, the chemical pattern of castes was not identical in all colonies and revealed to be variable in time. Nevertheless, these variations were not as profound as the geographical differences.

Conclusions: The results indicate that the chemical composition of epicuticular lipids varies among related colonies and in time, and suggest thus that also the caste recognition system is subjected to dynamic changes at a short-term scale.

Acknowledgements: Grant Agency of the Academy of Sciences of the Czech Republic (A600550614).

POSTER PRESENTATION

Impact of UV-absorbing greenhouse nets in the population increase and spatial distribution of *Macrosiphum euphorbiae* Thomas on lettuce crops

Saioa Legarrea, Beatriz M. Diaz, Ignacio Morales, Elisa Viñuela, Alberto Fereres

[1]Dpto Preotección Vegetal, CCMA-CSIC, Madrid, Spain, [2]Technical University of Madrid (UPM), Madrid, Spain

Introduction: The presence of *Macrosiphum euphorbiae* Thomas in lettuce involves cosmetic damage and high economic losses that forces to develop new control strategies.

Methods: In this context, UV-absorbing nets were tested under field conditions under two tunnels divided in four sealed identical compartments. The greenhouses were covered by 50 mesh nets, one of which had no UV-absorbing additives (Standard) while the other (BioNet®) filtered most of the UV incident light. Four lettuce plants were artificially infested with a density of 8 adult aphids/plant at the entrance of each tunnel compartment. Every plant in the tunnel was sampled twice or once a week by visual inspection in order to describe aphid population dynamics and their spatial distribution.

Results: The results show that the population increase of *M. euphorbiae* was significantly larger under the Standard net that under BioNet® from three weeks after infestation onward. In addition, the total number of aphids and the percentage of aphid-infested plants were significantly higher under the tunnel coverted by the standard net. The spatial distribution of aphids for each sampling date was analized using the SADIE and FOCI methodology. When the crop was half developed aphids were established in a more aggregated pattern under the BioNet cover. We also calculated the Shannon' entropia index as a measure of the degree of hetereogenity of population counts which was found to be highest for the Bionet tunnels. Marketable yield was also higher under the UV-absorbing nets.

Conclusion: Our results suggest that the reproduction rate and the dispersion of *M. euphorbiae* is significantly reduced under the UV-absorbing nets, which should be considered as a promising alternative pest-control strategy.

POSTER PRESENTATION

Geographical patterns, biodiversity hotspots and gaps in knowledge: Species-area relationships for moths and butterflies of Russia

Mikhail Kozlov[1], Sergey Sinev[2]

[1]University of Turku, Turku, Finland, [2]Zoological Institute, St. Petersburg, Russian Federation

Introduction: Until very recently, only scattered information was available on species richness of moths and butterflies of Russia. Publication of the first comprehensive catalogue in 2008 allowed biogeographical analysis aimed at exploration of large-scale geographical patterns.

Methods: We based our analysis on the numbers of species of different taxa calculated for 40 regions covering the entire territory of Russia, and compared species-area relationships with those in well-studied countries of Europe.

Results: The analysis demonstrated that fauna of moths and butterflies of Russia is explored much worse than in the rest of the Europe; only few regions of Russia (e.g. Murmansk district) fit species-area relationships based on data from European countries. The knowledge is generally biased, and 'microlepidoptera' are underrepresented in the majority of the regions. The most obvious shortage of information was detected for north-eastern parts of both Siberia (especially from territories adjacent to the Okhotsk sea) and the European Russia. Correction for these geographical and taxonomic biases allowed discovering both latitudinal and longitudinal trends in species richness and species-area relationships and identifying several biodiversity hotspots. We also estimated the numbers of species that are not yet reported but are likely to be found in each region of Russia and in the country as a whole.

Conclusions: Although information on local faunas of moths and butterflies of Russia is still incomplete, analysis of the data summarized in recently published catalogue has important ecological implications, including suggestion of tentative conservation targets for different regions.

POSTER PRESENTATION

Bt Cotton expressing the Cry1F and Cry1Ac protein in the management of *Alabama argillacea* Hueb, *Heliothis virescens* Fabr. and *Spodoptera frugiperda* Smith

Renan Gravena[1], Santos Antonio[2], Santin Gravena[1], Marcelo Batistela[1], Sergio Benvenga[1], Adriana Gravena[1]

[1]Gravena Ltd., Jaboticabal, SP, Brazil, [2]Dow Agro Sciences, São Paulo, SP, Brazil

Introduction: The insertion of genes of *Bacillus thuringiensis* in cotton crop promotes healthy crop and beneficial entomofauna. The efficiency of Bt Cotton, expressing Cry1F and Cry1Ac, was compared to the conventional, treated or not with spinosad to control *Alabama argillacea*, *Heliothis virescens* and *Spodoptera frugiperda*.

Methods: Randomized complete block design with 4 treatments and 5 replicates was used. Ten small larvae of *Spodoptera* and 5 of *Heliothis* larvae/plant were released natural ocurrence of *Alabama* was considered for evaluations. Percent of defoliation, number of eggs and larvae, and reproductive structures were evaluated. The application of spinosad on Bt-plot and the conventional plot was made from 2 to 5 days after the larvae release.

Results: *Heliothis* small larvae in Bt Cotton (with or without insecticide) presented infestations from 0 to 0.4 in contrast to the control, from 0.8 to 10.6/plant. The conventional plots showed from 0.2 to 3 larvae/plant with no difference with Bt and control plots. No large larvae were found in Bt Cotton. The oviposition of *Heliothis* was even less in control than the treatments. The average of damaged reproductive structures was less in Bt than in conventional and control plots. The density of *Spodoptera* was low even with larvae releases, with no statistical difference. The number of reprodoctive structures damaged by *Spodoptera*, in Bt Cotton (both systems) was less than in conventional and control plots statiscally.

Conclusion: The Cry1F/Cry1Ac Cotton is effective in the management of *Alabama*, *Spodoptera* and *Heliothis*, showing no damage to their reproductive structures.

POSTER PRESENTATION

Identification of a natural source of resistance to leaf miner species in melon (*Cucumis melo* L.)

Faiza E.E.Salah[1], M. T. Yousif[2], Y. G. Unis[2] , A. A. Gesmella[2]

[1]Faculty of Agriculture, Gezira University, Sudan; [2]National Institute for Promotion Horticultural Exports, Gezira University, Sudan

Melon (*Cucumis melo* L.) considered one of the most important vegetable crop. It is production facing the problem of insect infestation. Mainly white flies (*Bemisia tabac*i), aphids (*Aphis gossypyii*), leaf miners *(Liriomyza* spp.), beetles and fruit flies.

Objective of this study to identify natural source(s) for resistance to leaf miner. Surveys and collection missions carried out in some states in Central Sudan, to estimate damage caused and to collect promising accessions for resistance. Infestation found high in all visited areas. It observed leaf miners infestation is drastically decreased as you go north from Duem city in the White Nile State. The collected accessions with some introduced lines, kindly provided by the Plant Genetic Resource Unit of the Agricultural Research Corporation, were evaluated for resistance to leaf miner under field conditions of the Gezira University Research Farm, Medani, Sudan. The Complete randomized Block Design with four replications used in this study. Among the 102 screened accessions and lines only nine accessions, 7 indigenous accessions and 2 introduced lines, were found to be promising for leaf miner resistance under field conditions. The top resistant genotypes were HSD 2445, collected in Gezira State, with a general mean of infestation of 0.18% and HSD 1923, collected in the White Nile State, with a general mean of 1.77%, followed by the introduced lines Nantais Oblong (France) with a general mean of 24.7% and PI 313970 with a general mean of 36. 7%.

POSTER PRESENTATION

Identification of a natural source of resistance to leaf miner species in melon (*Cucumis melo* L.)

Faiza E.E.Salah[1], M. T. Yousif[2], Y. G. Unis[2] , A. A. Gesmella[2]

[1]Faculty of Agriculture, Gezira University, Sudan; [2]National Institute for Promotion Horticultural Exports, Gezira University

Melon (*Cucumis melo* L.) considered one of the most important vegetable crop. It is production facing the problem of insect infestation. Mainly white flies (*Bemisia tabac*i), aphids (*Aphis gossypyii*), leaf miners *(Liriomyza* spp.), beetles and fruit flies.

Objective of this study to identify natural source(s) for resistance to leaf miner. Surveys and collection missions carried out in some states in Central Sudan, to estimate damage caused and to collect promising accessions for resistance. Infestation found high in all visited areas. It observed leaf miners infestation is drastically decreased as you go north from Duem city in the White Nile State. The collected accessions with some introduced lines, kindly provided by the Plant Genetic Resource Unit of the Agricultural Research Corporation, were evaluated for resistance to leaf miner under field conditions of the Gezira University Research Farm, Medani, Sudan. The Complete randomized Block Design with four replications used in this study. Among the 102 screened accessions and lines only nine accessions, 7 indigenous accessions and 2 introduced lines, were found to be promising for leaf miner resistance under field conditions. The top resistant genotypes were HSD 2445, collected in Gezira State, with a general mean of infestation of 0.18% and HSD 1923, collected in the White Nile State, with a general mean of 1.77%, followed by the introduced lines Nantais Oblong (France) with a general mean of 24.7% and PI 313970 with a general mean of 36. 7%.

POSTER PRESENTATION

Optimization of methods for monitoring of *Oscinella frit* (L.) (Diptera: Chloropidae) on winter and spring barley

Hristina Krasteva, Olia Karadjova, Ventsislav Ventsislavov

Plant Protection Institute, Kostinbrod, Bulgaria

Introduction: *Oscinella frit* is the most damaging pest on winter and spring barley grains in Bulgaria. Yield reductions ranging from 3% to 35% have resulted from larvae feeding. The relationships between percent of damaged grains and density of flies in relations to barley growth stage and daily fly activity of adults were studied to formulate efficient sampling procedures.

Methods: Studies were conducted in winter and spring barley fields at the Plant Protection Institute in Kostinbrod during 1997-2007. Density dynamics of flies was observed by sweep-net using samples of 10 and 20 sweeps. Grain injury was presented in percentage of the total amount of grains per ear. Data were analyzed with program "Statistica 6" at $P \leq 0.05$. The relative standard error was used to compute the accuracy of estimations (Southwood, 1978).

Results: Significant positive correlations were found between per cent of damaged winter and spring barley grains and density of flies registered at the beginning of ear emergence stage (50-55 on Zadoks scale). Adult observation accuracy below 25 % was achieved in treatments in which the observation was carried out between one and four o'clock in the afternoon for the first generation and between ten and twelve o'clock in the morning for the second generation of *O. frit* by using samples of 10 sweeps.

Conclusion: The barley growth stage 50-55 is an optimum for sampling of frit fly adult density to make a decision for chemical control. For adult density observation accuracy below 25% is achieved by using samples of 10 sweeps.

POSTER PRESENTATION

Interspecific competition rather than predation explains host plant shift of a leaf beetle *Chrysomela lapponica*

Elena Zvereva[1], Mikhail Kozlov[1], Oksana Kruglova[2]

[1]University of Turku, Turku, Finland, [2]University of Belarus, Minsk, Belarus

Introduction: Leaf beetle *Chrysomela lapponica* sequesters major component of larval defensive secretion, salicylaldehyde, from salicyl glucosides (SGs) of host plant. However, some populations have shifted to SG-poor hosts; their defensive secretion does not contain salicylaldehyde. We tested whether these shifts allowed to escape from (i) specialist natural enemies and/or (ii) interspecific competition.

Methods: We compared field mortality in four populations of the leaf beetle feeding on SG-rich (in Kola Peninsula and Finnish Lapland) and SG-poor host plant species (in Ural and Belarus).

Results: Mortality from generalist enemies was highest in Belarus population, but mortality from specialists did not differ among four populations. Experiments showed that *C. lapponica* failed to escape from specialists by shift to SG-poor hosts because specialist enemies developed ability to use secretion of prey from SG-poor hosts as a search cue as effectively as salicylaldehyde.

Foliar damage of host imposed both by leaf puncturing and by feeding larvae of *Chrysomela vigintipunctata* decreased performance of *C. lapponica* indicating that indirect (host plant mediated) competition with early season specialist herbivores may have forced *C. lapponica* to escape from SG-rich host. Direct exploitative competition may also be strong during outbreaks of *C. vigintipunctata*. Moreover, populations of *C. lapponica* switched to SG-poor hosts are found mostly in the localities where distributions of these two leaf beetle species overlap.

Conclusions: Interspecific competition rather than escape from specialist enemies is the most plausible selection force that have caused host plant shift at least in some populations of *C. lapponica*.

POSTER PRESENTATION

Digestive proteaeses of the banana weevil, *Cosmopolites sordidus* Germar (Coleoptera: Curculionidae) and their response to protease inhibitors

Miguel Montesdeoca, Gloria Lobo, Félix Ortego, Aurelio Carnero, Pedro Castañera

ICIA, La Laguna,Canary Islands, Spain

Introduction: "Dwarf Cavendish" cv. banana is widely grown in Canary Islands with a production of approximately 400000 tons/year distributed in 8000 Ha. As the banana weevil larvae, *Cosmopolites sordidus* Germar (Coleoptera: Curculionidae) grows inside the rhizome, common practices as insecticide treatments and pheromones are poor effective in the control of this pest being an alternative the development of pest resistant banana expressing genes proteinase inhibitor. Thus, it is necessary to gain a comprehensive knowledge of the major digestive enzymes present in the banana weevil gut and their interaction with appropriate inhibitors.

Material and methods: Digestive protease activities of the banana weevil were characterized based on the ability of gut extracts to hydrolyze specific synthetic substrates, optimal pH and hydrolysis sensitivity to protease inhibitors.

Results: Adults of this species were found to use a complex proteolytic system for protein digestion that includes cathepsin D-, cathepsin B-, trypsin-, chymotrypsin-, aminopeptidase-, carboxypeptidase A- and carboxypeptidase B-like activities. According to this proteolytic profile, several serine and cysteine proteinase inhibitors were tested in vitro to establish their potential as resistance factors.

POSTER PRESENTATION

Digestive proteaeses of the banana weevil, *Cosmopolites sordidus* Germar (Coleoptera: Curculionidae) and their response to protease inhibitors

Miguel Montesdeoca, Gloria Lobo, Félix Ortego, Aurelio Carnero, Pedro Castañera

ICIA, La Laguna,Canary Islands, Spain

Introduction: "Dwarf Cavendish" cv. banana is widely grown in Canary Islands with a production of approximately 400000 tons/year distributed in 8000 Ha. As the banana weevil larvae, Cosmopolites sordidus Germar (Coleoptera: Curculionidae) grows inside the rhizome, common practices as insecticide treatments and pheromones are poor effective in the control of this pest being an alternative the development of pest resistant banana expressing genes proteinase inhibitor. Thus, it is necessary to gain a comprehensive knowledge of the major digestive enzymes present in the banana weevil gut and their interaction with appropriate inhibitors.

Material and methods: Digestive protease activities of the banana weevil were characterized based on the ability of gut extracts to hydrolyze specific synthetic substrates, optimal pH and hydrolysis sensitivity to protease inhibitors.

Results: Adults of this species were found to use a complex proteolytic system for protein digestion that includes cathepsin D-, cathepsin B-, trypsin-, chymotrypsin-, aminopeptidase-, carboxypeptidase A- and carboxypeptidase B-like activities. According to this proteolytic profile, several serine and cysteine proteinase inhibitors were tested in vitro to establish their potential as resistance factors.

POSTER PRESENTATION

Ovary structure and oogenesis in Dermaptera – New evidence for relationship within an order

Szczepan M. Bilinski[1], Fabian Haas[2], Waclaw Tworzydlo[1]

[1]Department of Systematic Zoology, Institute of Zoology, Jagiellonian University, Krakow, Poland, [2]icipe - African Insect Science for Food and Health, Nairobi, Kenya

Introduction: Dermaptera (earwigs) is an insect order comprising about 2200 extant described species classified in 11 families and 3 suborders. Some research has been conducted on phylogenic relationship within this group, including characters of the wing and male genitalia as well as molecular data. However, the studies still did not answer all the question about their relationships. It has been shown that representatives of various subgroups of earwigs may significantly differ in structure of ovaries and process of oogenesis.

Methods: The ovaries of earwigs were analysed using light and electron microscopy.

Results: In all cases, the ovaries were of meroistic – polytrophic type which means that developing oocytes are accompanied by the nurse cells. An individual ovary from representatives of more basal taxa (e.g. Labiduridae) comprises five long ovarioles, whereas in more derived taxa (e.g. Forficulidae) there are about 30-40 short ovarioles per ovary. In all studies species, ovarian follicles are composed of two cells only: an oocyte and a polyploid nurse cell that are connected by a simple intercellular bridge. Although, the final number of cells constituting the ovarian follicle is constant in Dermaptera, the processes that lead to their formation in various earwig subgroups are apparently different. In derived taxa, the cystoblast divides only once, whereas in more basic families, the cystoblast undergoes three mitotic divisions leading to the formation of 8-cell clusters that are secondarily split into 2-cell clusters. We also found that in taxa except the Pygidicranidae, the nurse cell nucleus is of an ameboid shape. In the Pygidicranidae its shape is rather discoidal.

Conclusions: We consider the ovaries and the oogenesis to be useful characters for phylogenic studies.

POSTER PRESENTATION

Tropical fly in European soup: *Sphyracefala europae*

Tamás Vásárhelyi

Hungarian Natural History Museum, Budapest, Hungary, Hungary

No abstract submitted, or incorrect abstract submitted, or abstract submitted in an inaccessible format.

POSTER PRESENTATION

Structure and functioning of the ovarian follicles in forficuloid dermapterans

Szczepan M. Bilinski, Waclaw Tworzydlo

Department of Systematic Zoology, Institute of Zoology, Jagiellonian University, Krakow, Poland

Introduction: The ovaries of the studied forficuloid earwig species (*Forficula auricularia, Chelidurella acanthopygia, Doru lineare* and *Opisthocosmia silvestris*) are meroistic-polytrophic and composed of numerous short ovarioles that consist of a terminal filament, germarium and vitellarium.

Methods: The ovaries of earwigs were analysed using light, fluorescence and electron microscopy.

Results: The germaria of adult females comprise meiotic (pachytene) and postmeiotic (differentiating) germ cell clusters, as well as small prefollicular cells. All germ cell clusters consist of two cells that are connected by a single intercellular bridge. In the vitellarium there are usually 2 ovarian follicles only. The individual follicle consists of a synthetically dormant oocyte and a single, polyploid nurse cell and is surrounded by a layer of somatic follicular cells (FCs). During previtellogenesis the nurse cell enlarges and becomes highly active. Concurrently its nucleus attains characteristic, irregular shape. In the nurse cell nucleus of one studied species, *F. auricularia* in addition to chromatin aggregations and RNA- and Ag-NOR-positive nucleoli, a single compact DNA- and Ag-NOR-positive body is present.Immunocytochemical tests showed that the body coantains snoRNAs. During advanced vitellogenesis the molecules synthesized in the nurse cells (RNAs, proteins, as well as nurse cell ogranelles) are transferred to the ooplasm *via* the intercellular bridge. During this transfer the nurse cell nucleus is retained in the cell center and does not occlude the intercellular bridge.

Conclusions: The results of hictochemical and immunocytochemical analyses indicate that the DNA-positive body is involved in the formation of the nucleoli.

POSTER PRESENTATION

Insect identification using Artificial Neural Networks (ANN)

Jaromir Vanhara, Peter Fedor, Igor Malenovský, Natália Murárikova, Josef Havel

[1]Masaryk University, Brno, Czech Republic, [2]Comenius University, Bratislava, Slovakia, [3]Moravian Museum, Brno, Czech Republic, [4]Masaryk University, Brno, Czech Republic, [5]Masaryk University, Brno, Czech Republic

Introduction: Entomology, as well as its application in many fields, such as agriculture, forestry, human and veterinary medicine, relies heavily on the accurate identification of species. Besides molecular diagnostic techniques, the progress in information technology has opened opportunities for the computer-assisted taxonomy. Artificial Neural Networks (ANN) seem to have been one of the most promising tools for the basis of such systems. The advantages of ANN include an ability to learn from examples and to generalize observed patterns.

Methods: The use of ANN requires a training database in which specimens, correctly identified by experts, are included. Each specimen has to be characterized by diagnostic variables (characters). For ANN inputs can be used digital images, optically sensed wing beat frequency spectra, near-infrared reflectance spectra, bioacoustic recordings, chemotaxonomy or morphometry. An ANN model is designed to find a relationship between the characters (=*input*) and species (=*output*). The quality of the training set is an essential prerequisite to obtaining reliable identifications.

Results: Our case studies on thrips and diptera used morphometric data mostly. The high percentage of correctly identified specimens (about 97 %) is promising for a wider use of ANN for insect identification in practice.

Conclusions: ANN is cheap and non-destructive suitable also for type material or permanently mounted slides. ANN have the potential to enhance the practice of routine identification with a non-expert as technical help. High reliability of classification is promising for a wider application of ANN in the practice of insect identification.

POSTER PRESENTATION

Efficiency of Cyflumetofen to manage the leprosis mite *Brevipalpus phoenicis* (Geijskes) (Acari: Tenuipalpidae) in a Brazilian citrus orchard (*Citrus sinensis* Osbeck).

Jose Silva[1], Toshiaki Shitara[2], Santin Gravena[1], Marcelo Batistela[1], Sergio Benvenga[1], Adriana Gravena[1], Renan Gravena[1]

[1]Gravena Ltd., Jaboticabal, SP, Brazil, [2]Iharabras, Sorocaba, SP, Brazil

Introduction: The citrus plantations in Brazil has as key pest the Citrus Leprosis (Flat) Mite (CLM), *Brevipalpus phoenicis (*Geijskes). This pest has also a high tendency to become resistant against acaricides needing to alternate the mode of actions of several compounds to monitor it. This paper deals with the study of the effect of the new compound Cyflumetofen to manage the CLM.

Methods: Cyflumetofen (OK-5101), in several doses, was compared with espirodiclofen and cyhexatin, spraying in citrus (*Citrus sinensis)* orchards, S. Paulo, Brazil. The trials were a semi-field to determine the Cyflumetofen residual effect and two field trials being one using plants 7 years old, variety Pera and the other with 3 years old. The Cyflumetofen dosages tested were 30, 35, 37.5 e 40 mL/hL. The field trials had as experimental design the randomized blocks and the semi-field design was complete randomized blocks. For this test, after application with a ground sprayer fruits were collected at 1, 3, 5, 7, 10, 12 and 15 after for mite exposition and mortality evaluation.

Results: The residual effect of Cyflumetofen (OK-5101) against CLM, in all dosages, was 7 days on citrus fruits. By the results of both field trials, all dosages of the new acaricide Cyflumetofen (OK-5101) were efficient to control the CLM, *B. phoenicis*, in fruits and branches, either in percent of population reduction or in number o mites per sample.

Conclusions: All dosages of the new acaricide Cyflumetofen were efficient to control the CLM with residual effect of 7 days.

POSTER PRESENTATION

Efficiency of Cyflumetofen to manage the leprosis mite Brevipalpus phoenicis (Geijskes) (Acari: Tenuipalpidae) in a Brazilian citrus orchard (Citrus sinensis Osbeck).

Jose Silva[1], Toshiaki Shitara[2], Santin Gravena[1], Marcelo Batistela[1], Sergio Benvenga[1], Adriana Gravena[1], Renan Gravena[1]

[1]Gravena Ltd., Jaboticabal, SP, Brazil, [2]Iharabras, Sorocaba, SP, Brazil

Introduction: The citrus plantations in Brazil has as key pest the Citrus Leprosis (Flat) Mite (CLM), *Brevipalpus phoenicis (*Geijskes). This pest has also a high tendency to become resistant against acaricides needing to alternate the mode of actions of several compounds to monitor it. This paper deals with the study of the effect of the new compound Cyflumetofen to manage the CLM.

Methods: Cyflumetofen (OK-5101), in several doses, was compared with espirodiclofen and cyhexatin, spraying in citrus (*Citrus sinensis)* orchards, S. Paulo, Brazil. The trials were a semi-field to determine the Cyflumetofen residual effect and two field trials being one using plants 7 years old, variety Pera and the other with 3 years old. The Cyflumetofen dosages tested were 30, 35, 37.5 e 40 mL/hL. The field trials had as experimental design the randomized blocks and the semi-field design was complete randomized blocks. For this test, after application with a ground sprayer fruits were collected at 1, 3, 5, 7, 10, 12 and 15 after for mite exposition and mortality evaluation.

Results: The residual effect of Cyflumetofen (OK-5101) against CLM, in all dosages, was 7 days on citrus fruits. By the results of both field trials, all dosages of the new acaricide Cyflumetofen (OK-5101) were efficient to control the CLM, *B. phoenicis*, in fruits and branches, either in percent of population reduction or in number o mites per sample.

Conclusions: All dosages of the new acaricide Cyflumetofen were efficient to control the CLM with residual effect of 7 days.

POSTER PRESENTATION

Tecia solanivora (Povolny 1973) (Lepidoptera: Gelechiidae) a new pest in Canary Islands

Aurelio Carnero, Angeles Padilla, Santiago Perera, Elena Trujillo, Estrella Hernández

ICIA, La Laguna,Canary Islands, Spain

Distribution: First reports in the Canary Islands of damage to potatoes by the Guatemalan moth *Tecia solanivora* were made in 1999, on the island of Tenerife. Although continental Europe is currently still free of *T. solanivora*, it is an important quarantine pest elsewhere and its spread to other islands posed a serious threat to the local staple potato crop. Initial incidence was established by placing pheromone traps in several field localities and in wholesale seed-potato warehouses throughout Tenerife. Data from December 2006 showed that the entire northern side of the island is affected, while infestations in the south remain restricted. Some evidences reports also cite its presence on the islands of Gomera, Grand Canary and La Palma.

Damages and losses: To date, the consequences of this pest are reductions in yield and in growing surface, and increased crop costs. Failure to adequately contain the moth could lead to the collapse of the local potato industry as well as the possibility of losing historically important cultivars, and the ever present threat of its spread to Mainland Spain and from there to the rest of Europe.

Control alternatives: Although most research to date has focussed on integrated management of the potato crop, ongoing research on fumigating harvested tubers with gases such as CO_2, O_2, and N_2 (alone or combined) appears promising: provisional results show a 100% mortality rate for larvae and adults in potatoes exposed to subjected to CO_2 (20%) Meanwhile the pupae were unaffected: pupal mortality was not significant.

POSTER PRESENTATION

The effect of vernalization on host plant resistance of wheat to Russian wheat aphid, *Diuraphis noxia*, biotype RWASA2

Robbie Lindeque[1], Vicki Tolmay[1], Maryke Labuschagne[2]

[1]ARC-Small Grain Institute, Bethlehem, Free State, South Africa, [2]University of the Free State, Bloemfontein, Free State, South Africa

Above-average late winter- and early spring temperatures during 2005 linked vernalization requirement of winter- and facultative varieties to field susceptibility of commercial varieties to RWA. The alternative hypothesis suggested that RWA damage of wheat varieties resulted from biotype development. In 2005 82% of winter and intermediate dryland wheat varieties available in South Africa contained host plant resistance through the dominant single genes, *Dn1* or *Dn2* from donor accessions PI 137739 and PI 262660. Although donors such as PI 294994 (*Dn-5, Dn-8 and Dn-9*) were also introduced into some varieties loss of *Dn-1* and *Dn-2* resistance in the field was greatly anticipated. Implications of lost host plant resistance to wheat breeding and seed production would however be significant and warranted investigations of both hypotheses. Mass screening of seedlings for RWA resistance under controlled conditions would also not be objective if vernalization is important in expression of RWA host plant resistance. Seedlings of Betta (susceptible check), CItr2401 (resistant check), Molen, Hugenoot, Limpopo, Gariep and Elands were subjected to 0-, 2-, 4-, and 6-weeks vernalization at 3°C (± 2°C) with a 10:14 hour light:dark photoperiod regime. Seedlings were removed simultaneously after vernalization and cultured at 18°C/ 12°C day/ night (± 2°C) - and 26°C/ 18°C day/ night temperatures (± 3°C) for four weeks. After a week seedlings were infested with 5 aphids per plant and visual damage rating (1 – 10) and fresh plant biomass (grams 2 plants^{-1}) was determined three weeks later. Main effects of variety on visual damage ratings and fresh biomass confirm susceptibility of Gariep, Limpopo and Elands to RWASA2. Application of the 2-week vernalization period in our experiment resulted in the best resistance by Elands to RWASA2, measured in percentage fresh biomass and corresponded with the vernalization recommendation for this variety. Our findings consequently also suggest that CItr2401 benefited from extended vernalization periods as the 6-weeks period produced significantly higher percentage biomass than 0-weeks, 2-weeks and 4-weeks periods. Results from our research however support findings in literature reporting no effect of non-vernalized or vernalized plants on RWA plant resistance ranking.

POSTER PRESENTATION

Thiamethoxam in the management of insect vectors of virus diseases and benefits to the tomato crop

Sergio Benvenga, Marcelo Batistela, Santin Gravena, Renan Gravena, Jose Silva, NIlton Araujo Jr, Luis Amorim

Gravena Ltd., Jaboticabal, Brazil

Introduction: *Frankliniella schultzei* (Trybom), *Thrips palmi* (Karny) (Thysanoptera: Thripidae), *Myzus persicae* (Sulzer) (Homoptera: Aphididae) and *Bemisia* spp. (Homoptera: Aleyrodidae) are key pests in tomato crops. The management is based on the treatment of plants in the pre-transplanting, followed by the population monitoring for new decision-makings according to the levels of action. The efficiency of thiamethoxam (Actara 250 WG at 600 g/ha), applied in plants by the transplanting date and complemented with eight weekly foliar applications of thiamethoxam + lambdacyhalothin (Engeo Pleno at 25, 50 and 75 mL/100 L), was evaluated in the management of insect vectors and beneficial aspects on a tomato crop.

Methods: The test was installed in staked tomato, *Lycopersicon esculentum*, hybrid Debora Max, County of Cravinhos, State of Sao Paulo, Brazil, with plots of 20 plants, in randomized blocks with 4 replications. The evaluation of insects density was made weekly through shaking the terminal branches on a plastic container, using 5 useful plants, complemented with a visual assessment. The benefits of the compounds on the crop were evaluated by the index of non-infected plants by viruses and productivity.

Results: The reduction rate of vectors with Thiamethoxan (Actara 250 WG) applied by the transplanting and complemented with foliar applications (Engeo Pleno; 25, 50 and 75 mL/100 L) was of 71, 73 and 81%, respectively.

Conclusions: Thiamethoxam (Actara 250 WG) and (Engeo Pleno) was efficient in the management of vectors and protected the plants against viruses, increasing the productivity related to the check.

POSTER PRESENTATION

Effect of rainfall and temperature on host plant resistance of wheat to Russian wheat aphid, *Diuraphis noxia*; biotype RWASA2

Robbie Lindeque[1], Vicki Tolmay[1], Maryke Labuschagne[2]

[1]ARC-Small Grain Institute, Bethlehem, Free State, South Africa, [2]University of the Free State, Bloemfontein, Free State, South Africa

Widespread reports of RWA virulence on commercial wheat varieties (containing *Dn-1*) were received from the eastern Free State in 2005. Virulence was confirmed by mass screening seedlings of all commercial varieties under controlled conditions and the new biotype was designated as RWASA2. In South Africa fluctuations from long-term average temperatures and rainfall coincided with lost resistance in the eastern Free State during 2005. This study firstly investigated changes in temperature and rainfall in the eastern Free State during 2005. The second objective was to determine visual damage of seedlings at 18°C/12°C, 22°C /16°C and 26°C /22°C by RWASA1 and RWASA2 and the relation with climatic variations in the eastern Free State. Thirdly, effects of RWASA2 on plant variables of Komati, Matlabas, SST 966 and SST 399 were determined at 26°C/ 20°C (± 3°C). High temperatures and soil-moisture stress occurred in the eastern Free State in 2005 during early developmental stages of dryland-wheat. A possible implication would have been reduced plant growth vigour and increased RWA population growth ultimately increasing virulence on wheat. Higher rainfall during the off–season ensured alternative host plant availability and increased over-wintering survival rate of RWA. In the second experiment resistance ratings to RWASA1 of Halt, Komati and Matlabas shifted to a less resistant- or susceptible category as developmental temperature increased and changed ranking of SST 966 substantially. RWASA2 was highly virulent on seedlings of all varieties except Halt regardless of temperature regimen. Komati, Matlabas, SST 966 or SST 399 did not express any significant resistance to RWASA2 through leaf area, leaf roll and chlorosis and support results obtained for the same varieties in the visual screening test.

POSTER PRESENTATION

Phylogeny of the tribe Athetini Casey, 1910 and its position in the subfamily Aleocharinae (Coleoptera: Staphylinidae)

Hallvard Elven, Vladimir Gusarov

Natural History Museum, University of Oslo, Oslo, Norway

Introduction: The staphylinid tribe Athetini has never been subjected to a thorough phylogenetic study. In our study molecular markers are used to infer the phylogeny of the tribe and its position within Aleocharinae.

Methods: Sequences were obtained from representative taxa of most subtribes of Athetini and several tribes related to Athetini. Sequenced regions include both mitochondrial (COI, COII, Leu1, Leu2, NADH1, 16S) and nuclear (18S) markers. RNA coding sequences were aligned manually using secondary structure information inferred by comparison with published structures. Data were analysed using maximum parsimony (PAUP) and bayesian inference (Phase). For the protein coding genes, both nucleotide and amino acid sequences were used in different analyses. For the RNA genes, secondary structure information was included in the analyses where possible.

Results: Our study supports the monophyly of a clade consisting of the tribes Athetini and Lomechusini, and a sister group relationship between that clade and the tribe Placusini. Lomechusini, together with the athetine genera *Geostiba* and *Earota*, forms a sister group to the remaining Athetini.

Conclusions: The monophyly of Athetini + Lomechusini is supported. Additional markers are needed to study relationships within Athetini in detail.

POSTER PRESENTATION

Insecticides against cone and seed insects in Norway spruce (*Picea abies*) seed orchards

Olle Rosenberg[1], Tiina Ylioja[2], Paal Krokene[3]

[1]Forestry Research Institute of Sweden, Uppsala, Sweden, [2]Finnish Forest Research Institute, Suonenjoki, Finland, [3]Norwegian Forest and Landscape Institute, Ås, Norway

Introduction: Seed production in Norway spruce (*Picea abies*) seed orchards may be severely reduced by insects attacking cones and seeds. Insects in several orders and genera are responsible for the damage, and at present there are no effective and environmentally acceptable control options. Studies in Sweden have shown promising results with spraying Bt (*Bacillus thuringiensis* var. *kurstaki* x *aizawai*) against species of Lepidoptera, but for other pests other control methods must be developed.

Methods: Tests with several insecticides were carried out in seed orchards in Sweden, Finland and Norway in 2006 and 2007. Insecticides were either conventionally applied by spraying cones (s) or injected into the lower stems (i). The following active ingredients were used: diflubenzuron (s), spinosad (s), esfenvalerate (s), imidacloprid (s), abamectin (i), acetamiprid (s) and azadirachtine (s).

Results: The efficacy of the insecticides ranged from low to negligible. Spinosad and abamectin showed most potential. Weather conditions, the fact that insecticides were applied only once during flowering and low infestation rates in some of the test sites in 2006 may explain the low efficacy of the applications. In 2007, very high infestation rates in the cones and early insect flight relative to insecticide applications may have contributed to the low efficacy.

Conclusions: The low efficacy was probably not only due to inefficient insecticides, but also due to problems with timing of insecticide application, weather conditions and insect density. To solve these problems more experimentation is called for in the future, including the use of semiochemicals for population monitoring.

POSTER PRESENTATION

Generalist fly pollination in *Ceropegia ampliata* and the role of trapping hairs

Gareth Coombs, Craig Peter, Tony Dold

Rhodes University, Grahamstown, South Africa

Introduction: Many species in the genus *Ceropegia* (Apocynaceae - Asclepiadoideae) have flowers with elaborate tubular corollas that are thought to mimic brood sites or food for pollinating flies. Pollinators are attracted to the unpleasant scent of the flowers where they are thought to be trapped by erect hairs lining the constriction of the bulbous base of the corolla tube, "forcing" prolonged visits and increasing pollen export and deposition. Pollinators are then released once the hairs have wilted.

Methods: Pollinators were collected and flowering phenology determined in a natural population of *C. ampliata* E.Mey. in the Eastern Cape, South Africa. Natural levels of pollination success were determined and the state of the hairs within the tube recorded. Histochemical stains where used to detect areas that emit scent and produce nectar.

Results: *C. ampliata* is visited by small, mainly female flies from at least 6 families but only flies of the Tachinidae (8 flies), Muscidae (2 flies) and Sarcophagidae (1 fly) bore pollinaria. Although the hairs may function to prolong pollinator visits, our data shows that pollinators can escape before hairs become flaccid and pollen transfer efficiency is generally very low. The flowers appear to accumulate small amounts of nectar in the nectaries located at the base of the gynostegium although the volumes are too small too accurately measure. Histochemical staining confirms metabolically active cells here as well as in the adaxial basal region of the petals which appears to be the site of scent of production.

Conclusion: This is the one of the first detailed studies to examine the pollination biology of a wild-growing population of *Ceropegia* and suggests generalist fly pollination in this species. Flies detained within the flowers may still escape, questioning the advantage of the trapping mechanism given the low pollination success.

POSTER PRESENTATION

Grooming behavior in the ant, *Lasius japonicus*, against entomopathogenic fungi

Masaki Okuno[1], Kazuki Tsuji[2], Kenji Fujisaki[1]

[1]Kyoto University, Kyoto, Japan, [2]University of the Ryukyus, Okinawa, Japan

Introduction: In social insects, grooming behavior is known not only for nestmate recognition, but also for immune defense system. Grooming behaviors have been indirectly studied in terms of survival rate or infection rate, under the vulnerable condition. We directly analyzed self-grooming and allogrooming to reveal the behavioral alteration as a measure of frequency of each behavior.

Methods: We tested 20 individuals in each Petri dish that was exposed to 1 of 3 fungal spore concentrations: low (10^4 spores/ml), high (10^7 spores/ml) and control (0 spore/ml). During 48h of exposure, we recorded grooming behaviors 7 times (30 min each time).The frequency of 2 types of behavior was calculated as the total number of observed behavioral events divided by the number of survival individuals. It was then converted into the mean frequency of grooming behavior and the percentage of self-grooming. Thus, we analyzed the total frequency of grooming behavior as a sum of self-grooming and allogrooming. We also observed the survival time as an indirect parameter.1

Results: When spore concentration increased from control (0 spore/ml) to high concentration (10^7 spores/ml), the mean frequency of self-grooming decreased, the mean frequency of allogrooming increased, the frequency of total grooming did not change and the percentage of self-grooming increased.

Conclusions: Frequency of self-grooming and allogrooming behaviors changes depending on spore concentration, indicating that it is an “allocation behavior”. Allogrooming behavior may play a role in the hygiene of nest, although we could not identify the significance of self-grooming.

POSTER PRESENTATION

Pathogenicity of blastospores and conidia of *Isaria fumosorosea* against pupae of the horse chestnut leaf-miner, *Cameraria ohridella*

Eva Prenerova[1], Rostislav Zemek[2], Frantisek Weyda[2]

[1]Laboratory of Plant Protection Olesna, Bernartice u Milevska, Czech Republic, [2]Biology Centre of Academy of Sciences of the Czech Republic, Institute of Entomology, Ceske Budejovice, Czech Republic

Introduction: The objective of this paper is testing the insecticidal activity of entomopathogenic fungus *Isaria fumosorosea* (Deuteromycetes) against the horse chestnut leaf-miner, a serious invasive pest spreading in Europe.

Methods: The experiments were carried out using strain of *I. fumosorosea* isolated from spontaneously infected hibernating pupa of *C. ohridella* (strain CCEFO.010.IFR) discovered in horse chestnut leaf samples. Blastospores were produced in an originally developed liquid medium, whereas conidia were produced on a Sabouraud agar. Toxicity of both types of spores was tested using a single-dosage dip assay. Diapausing pupae of *C. ohridella* were treated with a concentration of 6×10^7 conidia or blastospores/ml and incubated in Petri dishes at 23±1 °C and RH approx. 95 %. Pupae treated with destilled water served as control. Totally, 200 pupae were used in each treatment.

Results: Blastospores, conidia, and no-fungus control treatments averaged 100%, 88%, and 5% mortality of *C. ohridella* pupae, respectively, after a 3-day continuous exposure. The difference between blastospores and conidia treatments was statistically significant. Development of mycosis on pupae treated with blastospores was also faster compared to pupae treated with conidia (83 % versus 14%).

Conclusions: Our results demonstrate a high insecticidal activity of I. fumosorosea on C. ohridella pupae. It also show that blastospores kill the host faster than conidia.

Acknowledgments: This work was supported by MSMT grant No. 2B06005. The authors thank Ms. M. Krivanova for her help with experiments.

POSTER PRESENTATION

Molecular identification and characterization of two adipokinetic hormones in *Aedes aegypti* and *Culex pipiens*

Gerd Gaede[2], Christian Kaufmann[1], Hans Merzendorfer[1]

[1]University of Osnabrueck, Osnabrueck, Germany, [2]University of Cape Town, Rondebosch, South Africa

Introduction: Adipokinetic hormones (AKHs) are peptides that induce the mobilization of metabolites which are used to provide energy for such intense activities as, for example, flight in mosquitoes. We have cloned two AKH genes in each of two mosquito species under investigation, viz. *Aedes aegypti* and *Culex pipiens*.

Methods and Results: In each species one gene encodes for a novel "classical" AKH octapeptide, named Aedae/Culpi-AKH-I with the sequence (pELTFTPSWa), while the other gene in each species encodes for a "non-classical" AKH decapeptide which has the same sequence (pEVTFSRDWNAa) as the equivalent from *Anopheles gambiae* and is called Anoga-AKH-II. We investigated gene expression during the life cycle of *A. aegypti*. Northern blot analyses show expression of both AKHs in head and thorax but not in the abdomen of female mosquitoes, while males have, additionally, a significant AKH-I-mRNA amount in the abdomen. Immunocytochemistry performed with a polyclonal AKH antibody shows immunoreactivity in lateral neurosecretory cells of the brain, the corpora cardiaca, the x-cells, and in axons along the anterior midgut.

Conclusions: Comparing the translated coding sequences, *Aedes*-prepro-AKH-I has strikingly high similarity with *Culex*-prepro-AKH-I; the same is true for the prepro-AKH-II in the two species. This may point to conserved functions in the different mosquitoes. However, the classical and non-classical AKH preprohormones in any of the two mosquito species differ significantly, favouring the hypothesis of ancient gene duplication. Further studies using *in-situ* hybridization and bioassays will shed light on the localization of AKH synthesis and the functions of classical and non-classical AKHs.

POSTER PRESENTATION

Molecular identification and characterization of two adipokinetic hormones in *Aedes aegypti* and *Culex pipiens*

Gerd Gaede[2], Christian kaufmann[1], Hans Merzendorfer[1]

[1]*University of Osnabrueck, Osnabrueck, Germany,* [2]*University of Cape Town, Rondebosch, South Africa*

Introduction: Adipokinetic hormones (AKHs) are peptides that induce the mobilization of metabolites which are used to provide energy for such intense activities as, for example, flight in mosquitoes. We have cloned two AKH genes in each of two mosquito species under investigation, viz. *Aedes aegypti* and *Culex pipiens*.

Methods and Results: In each species one gene encodes for a novel "classical" AKH octapeptide, named Aedae/Culpi-AKH-I with the sequence (pELTFTPSWa), while the other gene in each species encodes for a "non-classical" AKH decapeptide which has the same sequence (pEVTFSRDWNAa) as the equivalent from *Anopheles gambiae* and is called Anoga-AKH-II. We investigated gene expression during the life cycle of *A. aegypti*. Northern blot analyses show expression of both AKHs in head and thorax but not in the abdomen of female mosquitoes, while males have, additionally, a significant AKH-I-mRNA amount in the abdomen. Immunocytochemistry performed with a polyclonal AKH antibody shows immunoreactivity in lateral neurosecretory cells of the brain, the corpora cardiaca, the x-cells, and in axons along the anterior midgut.

Conclusions: Comparing the translated coding sequences, *Aedes*-prepro-AKH-I has strikingly high similarity with *Culex*-prepro-AKH-I; the same is true for the prepro-AKH-II in the two species. This may point to conserved functions in the different mosquitoes. However, the classical and non-classical AKH preprohormones in any of the two mosquito species differ significantly, favouring the hypothesis of ancient gene duplication. Further studies using *in-situ* hybridization and bioassays will shed light on the localization of AKH synthesis and the functions of classical and non-classical AKHs.

POSTER PRESENTATION

A comparative study on the life cycles of *Liriomyza trifolii* (Burgess) and *Liriomyza sativae* (Blanchard)

Faiza Salah[1], Elamin M Elamin[2], Elameen Eltoum[1], Dominique Bordat[3]

[1]Dept. Crop Protection, Faculty of Agricultues, Gezira University, Medani, Sudan; [2]Agricultural Research, Medani, Sudan; [3]CIRAD, Montpellier, France

The life cycles of the leaf miners, *Liriomyza trifolii* (Burgess) and *Liriomyza sativae* (Blanchard), were studied in a growth chamber (25 ± 1°C; 75 ± 5% R.H.; 12 hL/12 LD and 3000 – 4000 LUX) at CIRAD, Montpellier, France. The host plant used was haricot bean, (*Phaseolus vulgaris)*. The egg incubation period of both species lasted for two days. Larval instars durations for both species was almost 6 days with no significant differences between the means. Regarding the pupal stage duration ranged between 9.14 and 10.66 days; the differences between the species were significant. The percentage of adult emergence for *trifolii* ranged between 62 to 76%, whereas that for *sativae* ranged was narrow 67.3 -68.8%; differences between the species were significant. Adult longevity was not studied. The total of the life cycle for the former was 16.6 – 18.0 days and for the latter was 17.7 -18.8 days; the difference was significant. Highly significant differences ($P<0.01$) were recorded between the number of feeding punctures caused by *L. trifolii* and *L. sativae.* Differences between the larval periods and number of emerging adults were not significant. Upon hatching, during 1996, the number of larvae of *L. trifolii* was significantly higher than that of *L. sativae,* but the total life span of *L. sativae* was significantly longer than that of *L. trifolii*.

POSTER PRESENTATION

A new species of the genus *Chionea* Dalman from Korea (Diptera: Limoniidae)

Sang Jae Suh, Yong Jung Kwon

Kyungpook National University, Sangju, Gyeongbuk, Republic of Korea

Snow crane flies, the *Chionea* species are characterized by the complete reduction of their wings and by the winter activity of adults. They are distributed over the whole Holarctic region. Only five species are known from Palaearctic Asian region: *Chionea araneoides* Dalman, *C. kanenoi* Sasakawa, *C. crassipes* Boheman, *C. nipponica* Alexander *and C. pusilla* Savchenko.

This new species is similar to *C. kanenoi* Sasakawa having 11 antennal segments which is differences from the other Palaeractic Asian species. But this species is distinctly differed from the known species by tibiae with a small node at apex respectively, conical outer gonostylus lobe, and the shape of gonostylus.

POSTER PRESENTATION

Spatial distribution pattern of cryptus mealybug and its optimal sample size for development of sampling plan in citrus groves, Korea

Jeong-Heub Song, Soon-Young Hong, Ki-Tek Kim

Jeju Agricultural Research and Extension Services, Jeju, Republic of Korea

Introduction: Cryptus mealybug, *Pseudococcus cryptus* is a serious scale pest of citrus in Jeju, Korea. To develop its sampling plan, it should take precedence over the others for its spatial distribution pattern in citrus orchard and determined the optimal sample size.

Methods: 14 datasets collected from a commercial citrus orchard were used for spatial pattern analysis by mean-variance relationship, probability distribution model, indices of dispersion and spatial autocorrelation. The linear strength of bivariate relations by season was summarized using covariance and correlation coefficients. The optimal sample size was determined by estimates of variability among primary (tree) and secondary (twig) sample units.

Results: The frequency distribution of cryptus mealybug follows a negative binomial distribution and iterative individual *k* was better fitted than others by χ^2 –test. The spatial continuity for 0° and 45° direction were 4 and 6m and for 90°, 135° and omnidirection was 12m. Morista's index and index of dispersion were shown the clumped distribution. Consider the bivariate scatterplot and summary statistics among March (after overwintering), May (1^{st} generation), June (2^{nd} generation), September (3^{rd} generation) collections. There was a positive and linear relationship between series seasons. The optimal sample size was determined as 7 twigs per tree and 8 trees per block.

Conclusions: The sampling plan for cryptus mealybug can be developed by the negative binomial probabilities and estimate the density precisely.

POSTER PRESENTATION

Comparative analysis of genes expressed from different castes of the termite *Coptotermes gestroi* (Isoptera: Rhinotermitidae).

Flávia Costa Leonardo[1], Anderson Ferreira da Cunha[2], Marcelo Falsarella Carazzolle[1], Fernando Ferreira Costa[2], Gonçalo Amarante Guimarães Pereira[1]

[1]Laboratory of Genomics and Expression, Department of Genetics and Evolution, Institute of Biology, State University at Campinas, Campinas, São Paulo, Brazil, [2]Center of Hematology and Hemotherapy, State University at Campinas, Campinas, São Paulo, Brazil

Introduction: Social insects such as termites present differential gene expression during development. Although *Coptotermes gestroi* has an important economic impact and is relevant from a biological point of view, to date only a few sequences have been produced from this species. The main objective of this study was to survey the gene composition of *C. gestroi*, comparing the gene expression between castes and find genes with biotechnological relevance.

Methods: To accomplish this study, we sequenced and analyzed expressed sequence tags (ESTs) isolated from libraries of workers' heads. Subtractive suppressive libraries using larvae, workers and soldiers were also constructed. Real time PCR was performed to confirm gene expression.

Results: From the workers' library, we obtained 2,332 sequences of appropriate standard quality that were clustered and assembled into contigs and singletons, revealing important biotechnology genes involved in cellulose degradation (endo-β-1,4-glucanase and β-glucosidase). Through the suppressive method we generated 529 ESTs that revealed genes involved in protein biosynthesis, digestive enzymes, iron and calcium transport, structural proteins, chitin catabolism and a variety of metabolic pathways.

Conclusions: These results provide novel insights into previously uncharacterized aspects of *C. gestroi* polyphenism and caste-associated biology.

POSTER PRESENTATION

Ecology of groundnut storage pests in Burkina Faso

Ouedraogo Issoufou, Traore N. Seydou, Dakouo Dona, Guenda Wendgoundi

INERA, Bobo-dioulasso, Burkina Faso

Introduction: In Burkina Faso, several groundnut varieties with good yield potential were developed and released. This leads to a significant development of groundnut production. Groundnut production increased from 180,532 tons in 1995 to 323,642 tons in 2003 (FAO, 2003). Despite this effort of production, groundnut is available only during a short period of the year due to damage caused by *Caryedon serratus* Olivier (Coleoptera: Bruchidae). It has been reported that in groundnut producing zones, about 70% of pods were damaged after four months of storage. This poster review aims at giving a better knowledge of the bio-ecology of the insect pest and at making some suggestions for managing groundnut storage in Burkina Faso.

Methods: In 2005 and 2007, pods from wild plants were sampled in groundnut production zones and belonging to the families of Mimosaceae, Papillionaceae and Cesalpiniacea. Adults emergence from these sampled pods and females egg laying were monitored in laboratory conditions.

Results: A total of 20 sites were visited and 64 samples were collected. Fruits were collected on 8 host plants belonging to four families (Caesalpiniacea, Mimosaceae, Papillionnaceae and Meliaceae). About 102 insects emerged from the harvested fruits. The majority of these insects were from three plant hosts (*Tamarindus indica*, *Piliostigma reticulatum* and *P.thonningii*). The identification of adults revealed that beetles emerged from the pods of *A. hypogea, P. reticulatum, P. thonningii* and *T. indica* all belong to the species of *C.serratus.* In laboratory, results on the behaviour of egg laying of *C. serratus* showed a significant difference between the number of eggs laid on groundnut varieties and those laid on other host plants.

Conclusions: Investigations carried out in different groundnut growing locations showed that *C. serratus* is the main insect pest during groundnut storage. The groundnut pods seem to the most suitable food support for this species of beetle.

POSTER PRESENTATION

1-Octen-3-ol as an important cue in fungal host finding of *Cis boleti*

Prodpran Thakeow, Sergio Angeli, Bernhard Weißbecker, Stefan Schütz

Forest Zoology and Forest Conservation, Goettingen, Lower Saxony, Germany

Introduction: The fungivorous insect *Cis boleti* (Coleoptera: Ciidae) belongs to a group of insects which colonize bracket fungi (Basidiomycetes: Polyporaceae) growing on tree trunks and wood logs. *C. boleti* is a host-specific species, selectively colonizing fruiting bodies of the genus *Trametes* generally known as important wood-rotting fungi. Fungal host volatiles were proposed to play an important role in its host finding.

Method: The electroantennographic responses of *C. boleti* antenna to *Trametes gibbosa* fruiting body volatiles and standard compounds (which are present in the fruiting body volatiles) were recorded by using gas chromatography-mass spectrometry, with parallel electroantennographic detection (GC-MS/EAD). In addition, the perception of *C. boleti* antenna to the standard compounds was carried out by electroantennography (EAG).

Results: *C. boleti* antenna responded consistently to 1-octen-3-ol, a major compound of *T. gibbosa* fruiting body volatiles. The GC-MS/EAD and EAG to pure standard compounds demonstrated that *C. boleti* antenna was additionally elicited by other host-fungal volatiles in different intensity.

Conclusion: Our discovery is the first evidence that 1-octen-3-ol is an important cue in fungal host finding of ciid beetles.

POSTER PRESENTATION

Males inhibit female remating using substances from accessory gland in the seed bug *Togo hemipterus* (Heteroptera: Lygaeidae)

Chihiro Himuro, Kenji Fujisaki

Kyoto University, Kyoto, Japan

Introduction: Females of many insect species mate repeatedly throughout their life. However, multiple mating by females increases both the risk and intensity of sperm competition for males. Thus males adopt various strategies to reduce the risk of sperm competition from future males. In Heteropteran species, many studies have reported that males guard females after ejaculation to reduce the risk of sperm competition. The seed bug *Togo hemipterus* males do not guard females. On the other hand, females show long refractory period. We hypothesized that *T. hemipterus* males inhibit female remating using some kind of seminal fluid, as in the case of *Drosophila melanogaster*.

Methods: Firstly, to examine the relationship between the mating duration and the refractory period, we adjusted mating duration artificially and examined the refractory period. Secondly, we injected each of three kinds of extracts from accessory gland (A and B) or seminal vesicle to virgin females. Then, we examined the effect of those solutions on the duration from the injection to the mating in females.

Results: There was a significantly positive relationship between the mating duration and the refractory period. The duration from injection to mating in females was significantly longer in females which was injected the solution from accessory gland B than in females which was injected the solution from seminal vesicle, accessory gland A and control (only saline).

Conclusions: We showed that *T. hemipterus* males inhibit female remating using substances from accessory gland B, and the seminal fluid has dose-dependent inhibition effect. This is the first report showing that substances from male reproductive tract reduce female mating receptivity in Heteropteran species.

POSTER PRESENTATION

Ecology of the Salticid spider *Afraflacilla epiblimoides*; Implications for conservation of central European low-land forests

Vladimír Hula, Martin Jarab

Agronomical Faculty of Mendel university of Agriculture and, Brno, Czech Republic

Introduction: Salticid spider *Afraflacilla epiblimoides* is one from endangered species of spiders in the Czech Republic. Only one male was recorded at 2001 and population was found in Lednice Castle Park in 2006. This species strictly inhabits old oak (*Qurcus robur*) trees with population of basically Pannonian ant *Liometopum microcephalum*.

Methods: So far we know only the distribution across Europe, furthermore it was known that this species mimics *Liometopum* ants and that it prefers old oak trees. We studied the species' life history, phenology, prey, protection strategy again ants, spider species composition and preferences for particular trees (by ordination analyses).

Results: It was theorised that the spiders prey on *Liometopum* ants. However, we found, that the spider must protect itself against the ants and that it has special strategies against the aggressive ant species. As a prey *A. epiblimoides* uses everything that they can to overpower the ants. The species prefers mainly solitary trees about 100 cm in diameter, with insulated bark, inhabited by rich population of *Liometopum* ants. For survival of the spider it is necessary to conserve all alive oak trees in Lednice Castle Park. However, as all trees are old and the majority of them are, in reality, dead, there are no available younger trees for the future. In the area there is a lack of trees in age category about 70 years.

Conclusions: Management of protected areas must help by making new possible habitats in surrounding forests, where there exist some threes of a suitable age. This study was supported by the project VaV-MZP-CR-SP/2D4/59/07.

POSTER PRESENTATION

The effect of thiopentone sodium on the development rate of *Chrysomya megacephala* (Diptera: Calliphoridae) and its importance for the post-mortem interval estimate in Brazil

Dora Amparo Estrada[1], Patricia Jacqueline Thyssen[2], Aricio Xavier Linhares[1]

[1]Department of Parasitology, Institute of Biology, State University of Campinas, Campinas/SP, Brazil, [2]Department of Parasitology, Institute of Biosciences, UNESP, Botucatu/SP, Brazil

Introduction: Recent research has demonstrated that the presence of drugs in decomposing tissues may affect the insect development rate when they using such tissues as food, thus potentially altering estimates of the post-mortem interval (PMI). The thiopentone sodium is a short-acting barbiturate and is most commonly used in the induction phase of general anesthesia in veterinary medicine. In this study, we investigated the effect of the thiopentone sodium on the development rate of *Chrysomya megacephala* (Diptera: Calliphoridae) immatures.

Methods: Groups of larvae were placed in artificial diet containing thiopentone sodium in 3 different concentrations: 0.5 x LD (lethal dose), 1 x LD and 2 x LD. The control group was reared on the diet without any drug. Weights were recorded for groups of 10 larvae at 12 h intervals up to the end of the larval stage.

Results: There was a significant effect of the drug concentration on larval development as measured by weight ($F = 1154.20$; $p < 0.0001$). Immatures from the 2 x LD and 1 x LD groups died in the third instar (96 h). The survivorship rates up to the pupae stage were 70.7% and 34% at control and 0.5 x LD groups, respectively.

Conclusion: Studies done with different drugs in several species of Calliphoridae suggest that larval development respond differently to the presence of each drug. These results evidenced that the effects of thiopentone sodium on maggots development may lead to errors in estimating the PMI, especially when is necessary to use entomological means.

POSTER PRESENTATION

Atlas of the burnets of the Iberian Peninsula (Lepidoptera: Zygaenidae)

José Martin, Juan M. Jambrina, M. Pilar Gurrea

Universidad Autónoma de Madrid, Madrid, Spain

Introduction: Here is presented the atlas of burnets in the Iberian Peninsula based on the10 x 10 km UTM grid. This atlas consists of 22 maps with all 22 *Zygaena* species present in the Iberian Peninsula. One of these species, *Zygaena ignifera*, is endemic, while all the others can be found in other regions of Europe.

Material and Methods: The atlas has been built up from a database specifically created to this end. The database consists of almost 4000 records from two main sources of information, the MNCN (Museo Nacional de Ciencias Naturales de Madrid) collection and the references in SHILAP Revta lepid. The MNCN which collection has 3969 iberian specimens of *Zygaena*, is the most important zoological and entomological museum of Spain and one of the most in Europe. Both of these sources contribute with about 3200 records. In addition to this, other periodical journals and books related to Lepidoptera in the Iberian Peninsula have been checked as well.

Results: The results show that all the Iberian species except *Z. ignifera* live en the Pyrenees. There are 2 groups rather differenced attending to their geographic distribution. On one side we have a group of 9 species that have a very restricted distribution, taking up just a few number of 10 x 10 km squares, 4 of these species are completely included in the Pyrenees. The rest of them have a wider distribution, they also live in the Pyrenees but also in other regions of the Iberian Peninsula.

POSTER PRESENTATION

Artificial Neural Network in forensic entomology: Contribution to PMI estimates

Lucila Maria L Carvalho[1], Fernando J von Zuben[2], Aricio Xavier Linhares[3], Cláudio J von Zuben[1]

[1]Departamento de Zoologia, UNESP, Rio Claro/SP, Brazil, [2]Faculdade de Engenharia Elétrica, laboratório de Bioinformática e Computação Bioinspirada, State University of Campinas, Campinas/SP, Brazil, [3]Departamento de Parasitologia, State University of Campinas, Campinas/SP, Brazil

Introduction: In forensic entomology the knowledge of fly life cycle and environmental conditions taken on the death scene is crucial. With the new perspectives of FE in Brazil a computer-based database is important to get quick results during an investigation. In order to attend this necessity a computational program was developed using artificial neural networks (ANN). The key element of this paradigm is the novel structure of the information processing system, composed of a large number of highly interconnected processing elements working together to solve specific problems. ANNs learn by example and training and is configured for a specific application, such as pattern recognition or data classification, through a learning process.

Methods: Dynamic phenomena such as weight of insect, developmental time, threshold and temperature (environmental and controlled) were used to elaborate the model. After data simulation, they were divided in groups of training, validation and tests. The Matlab program was used to train the different situations.

Results: The relation among the studied factors showed non-linear associations between the independent variable (input pattern) and dependent variable (output pattern). A non linear performance of input/output was determined with available data on insects. The model using ANN is recommended when time of larval development is required, whereas a table is indicated to determine the pupation time,

Conclusions: ANN is an alternative methodology to estimate the PMI once neural networks, with their ability to derive meaning from complicated or imprecise data, can be used to extract patterns and detect trends that are too complex to be noticed by either humans or other computer techniques.

POSTER PRESENTATION

Geographical variation in the susceptibility of the African cotton bollworm to a baculovirus

Michelle Grant, Gustav Bouwer

University of the Witwatersrand, Johannesburg, South Africa

Introduction: The susceptibility of *Helicoverpa armigera* (Hübner) (Lepidoptera: Noctuidae) populations of varying geographical origin in South Africa to a baculovirus, *Helicoverpa armigera* single nucleopolyhedrovirus (*Hear*SNPV), was examined.

Methods: Field-collected *H. armigera* populations from Brits and Groblersdal were compared to a laboratory reared population (ARC). The volumes imbibed by the larvae from each *H. armigera* population was determined by fluorescent spectrophotometry. The droplet feeding assay was used to determine a lethal dose range and the survival time for each *H. armigera* population in order to compare their susceptibility to *Hear*SNPV.

Results: The fluorescent spectrophotometry showed that there was no significant difference in the volume imbibed by larvae from the different populations. Bioassays showed that in comparison to the ARC population, the Brits and Groblersdal populations were 1.9 and 1.3 times respectively, more susceptible to *Hear*SNPV. At the calculated population-specific LD_{90} values, the median survival time (ST_{50}) of each population was compared. On the basis of the ST_{50} values, the Brits and Groblersdal populations were 0.74 and 0.81 times as susceptible to *Hear*SNPV as the ARC population.

Conclusion: These findings have significant implications for the future use of baculoviruses as biopesticides, because a dose that is adequate to control *H. armigera* populations in one geographical area may not be adequate in another area. It also implies that lethal dose studies using a *H. armigera* population from one geographical area are not comparable to studies done using populations from another geographical area.

POSTER PRESENTATION

Phylogeny, historical biogeography, and evolution of parasitic myrmecophily in the Glaucopsyche-section (Lepidoptera: Lycaenidae)

Pavel Pech[1], Zdenek Fric[1], Jan Zrzavy[2]

[1]Institute of Entomology, BC CAS, Ceske Budejovice, Czech Republic, [2]Faculty of Sciences, University of South Bohemia, Ceske Budejovice, Czech Republic

Introduction: The vast majority of lycaenid butterflies exhibits some kind of relationship with ants. The obligate parasitic blues of *Phengaris* Doherty, 1891 belong to the most intensively studied butterflies in Eurasia. Although several studies concerning their phylogeny, population biology, and evolution have been published recently, a more complete phylogenetic study including a wider taxon sampling of putatively related taxa has not yet been done. At present, we can reliably reconstruct ecology of the *Phengaris* ancestor; however, more comprehensive analyses are required to reconstruct evolutionary processes that have constrained deeper origins of the obligate parasitism.

Methods: We used morphological and molecular data for 77 analysed taxa. We used the maximum parsimony program NONA (Goloboff, 1999), with bootstrap and Bremer values. Historical biogeographical analyses were computed for combined all-species trees using the dispersal-vicariance analysis (DIVA).

Results: The combined morphological-molecular analysis showed that *Glaucopsyche*-section was monophyletic, with the exception of *Lachides*. Within the *Glaucopsyche*-section, several clades could be recognised, with the basalmost *Iolana-Turanana* group (including *Iolana*, *Turanana*, *Otnjukovia*, *Micropsyche*), followed by *Palaeophilotes* and two major clades, namely, “Glaucopsychiti” (= *Phengaris* s.lat., *Glaucopsyche*, *Praephilotes*, *Philotiella*, *Shijimiaeoides*, and *Caerulea*) and “Scolitantiditi” (= *Sinia*, *Scolitantides*, *Philotes*, *Euphilotes*, *Pseudophilotes*). Several genera seemed to be nonmonophyletic: they included *Glaucopsyche* (paraphyletic in respect of *Shijimiaeoides* and *Caerulea*), *Sinia* (polyphyletic), and *Turanana* (paraphyletic in respect of *Micropsyche*). Obligate myrmecophily developed in the common ancestor of *Phengaris*. The origin was also connected with change of host plant family and the origin was situated in Manjuria.

POSTER PRESENTATION

The effect of alpha-cypermethrin on the cyclic gas exchange of bumblebee *Bombus terrestris* L. foragers

Reet Karise, Marika Mänd, Anne Luik

Estonian University of Life Sciences, Institute of Agricultural and Environmental Sciences, Tartu, Estonia

Introduction: Minor effects of pesticides may remain unnoticeable in adult bees because of no visible changes in their behaviour throughout several days after coming into contact with pesticides. The hypothesis of this work is that changes which are not observable through the behaviour of the bee can be seen through physiological patterns. The aim of the present research was to study the effect of a low concentration of alpha-cypermethrin on discontinuous gas exchange cycles of bumblebee *Bombus terrestris* foragers.

Methods: Using a system of flow-through CO_2 respirometry, the effect of low concentration of alpha-cypermethrin on bumblebee *Bombus terrestris* foragers was studied.

Results: We found an increase in CO_2 emission rate at high relative humidity (RH = 95%) (0.130 ± 0.01 ml h^{-1}), compared to low relative humidity (RH = 2%) (0.074 ± 0.01 ml h^{-1}). Treatment with alpha-cypermethrin decreased significantly the frequency of bursts of CO_2 release during discontinuous gas exchange (DGC) in dry conditions. In humid conditions no significant differences were found.

Conclusions: Alpha-cypermethrin caused changes in the respiration patterns of *B. terrestris* foragers although not seen through the behaviour. These changes could potentially lead to the decreasing individual and colony survival.

POSTER PRESENTATION

Susceptibility of some varieties and breeding lines of tomato to *Liriomyza* spp. infestation in Central Sudan

Faiza Salah[1], Elamin Elamin[2], Elameen Eltoum[1] , Dominique Bordat[3]

[1]Dept. Crop Protection, Faculty of Agriculture, Gezira University, Medani, Sudan; Agricultural [2]Research, Medani, Sudan; [3] CIRAD, Montpellier, France.

Tomato crop in the central Sudan is liable to heavy infestation by the leaf miners (LM). Field experiments indicated significant differences between susceptibilities of varieties and breeding lines of tomato to the damage in terms of infestation percentages caused by Liriomyza spp. The variety Flora Dade and the breeding lines Omdurman, UG Fireset A3 36L and UG Fireset A6 30R were the most infested (susceptible). The breeding line Trop G 9–18 and the varieties, Alfa, Peto 86 and Strain B were the least infested (resistant). Moderate susceptibility was exhibited by the breeding lines, Hillo, UG 46 and UG Fireset A4 20R and the variety Red Star.

The laboratory tests revealed that Flora dade was more susceptible to sativae than Trop-G, whereas the latter was absolutely resistant to trifolii. The mean number of larvae/leaf and the larval period were tahen as parameters to evaluate the susceptibilities of two breeding lines and two varieties. Omdurman harbored the highest number and Trop-G was not attacked. The two varieties showed moderate resistance. No differences were found in larval duration of the varieties and Omdurman breeding line. Resistance is attributed to antiffedents and associated with the glandular trichomes on the leaves.

POSTER PRESENTATION

Dispersal abilities in marsh fritillary, *Euphydryas aurinia* (Lepidoptera: Nymphalidae): A large scale study

Kamil Zimmermann[2], Martin Konvicka[1], Vladimir Hula[3], Petr Jiskra[4], Michala Kopeckova[5], David Novotny[1], Petr Vlasanek[1], Michal Zapletal[1], Zdenek Fric[2]

[1]University of South Bohemia, Ceske Budejovice, Czech Republic, [2]Institute of Entomology, Czech Academy of Sciences, Ceske Budejovice, Czech Republic, [3]Mendel Agricultural University, Brno, Czech Republic, [4]Czech Conservation Authority, Karlovy Vary, Czech Republic, [5]Ametyst o.s., Plzen, Czech Republic

Introduction: *Euphydryas aurinia* is a continentally endangered butterfly, depending on nutrient-poor seminatural meadows in Central Europe. While it has been subject to intensive research in many countries, there was a spectacular lack of large-scale mark-recapture projects that would assess status of populations on large scale.

Methods: We carried out mark-recapture study of all known colonies in W Bohemia, Czech Republic. It encompassed 100 local colonies in seven regional clusters, studied by 24 persons for entire 2007 flight period. In total, we marked 9,466 individuals and recaptured 5,212 individuals in 14,678 capture events.

Results: We found a high degree of interconnection among seemingly isolated local populations. Out of the 5,212 individuals recaptured at least once, 69 (56 males, 13 females) moved over 5 km, and 20 (18 males, 2 females) moved over 10 km, the longest flights being 23.1 km (a male) and 15.2 km (female). The populations thus form a superpopulation distributed across over 1000 km^2 of land area – however, the actual summed area of occupation is just 300 hectares. The total population size in the Czech Republic, estimated using constrained linear models, approaches 30,000 adults, and various estimation methods converged at this number.

POSTER PRESENTATION

Investigation of *Myzus persicae* salivary proteome and potential role in plant defence mechanisms following aphid infestation

Nicolas Harmel[1], Frederic Francis[1], Edwin De Pauw[2], Eric Haubruge[1]

[1]Gembloux Agricultural University, Functional and Evolutionary Entomology, Gembloux, Belgium, [2]University of Liege, Mass Spectrometry Laboratory, Liege, Belgium

Introduction: Salivary secretions are a key component in plant-aphid interactions and constitute the first contact between insect and plant. Proteic and non-proteic elicitors have been discovered in saliva of some chewing insects but no aphid elicitor is known to date although some enzymatic activities have been detected. Moreover aphid induces plant volatiles emission and plant phloem proteins modification.

Method: We investigate salivary proteome of the green peach aphid, *Myzus persicae*, in search of an elicitor. Proteins were isolated from artificial diets and salivary glands. Proteins were either directly in-solution digested or separated by 2D SDS-PAGE before being digested. Resulting peptides were then identified by mass spectrometry coupled with data bank investigations constituted with ESTs from the pea aphid *Acyrtosiphon pisum* and *M. persicae*. These specific databases were used to identify proteins related to this organism with non-sequenced genome.

Results: This procedure allowed us to discover glucose oxidase, glucose dehydrogenase, NADH dehydrogenase, α-glucosidase and α-amylase in *M. persicae* saliva. Implication of these enzymes was discussed in term of plant-aphid interactions.

POSTER PRESENTATION

A fluorescent sperm-specific marker for the medfly, *Ceratitis capitata*

Francesca Scolari[1], Marc Schetelig[2], Sabrina Bertin[1], Anna Malacrida[1], Giuliano Gasperi[1], Ernst Wimmer[2]

[1]University of Pavia, Pavia, Italy, [2]Georg-August-University Göttingen,, Göttingen, Germany

The medfly, *Ceratitis capitata* (Diptera: Tephritidae) is an invasive pest species of agricultural importance. Its polyphagous behavior and its high reproductive capacity are responsible for the spread of this species in the last two centuries from sub-Saharan Africa to several tropical and sub-tropical regions worldwide.

The environmental-friendly Sterile Insect Technique (SIT) has been effectively applied as a component of area-wide integrated pest management (AW-IPM) for *C. capitata* since the 1970s. Effective monitoring to assess the number and mating success of the released medflies is essential.

Using a transgenic approach we developed a direct sperm visualization system which makes it possible to follow the fate of sperm from different males in the female reproductive tract of the medfly.

For this purpose, we generated a sperm-specific marking system based on the spermatogenesis-specific *C. capitata beta2-tubulin* (*Ccbeta2t)* promoter driving the expression of the reporter genes GFP or DsRed.

Monitoring of the mating success of sterile released males by trapping females and examining their spermathecae is possible with these strains.

Moreover, the availability of differently sperm-marked lines will help us to understand the relationship between sperm allocation, remating frequency and sperm displacement in the medfly, given that in wild populations females can remate with a strong paternity skew.

In preliminary laboratory competitiveness assays we determined that the marker does not cause general fitness disadvantages. Therefore, such harmless transgenic markers represent an ideal springboard to transfer insect transgenesis technology from the laboratory to field applications.

POSTER PRESENTATION

Surveys of Chilean indigenous entomopathogenic fungi and nematodes and studies on their pathogenicity against pests of economic importance

Loreto Merino, Steve Edgington, Dave Moore, Marcos Gerding, Andrés France

INIA Quilamapu, Chillan Bio bio zone, Chile

The Insect Pathology Program of the Institute of Agricultural Research (INIA) Quilamapu, Chile, is working in collaboration with CABI (Commonwealth Agricultural Bureaux International, UK) on a Darwin Initiative (DEFRA, UK) to conserve and use Chilean entomopathogenic microorganisms. The aim was to collect entomopathogenic fungi and nematodes from some of the major ecological habitats in Chile. Six survey transects were chosen: 1) Latitude 20^{o}, with sections of Altiplano and on the periphery of the Atacama Desert; 2) Latitude 30^{o}, desert with remnants of ancient tropical forests; 3) Latitude 33^{o}, an area of Mediterranean vegetation; 4) Latitude 37^{o}, a transitional zone from dryland to wetland; 5) Latitude 46^{o}, heavy rainfall, relatively cold, with humid forests and areas of pampas, 6) Latitude 52^{o}, Tierra del Fuego, with almost Antarctic conditions and flora and fauna adapted to low temperatures. The first two transects have been surveyed, revealing 157 isolates of entomopathogenic fungi, predominately *Metarhizium* and *Beauveria* spp. and 14 isolates of nematodes *Heterorhabditis* and *Steinernema* spp. The isolates will be maintained in the Genetic Resource Collection of INIA, significantly enhancing the bank of indigenous germplasm already present. It is likely that indigenous isolates will show stronger adaptations to Chilean conditions compared to exotic isolates and could be important pest control alternatives

POSTER PRESENTATION

Surveys of Chilean indigenous entomopathogenic fungi and nematodes and studies on their pathogenicity against pests of economic importance

Loreto Merino[1], Steve Edgington[2], Dave Moore[2] y Marcos Gerding y Andrés France[1]

INIA Quilamapu, Chillan Bio bio zone, Chile

The Insect Pathology Program of the Institute of Agricultural Research (INIA) Quilamapu, Chile, is working in collaboration with CABI (Commonwealth Agricultural Bureaux International, UK) on a Darwin Initiative (DEFRA, UK) to conserve and use Chilean entomopathogenic microorganisms. The aim was to collect entomopathogenic fungi and nematodes from some of the major ecological habitats in Chile. Six survey transects were chosen: 1) Latitude 20°, with sections of Altiplano and on the periphery of the Atacama Desert; 2) Latitude 30°, desert with remnants of ancient tropical forests; 3) Latitude 33°, an area of Mediterranean vegetation; 4) Latitude 37°, a transitional zone from dryland to wetland; 5) Latitude 46°, heavy rainfall, relatively cold, with humid forests and areas of pampas, 6) Latitude 52°, Tierra del Fuego, with almost Antarctic conditions and flora and fauna adapted to low temperatures. The first two transects have been surveyed, revealing 157 isolates of entomopathogenic fungi, predominately *Metarhizium* and *Beauveria* spp. and 14 isolates of nematodes *Heterorhabditis* and *Steinernema* spp. The isolates will be maintained in the Genetic Resource Collection of INIA, significantly enhancing the bank of indigenous germplasm already present. It is likely that indigenous isolates will show stronger adaptations to Chilean conditions compared to exotic isolates and could be important pest control alternatives

[1] Instituto de Investigaciones Agropecuarias, Centro Regional de Investigaciones Quilamapu, Casilla 426, Chillán, Chile. lmerino@inia.cl

[2] CABI UK Centre (Ascot) Silwood Park Buckhurst Road Ascot Berks SL5 7TA United Kingdom

POSTER PRESENTATION

Sublethal effects of entomopathogenous fungus B*eauveria bassiana* (Bals.) Vuill. on European paper wasp *Polistes dominulus* (Hymenoptera: Vespidae)

Merino Loreto, Gerding Marcos, France Andres

Inia Quilamapu, Chillan, Bio Bio zone, Chile

The sublethal effects of an infection is an aspect of entomopathogenic fungi efficacy that not include insect mortality but affect or decrease various aspects of its biology. The objective of this research was evaluating sublethal effect of Qu-B933 isolates of *Beauveria bassiana* over *Polistes dominulus* wasps. A matrix was build to establish activities and distribution of time on healthy wasp colonies, comparing with wasps belonging to colonies receiving a liquid bait with a dose of 10^8 espores mL^{-1} using The Observer™ software and grouping activities in active and inactive times.

The test results showed significant decreases ($P<0,05$) in total active time of inoculated wasps, reaching 79.89% decrease at day 11 of test, isolate application caused a progressive reduction in activities as drinking, washing, nest expansion, larva feeding, flying, walking, and interaction with other individuals, also increasing inactive time in inoculated wasps, finally causing insect death since 10^{th} day and collapse of inoculated colonies due to a lack of defense work, cleaning and nest maintenance.

POSTER PRESENTATION

The isoprenoid pathway in aphids: Focus on geranyl/farnesyl diphosphate synthase

Sophie Vandermoten[1], Stephanie Sen[2], Frederic Francis[1], Michel Cusson[3], Eric Haubruge[1]

[1]Gembloux Agricultural University, Functional and Evolutionary Entomology, Gembloux, Belgium, [2]Indiana University-Purdue University at Indianapolis, Department of Chemistry, Indianapolis, United States, [3]Natural Resources Canada, Laurentian Forestry Centre, Quebec, Canada

Introduction: Short-chain isoprenyl diphosphate synthases (scIPPSs) catalyse condensation of an allylic diphosphate substrate with isopentenyl diphosphate to generate C10, C15 or C20 products.

Methods: We report on the cloning of two scIPPS cDNA isoforms from the aphid *Myzus persicae* (MpIPPS-S and MpIPPS-L), including one with an N-terminal extension containing a putative mitochondrial targeting peptide. Expression in *Escherichia coli* of each *M. persicae* cDNA were performed

Results: Active prenyltransferase activities were obtained from both *M. persicae* cDNA.. However, although the cloned *M. persicae* enzymes were predicted to be farnesyl diphosphate synthases by BLASTP analysis, the rMpIPPS-S, when supplied isopentenyl diphosphate and dimethylallyl diphosphate as substrates, typically generated geranyl diphosphate (C10) as its main product, along with significant quantities of farnesyl diphosphate (C15), suggesting that it is a bifunctional enzyme. Analysis of an MpIPPS-S homology model pointed to some aphid-specific substitutions that could confer bifunctionality to the *M. persicae* enzyme.

POSTER PRESENTATION

Development of a biopesticide from proteic waste issued from pea processing

Gaetan Cuartero Diaz, Frederic Francis, Eric Haubruge

Gembloux Agricultural University, Functional and Evolutionary Entomology, Gembloux, Belgium

Introduction: Some components of the pea seed are known as antinutritional factors. During the industrial process aiming to valorize proteic isolate from pea, some of those factors are removed by clarification. Among them are the proteins from the albumin class. Very often those antinutritional factors can act also against insect.

Methods: To evaluate the potential for the crop protection of the waste issued from the clarification, active components have been detected through their enzymatic activity. Then the proteins present in this sample have been separated by gel filtration with a Sephadex® G-75 media. Lectins are collected with an affinity chromatography with the same media. Each fraction issued from the chromatography has been identified by MSMS. Toxical assays have been performed on the aphid *Myzus persicae*.

Results: Several toxic components have been highlighted and caracterized in these waste. Among them: the pea lectin, trypsin inhibtors and the pea albumin 1b (PA1b). Those substances showed toxicity activity against *Myzus persicae* feeded with an artifical diet.

Conclusion: The waste issued from clarification contains insecticidal components. The challenge now is to valorize such substances in the crop protection. It would allow in the same time to increase the yield of pea's industry by reducing the wastes and to reduce pressure on environment by the use of a natural product in crop protection.

POSTER PRESENTATION

Control of *Dysaphis plantaginea* in IPM orchards: Effect of cultivar and predatory arthropods

Sylvaine Simon, Emilie Durand, Karine Morel, Hubert Defrance, Benoit Sauphanor

[1]INRA, St Marcel les Valence, France, [2]INRA, Avignon, France

Introduction: The rosy apple aphid *Dysaphis plantaginea* is a major pest in European apple orchards. Its treatment threshold is very low, due to the detrimental effect of spring infestation on trees and fruits. The development of sustainable and relevant new strategies for aphid control is thus a challenge in IPM orchards.

Results: We investigated the effect of cultivar and predatory arthropods within the apple tree-rosy aphid-natural enemies system in three organic apple orchards. Shoot growth was reduced during aphid infestation, but more leaves were emitted after the migration of the aphid towards its secondary host in late spring, compared to uninfested shoots. The Golden and Ariane cultivars were always affected whereas the Melrose cultivar was not affected for low levels of infestation. For all cultivars, fruit growth and nitrogen leaf content were not significantly different within low-infested trees compared with uninfested ones. Beneficial arthropods that were assessed within infested shoots mainly comprised Syrphidae, Cecidomyiidae and Coccinellidae, but the predator/prey ratio remained the same along the period of infestation and only increased when the migration of *D. plantaginea* occurred.

Conclusion: A moderate infestation in orchards can be tolerated by some cultivars such as Melrose, without effect on yield, calibre or shoot growth. A higher treatment threshold can be recommended for these cultivars, which should contribute to more sustainable control strategies. From this study, it seems that the plant tolerance to infestation rather than the control by natural enemies may contribute to the management of the apple rosy aphid in orchards.

POSTER PRESENTATION

Bringing biological control to the heartland: A South Dakota PPQ 526 story

Kelley Tilmon

South Dakota State University, Brookings, SD, United States

There are many obstacles to overcome when instituting a classical biological control program for the management of a given pest. Apart from the logistic, scientific, and regulatory aspects of the process, there are also frequently social and political forces involved. This poster details the unusual political circumstances surrounding the issuance of a regulatory permit to ship and release the soybean aphid parasitoid *Binodoxys communis* in South Dakota, USA.

POSTER PRESENTATION

IMGD: An integrated platform for dissecting insect mitochondrial gene sequences

Wonhoon Lee[1], Jongsun Park[1], Jaeyoung Choi[1], Bongsoo Park[2], Kyongyong Jung[1], Seogchan Kang[2], Yong-Hwan Lee[1], Seung-Hwan Lee[1]

[1]Seoul National University, Seoul, Korea, Republic of, [2]Penn State University, University Park, United States

Introduction: Two databases, AMIGA and MITOME, provide web-based useful tools for analyzing mitochondrial genome sequences used for phlylogenetic studies. Because two databases archived only completely sequenced mitochondrial genomes, comparative analyses across broad ranges of insect species in these databases are limitated. In addition, they do not support comprehensive phylogenetic tools on the web, so that phylogenetic analyses of mitochondrial genes are not conducted efficiently in one place.

Methods: For collecting both completely and partially sequenced mitochondrial genomes, standardized genome database structure implemented in Comparative Fungal Genomeics Platform (CFGP; http://cfgp.snu.ac.kr/) were used in IMGD. Components of Phyloviewer (http://www.phyloviewer.org/) support three different methods, such as neighbor-joining, maximum parsimony, and maximum likelihood for drawing phylogenetic trees via user-friendly interface of the web.

Results: IMGD archives fully sequenced mitochondrial genomes of 113 species and 86,214 genes in partially sequenced mitochondrial genomes covering 17,839 insect species. For manipulating large species, Species-driven User Interface (SUI) was developed in IMGD, providing an interface similar to on-line shopping site. In SUI, eight analysis functions were supported including downloading sequences with various options, drawing phylogenetic tress with three methods, and BLAST search.

Conclusions: The IMGD will serve as a versatile informatics platform not only for archiving rapidly increasing insect mitochondrial genes but also for conducting efficient phylogenetic and comparative analyses.

POSTER PRESENTATION

Molecular analysis of trophic links within an autumn- and winter-active invertebrate community

Bernhard Eitzinger, Michael Traugott

University of Innsbruck, Innsbruck, Austria

Many arthropods, such as linyphiid spiders and beetle larvae, are active during the cold months of the year; some of them are important natural enemies of pests during summer. A better understanding of the feeding ecology of these autumn- and winter-active predators is essential to promote these species in agroecosystems and maximize natural pest control.

Within this project we address two main objectives: (1) recording species spectrum, activity-densities and abundance of winter-active epigeic invertebrates in an organically cultivated spelt field and a bordering meadow near Innsbruck, Austria, and (2) assessing trophic links within this invertebrate community.

Throughout the winter catches were dominated by larval *Cantharis* and carabid beetles as well as linyphiid spiders. Collembolans and earthworms were also abundant, possibly representing important food sources. As the predators are fluid feeders, a PCR-based approach was used to screen the predators' guts for DNA of specific prey taxa. Using group-specific markers, the importance of collembolan and earthworm prey will be assessed for the different predator groups. First results indicate that cantharid- and carabid beetle larvae regularly feed on collembolans and earthworms. Newly designed markers - targeting cantharids, carabids and linyphiid spiders - will be used to determine the levels of intraguild predation.

POSTER PRESENTATION

Dispersal abilities of adult click beetles in arable land revealed by analysis of carbon stable isotopes

Nikolaus Schallhart, Corinna Wallinger, Anita Juen, Michael Traugott

University of Innsbruck, Innsbruck, Austria

Larvae of the genus *Agriotes* feed on roots and tubers of plants and are serious pests on a variety of crops. Albeit highly relevant for the control of agrioted beetles, their dispersal abilities are poorly known, as it is difficult to track the movements of the beetles in the field. Here we used, for the first time, a stable isotope approach to assess the dispersal abilities of these insects in arable land.

Pheromone traps, lured for *Agriotes* sp., were installed at two study sites in Western Austria, each comprising a maize field and adjacent grassland. Traps were installed in the centre of each maize field and along transects into the grassland.

The different $\delta^{13}C$ signatures of grassland and maize habitats are reflected in the herbivorous larvae. During metamorphosis, the $\delta^{13}C$ signature of the larval diet is translocated to the adult beetle, allowing the identification of the beetles' larval habitat (maize or grassland). By measuring the $\delta^{13}C$ signatures of wing covers from adults, we were able to estimate the dispersal by *Agriotes* beetles developing in maize fields into the adjacent grasslands.

Beetles covered distances of at least 80 m beeline and up to 13 % of individuals caught in traps at 80 m distance from the maize field emigrated from the maize habitat. These findings show that *Agriotes* beetles are capable to migrate over larger distances than previously assumed. Moreover, the stable isotope approach has been proven to be a useful tool to assess migration in arthropods.

POSTER PRESENTATION

Impact of wildflower strips and companion plants on pest control in organic cabbage crops

Johannes Schied[1], Andrea Leimgruber[3], Martin Willareth[3], Peter Nagl[3], Lukas Pfiffner[2], Henryk Luka[2], Eric Wyss[2], Christian Schlatter[2], Michael Traugott[1]

[1]University of Innsbruck, Innsbruck, Austria, [2]Research Institute of Organic Agriculture, Frick, Switzerland, [3]University of Basel, Basel, Switzerland

The promotion of natural antagonists is an important strategy of pest management in organic agriculture. In organic cabbage cultures the lepidopterans *Plutella xylostella, Mamestra brassicae* and *Pieris rapae* are the main pests, under attack by a guild of insect natural enemies, including parasitoids and generalist predators.

Within this project we assess whether wildflower strips and companion plants increase the level of pest control exerted by (i) natural enemies and (ii) mass-released *Trichogramma* egg parasitoids.

At Alten (Switzerland), two organic cabbage fields were used for this project: adjacent to each field a wildflower strip was sown and cornflowers (*Centaurea cyanus*) used as companion plants, sown intermixed within the crop. Within each field ~15,000 *M. brassicae* eggs were placed out to determine the parasitism rates by mass-released *Trichogramma brassicae* and assess the levels of egg predation. Over 1,000 lepidopteran larvae were collected and screened for hymenopteran and tachinid parasitoid DNA using am multiplex PCR assay. Invertebrate generalist predators (n=1,063) were collected for DNA-based gut content analysis to assess predation on healthy and parasitized lepidopteran pests. The epigaeic and plant dwelling invertebrate community was recorded by the use of pitfall traps, yellow bowls and sweep nets.

Currently the extensive sample set is being analysed: first results indicate that the wildflower strips increase egg parasitism rates and that companion plants enhance invertebrate predation on *M. brassicae* eggs suggesting that both wildflower strips and companion plants provide a effective measure to enhance pest control.

POSTER PRESENTATION

DNA-based identification of *Agriotes* wireworms

Karin Staudacher[1], Lorenzo Furlan[2], Michael Traugott[1]

[1]University of Innsbruck, Innsbruck, Austria, [2]University of Padova, Padova, Italy

This study focuses on larvae of European *Agriotes* species (Coleoptera: Elateridae), which are abundant below-ground living herbivores and cause considerable damage to field crops. There are up to 20 species occurring in arable land, which differ in regard to ecology, abundance and pest status. The basis of any wireworm risk assessment is the correct identification of the larvae; however, this is considerably hampered when morphological features are being used: current identification keys do allow identifying just eight of the 20 species in larval stage. Moreover, some morphological characters used for identification look very similar among some of the described species and their intraspecific variability has yet not been assessed.

Here we used a DNA-based approach to identify the different Agriotes species in larval stage. Within each species adult beetles, which are readily identifiable, were collected from different locations all over Europe. From these beetles, part of the mitochondrial cytochrome oxidase subunit I gene was sequenced to estimate the genetic variation within and between species. A non-destructive DNA-extraction method was used to gain DNA of rare specimens from insect collections. Species-specific markers were designed and applied in a multiplex-PCR approach, allowing to discriminate between the different *Agriotes* species within a single-step reaction.

Once the feasibility of this molecular identification system has been evaluated, it can easily be used by other researchers to routinely and securely differentiate between *Agriotes* wireworms, which will improve our ability to determine subtle differences in their specific ecology.

POSTER PRESENTATION

Detecting prey-DNA in invertebrate predators: The influence of predator taxon and storage method

Thomas Waldner, Michael Traugott

University of Innsbruck, Innsbruck, Austria

Molecular gut content allows studying the trophic connections of predatory invertebrates under natural conditions, often not accessible by conventional approaches. However, our knowledge on predator-specific prey DNA digestions rates, important to correctly interpret field data, still is scarce. Moreover, the influence of different storage methods on the quality of prey DNA within invertebrate predators has not been evaluated yet.

Were we compare DNA digestion rates between several ground-living predator groups including adult carabid and histerid beetles, cantharid and elaterid beetle larvae, and centipedes (Geophilidae and Lithobiidae). Predators were fed with larvae of the summer chafer, *Amphimallon solstitiale*, and frozen after several time points (0 - 60 h) post feeding. Using summer chafer-specific markers and diagnostic PCR, prey DNA detection rates for three differently sized mitochondrial DNA fragments (127 bp, 463 bp and 856 bp) are being compared among the different predator groups.

Within another experiment we assess how different storage conditions – freezing at -28°C or -80°C, storage in 80% ethanol - affect prey DNA detection success in carabid beetles fed with *A. solstitiale*.

The outcomes of these experiments will provide new insights into prey DNA digestion rates across a wide range of soil-dwelling invertebrate predators and guide us on how to store field-collected predators to preserve high-quality prey DNA.

POSTER PRESENTATION

Exploitation of plant biodiversity by below-ground herbivores: Tracking dietary choice in elaterid larvae using a molecular approach

Corinna Wallinger, Nikolaus Schallhart, Karin Staudacher, Michael Traugott

University of Innsbruck, Innsbruck, Austria

In the last decades the importance of biodiversity in ecosystem functioning has been increasingly acknowledged. To understand the structure of floral and faunal communities and the interactions within them, the investigation of trophic relationships is crucial. Upon now, research on trophic interactions in natural and agricultural ecosystems focussed mainly on above-ground relationships, whereas our knowledge on below-ground trophic interactions is limited.

This project, started in spring 2008, focuses on the trophic links within a plant-soil insect system. As soil-insects wireworms, the larvae of click-beetles (Coleoptera: Elateridae), have been selected. They are highly abundant herbivores in grassland and arable land and can cause considerable damage to crops. Additionally, weeds are known to be regularly fed on by wireworms. We will use stable isotope and molecular gut content analysis combined with an analysis of plant assemblage structure to assess the wireworms' feeding preferences under field conditions. Moreover, the affects of plant diversity on the insects' dietary choices will investigated experimentally. Besides addressing functional biodiversity in a below-ground food web, our research aims at providing a better understanding of plant biodiversity–wireworm trophic interactions, creating new ways of sustainable control strategies for these pests.

POSTER PRESENTATION

Arthropods associated with commercial Proteaceae in the Western Cape, South Africa: Preliminary results

Archbold Sasa, Michael. J. Samways, Melodie. A. McGeoch

Stellenbosch University, Western Cape, South Africa

Introduction: Commercial Proteaceae industry is growing in South Africa but the greatest problem is that of insect pests. Research on insects associated with plant species in the family Proteaceae in South Africa over the past three decades shows that these plants have a rich and diverse insect fauna. However, the data are insufficient for a number of reasons: (a) confirmation of insect identification requires expert advice and a comprehensive reference collection, (b) the list of insects covered is incomplete and (c) most of the studies were carried out on wild Proteaceae species and this is a ground breaking study on commercial Proteaceae.

Methods: Infructescences and leaves of commercial Proteaceae are being sampled for arthropods seasonally for a period of 12 months through use of active collection and active searching (spot check) methods.

Results: These plants have a rich and diverse insect fauna, which includes insects across a full range of plant-feeding guilds: leaf miners, leaf chewers, flowers bud borers, sap suckers and seed feeders. In addition to phytophages, there is a large suit of insect predators and parasitoids. A large percentage of the arthropods are indigenous and have pest status, in that they cause significant damage to the protea plants. Arthropods such as *Capys alphaeus* (Protea butterfly) and *Phyllocnistis* sp. (Channel leaf miner) appear to be specialist pests, as they only attack *Protea cynaroides* and Susara cultivar (*P. magnifica* x P. sussane) respectively.

Conclusions: A large percentage of arthropods associated with commercial protea plants are of economic importance.

POSTER PRESENTATION

Insecticidal activity of some wood-oils against the large pine weevil, *Hylobius abietis* L. (Coleoptera: Curculionidae)

Ivar Sibul, Linnar Pärn, Angela Ploomi

Estonian University of Life Sciences, Tartu, Estonia

Introduction: *H. abietis* is the major damaging pest in conifer reforestation areas in Northern and Eastern Europe. Weevil feeds on the bark causing newly planted trees mortality. The effect of some wood-oils was tested on the large pine weevils feeding.

Methods: Wood-oils extracted from native tree species (*Alnus incana*, *A. glutinosa*, *Populus tremula*, *Betula pendula*, *Picea abies*, *Tilia cordata*) by pyrolysis were studied in laboratory and field conditions. In laboratory tests the preferences and feeding activity of *H. abietis* for treated and untreated food (*Pinus sylvestris* branches) were assayed in simple choice and no-choice tests in spring 2007. Field experiment assayed the repellent or deterrent effect of wood-oils on weevil feeding activity in different conifer transplants over a 4-month period during 2007.

Results: Weevils feeding activity was depressed and wood-oils toxic effect caused many insects death in laboratory tests. The results from field tests indicated that wood-oils had deterrent influence to weevils. There was revealed a phytotoxic influence, a part of treated seedlings died. Although the wood-oils had only some weeks persistent effect nevertheless in autumn were the treated conifer trees less damaged than control plants.

Conclusions: The results indicate that wood-oils may have a role to play in protecting transplanted conifers from attack by pine weevil.

This research is supported by ETF grant no 6781.

POSTER PRESENTATION

Effects of isolation and landscape fragmentation on dispersal abilities of butterflies

Martina Klimova, Zdenek Fric

[1]Czech Conservation Authority, Zlin, Czech Republic, [2]School of Sciences, University of South Bohemia, Ceske Budejovice, Czech Republic, [3]Institute of Entomology, Czech Academy of Sciences, Ceske Budejovice, Czech Republic

Introduction: Biomechanical design of butterflies (allocation of flight muscles, shape and area of wings, wing loading) is directly related to flight abilities of species and individuals. We compared the changes in design of several butterflies differing in habitat requirements and both increasing and decreasing during the 20th century. We hypothesized that in decreasing species, traits associated with good dispersal should prevail in samples from early-20th century, when the habitats were less fragmented than in present.

Methods: We used specimens from large public and private collections, and recent material from identical sites. We then digitized the material and measured it using ScionImage (ScionCorp). Using discriminant function analyses, we compared changes of body design in time.

Results: We found significant changes in dispersal-related biomechanical traits in time in all studied species, indicating a shift in dispersal with changing landscape structure.

POSTER PRESENTATION

Chemical ecology in forensic entomology: Investigation of volatile infochemicals from pig cadaver on necrophagous insect behaviour

Jessica Dekeirsshieter, Francois Verheggen, Frederic Francis, Eric Haubruge

Gembloux Agricultural University, Functional & Evolutionary Entomology, Gembloux, Belgium

Introduction: The « chemistry of death » is poorly studied and information regarding the volatile organic compounds (VOCs) released after death is limited. Nevertheless, the VOCs from cadaver may attract a wide range of insects. These necrophagous insects, mainly Diptera and Coleoptera, may easily detect a dead body sometimes at long distances. Insects perceive chemical cues, the cadaveric odorant molecules or VOCs, that contribute to the dispersal and reproductive behaviour. Chemical ecology is a particular branch of ecology that focuses on the chemical communications between "living" organisms, such as the necrophagous insects and the dead body.

Methods: The chemical ecology approach is divided in three steps: (1) the volatile collection from a dead body (from pig's carcasses) and their identification by analytical techniques (GC-MS). (2) The study of the perception of these volatile organic compounds by a selected necrophagous insect (e.g. blowflies and Silphidae such as Silpha sinuata F.) with electrophysiological techniques (EAG). Third, the behavioural approach that study the insect behaviour to an odorant stimuli.

Results: Volatile compounds from pig cadaver were identified according to increasing durations of decomposition. Most interesting molecules were tested in both EAG and behavioural assays using olfactometry. Results from these experiments will be discussed in relation to the use of necrophagous insects and VOCs as bio-indicators or bio-sensors in the environment of a corpse.

POSTER PRESENTATION

Variation of the arthropod communities associated with repopulated plots with native shrub species at the micro-basin of Santa Helena–Suesca (Cundinamarca, Colombia)

María Catalina Cotes-Bravo[2], Giovanny Fagua[1], José Ignacio Barrera[1]

[1]Pontificia Universidad Javeriana, Bogotá, D.C., Colombia, [2]AKÁSIHA, Fundación para la Conservación y Biodiversidad Tropical, Bogotá, D.C., Colombia

Introduction: The change of both composition and structure of the arthropod community associated to native shrubs along the establishment of a riparian corridor in a micro-basin was studied.

Methods: The study was made in two zones of the micro-basin, one at 3000 m of altitude, and the other at 2800 m. Five samplings were made every two months from June 2004 to April 2005. The captures were made using the following traps: pitfall, Malaise, net transects, and Berlesse funnels, in twelve plots of 100 m² (10x10 m), six per zone.

Results: 108 families, 351 morph species and 30.900 individuals were colleted. Collembola and Diptera were the orders with the highest number of morph species and individuals. In both zones the abundance between the plots tending to increase and for the richness, which tends to diminish during the sampling time. It was found a tendency to increase of the diversity during the sampling time and the dominance diminished in both type plots. The Bray-Curtis analysis for the four capture methods showed that the similitude was higher between every sampling for the two types of plots that between each plot for the total sampling.

Conclusions: the composition of the arthropods community was associated to the complex structure of plants that is formed with the time of succession. The comparisons between communities of the two zones showed an increment of the diversity and a low dominance in the time, associated with an incipient succession at planted shrubs.

POSTER PRESENTATION

Understanding the role of symbionts in *Diaphorina citri* Kuwayama (Hemiptera: Psyllidae) by developing symbiont free lines

Izabela Salvador, Fernando Cônsoli

ESALQ-University of São Paulo, Piracicaba, São Paulo, Brazil

Introduction: Many insects harbour primary symbionts within specialized cells or structures for their growth and maintenance, while secondary symbionts may infect other tissues. These symbionts, mainly bacteria, may affect the host physiology and its interactions with the trophic levels, besides being necessary for the production of required nutrients. Because symbionts play a major role in determining host fitness, their use in developing new technologies for pest and disease control has been investigated. However, a candidate symbiont with a known effect on host biology has to be selected for the development of such technologies. The citrus psyllid *Diaphorima citri* vectos greening disease in Brazil, and is known to harbor the symbionts *Carsonella*, *Wolbachia* and the syncitium symbiont.

Methods: We proposed to develop symbiont lines of the citrus psyllid to understand the role symbionts play on *D. citri* development and reproduction as a step forward to develop strategies to control the disease it vectors. Ten-days old adults were fed antibiotic solutions (tetracycline, streptomycin, ampicillin, cefotaxime and rifampicin) for three days, and transferred to mating cages for egg collection and immature development.

Results: The syncitium symbiont was the most affected, followed by *Wolbachia.* Streptomycin and tetracycline were the most effective antibiotics in eliminating or reducing the symbiont load associated with the citrus psyllid, resulting in lower egg and nymphal survivorship, respectively. *Carsonella* was not affected by any of the antibiotics tested.

Conclusion: The secondary symbiont associated with the syncitium of the bacteriome holds a mutualistic association with the citrus psyllid.

Funding: FAPESP

POSTER PRESENTATION

Emission of alarm pheromone in aphids: A contagious phenomenon?

Francois Verheggen[1], Mark Mescher[2], Frederic Francis[1], Eric Haubruge[1], Consuelo de Moraes[2], Ezra Schwartzberg[2]

[1]Gembloux Agricultural University, Functional and Evolutionary Entomology, Gembloux, Belgium, [2]The Pennsylvania State University, Department of Entomology, State College, United States

Introduction: In response to attack by natural enemies, most aphid species release an alarm pheromone that causes nearby conspecifics to cease feeding and disperse. The primary component of the alarm pheromone of most studied aphid species is (E)-ß-farnesene. We recently demonstrated that the production and accumulation of (E)-ß-farnesene during development by juvenile aphids is stimulated by exposure to odor cues, most likely (E)-ß-farnesene itself, emitted by other colony members.

Methods: Volatiles from aphids were determined by gas chromatography – mass spectrometry. Here we examined whether the release of (E)-ß-farnesene can be triggered by exposure to the alarm pheromone of other individuals and thereby amplify the signal. Such contagious emission might be adaptive under some conditions because the amount of (E)-ß-farnesene released by a single aphid may not be sufficient to alert an appropriate number of individuals of the colony to the presence of a potential threat. Using a push-pull headspace collection system, we quantified the (E)-ß-farnesene released from aphids exposed to conspecific alarm signals.

Results: Typical avoidance behavior in aphids was observed with exposure to (E)-ß-farnesene (i.e., they ceased feeding and dropped from host-plant); however, no additional alarm pheromone was detected, suggesting that contagious release of (E)-ß-farnesene does not occur.

POSTER PRESENTATION

Microsatellite loci analysis in population of *Melipona marginata*

Alisson Roberto Campos Moresco, Maria Cristina Arias

USP, São Paulo, SP, Brazil

Introduction: *Melipona marginata* is a species of Meliponini found in eight Brazilian states, RS, SC, PR, SP, RJ, ES, MG, BA. This specie is considered the most ancestral from the genus, and like others species from this genus, makes nests in tree hollows. Due to the forest devastation, this species is considered endanger in some states. Also the uncontrolled transportation of colonies mediated by humans can increase the genetic drift among natural and isolated populations.

Methods: To study the population structure of *M. marginata* we collected specimens from 54 colonies along the geographical distribution of *M. marginata*, and we tested the amplification via PCR of 3 microsatellite loci (Mbi 201, Mbi 215 and Mbi 278), characterized originally in *M. bicolor*.

Results: The loci Mbi 278 and Mbi 201 presented a high number of alleles (6 each) and high level of heterozygosity, however the locus Mbi 215 presented only two alleles, being one of them extremely rare.

Conclusion: The use of heterospecific primers in order to amplify microsatellite loci in *M. marginata* was not so promising. It is necessary a survey of more loci, including others characterized in *M. bicolor* and *Scaptotrigona postica*.

POSTER PRESENTATION

Plutella xylostella (L.) (Lepidoptera: Plutellidae): strategies for integrated pest management

Sergio De Bortoli, Robson Thuler

FCAV-UNESP, Jaboticabal, São Paulo, Brazil

Introduction: This work was developed to evaluate the effect of the interaction between resistance of cabbage cultivars, insecticides and *Trichogramma* on the *Plutella xylostella* control.

Methods: The biology of *P. xylostella* was evaluated in the following cabbage cultivars: Chato de Quintal (CQ), Midori (MD), Roxo Precoce (RP) and Roxo Hybrid (RH), and kale cultivars: Geórgia (CM) and Geórgia Hybrid HS20 (HS20), in laboratory. The toxicity of the insecticides lufenuron and deltamethrin and, the vegetal products neem oil and pyroligneous extract, were evaluated for the adequacy of the lethal concentrations (LC50) of the products. With those products, the effect on *Trichogramma* was also evaluated. Finally, it was evaluated the association of the methods tested, using cabbage cultivars, chemical insecticides and vegetal products, and the effect on *Trichogramma*.

Results: The cultivar CQ was classified as moderately resistant; RP and MD as susceptible, and CM, HS20 and HR as highly susceptible, being also observed, that the cultivars tested did not present sinigrin. Lufenuron, Neem oil and pyroligneous extract caused up to 100% of *P. xylostella* mortality and deltamethrin was not efficient. Deltamethrin was most harmful product to the parasitoids *T. exiguum* and *T. pretiosum*, while neem oil and lufenuron were less harmful.

Conclusion: The interaction of chemical and plant resistance methods, increased the potential to *P. xylostella* control, but this strategy must be well evaluated, as it can affect negativity the parasitoid performance, reducing its control potential.

POSTER PRESENTATION

Resistance of citrus varieties and hybrids to the citrus psyllid *Diaphorina citri* Kuwayama (Hemiptera: Psyllidae)

Paulo Bogorni, José Vendramim, André Lourenção, Marcos Machado, Cristina Vasconcelos

ESALQ/USP, Piracicaba, São Paulo, Brazil

Introduction: The *greening* disease was detected in Brazil only in 2004, where it is vectored by the citrus psyllid *Diaphorina citri*, which is commonly found all over the country.

Methods: As a possible strategy to control the vector of this disease, was evaluate the resistance of Citrus varieties and hybrids and three related genera to the citrus psyllid. Twenty-two genotypes were evaluated. They were distributed in three groups of three genotypes each, and sweet orange (Pêra) was used as control. Each group was caged and 30 psyllid adults were released inside. Each group was replicated 8 times. Data was analyzed by applying the resistance index R.I.= [(A – B) / (A + B)] x 100, where: A = number of psyllid eggs, nymphs or adults in the tested genotype; B = number of psyllid eggs, nymphs or adults in the control. The number of insects was assessed from the 18^{th} to the 21^{st} day after adult release into the cages.

Results: *Poncirus trifoliata* was the most resistant genotype, and none of the psyllid stages of development evaluated were found associated to this plant. Other genotypes, such as grapefruit, *Fortunella margarita*, sweet orange (Natal), hybrid (*Poncirus trifoliata* x *C. sinensis*) and hybrid (*Citrus paradisi* x *Poncirus trifoliata*) were also resistant to the citrus psyllid, while the genotypes pummelo, citron, sweet orange (Hamlin), *Murraya paniculata*, sweet orange (Valência), lemon, hybrid mandarin x sweet orange (*C. reticulata* x *C. sinensis*), mandarin and hybrid (*C. reticulata* x *Poncirus trifoliata*) were the most susceptible.

POSTER PRESENTATION

Aphid - ant mutualism : How do aphids focus ant foraging?

Francois Verheggen[1], Lise Diez[1], Claire Detrain[2], Bernard Wathelet[3], Frederic Francis[1], Eric Haubruge[1]

[1]Gembloux Agricultural University, Functional and Evolutionary Entomology, Gembloux, Belgium, [2]Free University of Brussels, Department of Social Ecology, Brussels, Belgium, [3]Gembloux Agricultural University, Department of Biological Chemistry, Gembloux, Belgium

Introduction: The mutualistic relationships that occur between myrmecophilous aphids and ants are based on the rich food supply that honeydew represents for ants and on the protection they provide against aphid natural enemies. Scouts of aphid-tending ant species would benefit from locating honeydew ressources by orienting toward aphid pheromone sources. The present study aims to identify the chemical factors that attract ants and that maintain their mutualistic relationships with aphids.

Methods: The perception and behavioral impact of *Aphis fabae* alarm pheromone, namely (E)-β-farnesene, on *Lasius niger* were firstly investigated using electroantennography and a four-arm olfactometer. *Aphis fabae* honeydew sugar composition was subsequently analyzed and the preference and recruitment operated by individual *L. niger* scouts for each of the identified sugars was studied.

Results: Clear electrical depolarisations were observed from *L. niger* scout antennae to stimulations of *A. fabae* alarm pheromone. Scouts were significantly attracted toward (E)-β-farnesene in the four-arm olfactometer, suggesting for the first time that the latter compound is a key chemical in the establishment of the mutualism. *Aphis fabae* honeydew composition consisted of 9 identified mono-, di- and tri-saccharides and 8 hydrocarbons that could not be identified. Individual *L. niger* scouts showed the following preferences for the tested sugars: melezitose = sucrose = raffinose > glucose = fructose > maltose = trehalose = melibiose = xylose. Ant scouts are therefore presumed to use aphid semiochemicals to locate at distance an aphid colony and subsequently to estimate honeydew quality by tasting it before recruiting conspecifics and establishing mutualistic relationship.

POSTER PRESENTATION

Mixed forests – a strategy to avoid pest outbreaks? How euryphages and stenophages could react: A case study of temperate forests

Julian Heiermann, Stefan Schütz

Büsgeninstitute, Georg-August-University Göttingen, Göttingen, Germany

Introduction: Mixed forests are assumed to be less prone to insect outbreaks than monocultures. This common thesis was tested by observing two Lepidoptera pests with various diet widths. *Lymantria monacha* L. (Nun moth) as a euryphagous pest on coniferous and deciduous tree species, and *Calliteara pudibunda* L. (Pale tussock moth) as stenophaguous pest on broad-leaved trees.

Methods: The relative abundances and species dominance of both target pests were investigated in six forest types (with five replications): pure spruce (Norway spruce (*Picea abies* (L.) Karst.), pure beech European beech (*Fagus sylvatica* L.) and four mixed stands with different ratios of both tree species. Light traps were used for catching the moths.

Results: Both target species react different. The relative abundances of *C. pudibunda* appear to be linked to the tree species compositions of the test forests. Both the number of individuals and the dominance of the pest species increased from pure spruce forests to above mixed forests with rising beech ratio towards pure beech stands. Remarkable is that beech forests with a small portion of spruce (25 %) show a strong effect of decreasing number of individuals. No significant effects were observed concerning to *L. monacha* and beech/spruce ratio of forests. The only clear trend was that the dominance of this pest decreased with rising beech ratio in forests.

Conclusions: Overall, our findings confirm the assumption that mixed forests are less prone to insect outbreaks in comparison to monocultures.

POSTER PRESENTATION

Selectivity of pesticides for two species of *Trichogramma* (Hymenoptera: Trichogrammatidae) in different hosts

Sergio De Bortoli, Roberto Goulart, Robson Thuler

FCAV-UNESP, Jaboticabal, SP, Brazil

Introduction: The aim of this work was to evaluate the selectivity of pesticides triflumurom, etofenprox and endosulfan for two species of *Trichogramma*; *T. pretiosum* and *T. exiguum*, in different hosts: *A. kuehniella*, *S. frugiperda* and *P. xylostella*, under laboratory conditions.

Methods: This research was conducted at Faculdade de Ciências Agrárias e Veterinárias de Jaboticabal (FCAV-UNESP), in the Laboratório de Biologia e Criação de Insetos. The tests were based on two methodologies: a new methodology for selectivity tests which was developed in LBCI and the IOBC/WPRS methodology. Using LBCI methodology parasitized eggs, percentage of emergence, percentage of parasitism, longevity and sex ratio were evaluated for generations F_1 and F_2. Using IOBC methodology were evaluated parasitized eggs, percentage of emergence, percentage of parasitism and parasitism reduction.

Results: The endosulfan and etofenprox were harmful to parasitoids inhibiting the parasitism in all hosts or killing the insects by two methodologies. Triflumurom was selective to parasitoids just in natural host eggs when the new methodology was applied. When the IOBC methodology was applied triflumurom showed selectivity for both species of parasitoids.

Conclusion: The use of these methodologies influenced the results of insect selectivity.

POSTER PRESENTATION

Traps used in different European countries for the monitoring of vectors of Bluetongue (BT) and African Horse Sickness (AHS)

Ricardo del Rio Lopez[1], Miriam Monerris Mascaró[1], Miguel Angel Miranda Chueca[1], Carlos Calvete[2], David Borras[3], Margalida Miquel[1], Rosa Estrada[4], Javier Lucientes[4]

[1]University of Balearic Islands, Palma de Mallorca, Spain, [2]CITA, Aragon, Spain, [3]IBABSA, Palma de Mallorca, Spain, [4]University of Zaragoza, Palma de Mallorca, Spain

Bluetongue is a disease of ruminants caused by a virus transmitted by the bites of midges species from genus *Culicoides* (Diptera; Ceratopogonidae).Several types of light traps are being used in different European countries for capturing the major vector species of BTV. The four different traps used for the study were: i) OVI-Ondestepoort trap, black light trap provided with 8W U.V. light tube, used in UK and Italy ii) Mini CDC, black light model 912 provided with 4W U.V. light tube, John Hock Company, used in Spain and Portugal iii) Rieb trap, white light model provided with 4W U.V. light tube, used from 2000-2006 in France iv) UK trap, provided by 4W standard incandescent bulb, used in the past in UK and other European countries for AHS surveillance. All traps are provided with a draught back suction fan. Here we have compared the performance of the four types of traps used for the surveillance of the *Culicoides* vector species. The Comparison consisted on a randomized block design. During nine non-consecutive nights the traps were placed in four different positions in a cattle farm located in the island of Mallorca (Balearic Islands, Spain). Results showed important differences in collecting *Culicoides*. The catches were less abundant compared with previous years because of heavy rains and strong winds during the sampling OVI trap showed the best performance in terms of total amount of *Culicoides* captured. However, all four traps captured a similar range of species making non difference in specificity when comparing traps.

POSTER PRESENTATION

Phylogenetics relationships among species of genus *Scaura* (Hymenoptera: Meliponini) inferred from mtDNA sequences

Alayne Domingues, Maria Cristina Arias

USP, São Paulo, SP, Brazil

Introduction: The genus *Scaura* contains species of stingless bees of small size and dark color pattern. The group presents variation in the nesting behavior including several types of cavities as tree hollows or within active termite nests. Currently, four species are recognized: *Scaura latitarsis*, *S. atlantica*, *S. longula* e *S. tenuis*. This genus is of particular interest in terms of taxonomy and phylogenetic relationships. However all the literature are based on morphology and behavior data. The present work aim at to establish the pattern phylogenetic in the genus *Scaura* by using molecular approaches as a new contribution to this bee group.

Methods: Samples were collected from nests in different regions of Brazil. Five mitochondrial genes (12S, 16S, CO I, CO II and Cyt *b*) were amplified and sequenced for *Scaura* species and *Schwarzula timida* and *Schwarziana quadripunctata* (outgroups). Phylogenetic relationships among the included taxa were inferred using neighbor-joining and maximum parsimony methods.

Results: The results show high A+T content. The tree obtain allowed discrimination of species closely related, making part the same monophyletic group.

Conclusion: Further studies using more molecular techniques will contribute to a better understanding of the mechanisms involved in the evolution and to contribute to the correct taxonomic classification of the genus.

POSTER PRESENTATION

A survey of ticks in sheep in the Serra de Tramontana in Mallorca (Balearic Islands, Spain)

Miriam Monerris[1], Ricardo Del Rio[1], Marga Miquel[1], David Borràs[2], Cristina Rincón[1], Miguel Angel Miranda[1], Agustín Estrada-Peña[3]

[1]University of Balearic Island, Palma de Mallorca, Baleares, Spain, [2]IBABSA, Palma de Mallorca, Baleares, Spain, [3]Universidad de Zaragoza, Zaragoza, Aragón, Spain

Ticks are ectoparasites of vertebrates, being identified as highly competent vectors. In fact, ticks have a great medical and veterinary importance, because of its capacity for transmitting a large number of pathogens, including viruses, bacteria and protozoa.

The objective of this work was to survey the species of ticks found on sheep in the island of Mallorca (Balearic Islands). The study took place in the Serra de Tramontana, located in the north of the island. Six farms were chosen and 15 to 30 sheep were sampled in each one. The ticks were directly collected from the head and perianal area of the animals and preserved in ethanol 70 % until identification.

A total of 558 ticks were collected. The farm with a higher abundance of ticks was Sollerich (212 ticks), followed by Son Sales (136), Sòller (82), Son Alzines (49), Es Clot (45) and finally Es Pujol (24). The species of ticks found were *Rhiphicephalus turanicus* (64.3%) and *Rhipicephalus sanguineus* (31.7%). Only one specimen of *Haemophysalis punctata* was collected.

Results showed a high infestation of animals by ticks. From the total of sheep sampled (171 animals), a 77.7 % were infested with ticks. The average of infestation per animal was 5 ± 2,74 ticks. The free range management of the sheep herds in the mountains of Mallorca seems to be directly related with the high abundance of ticks found in the animals.

POSTER PRESENTATION

Genetic variability of a small population of *Frieseomelitta varia* (Hymenoptera, Apidae: Meliponini) through RFLP of mitochondrial DNA

Paulo Henrique Pereira Gonçalves, Maria Cristina Arias

Universidade de São Paulo, São Paulo/SP, Brazil

Introduction: The stingless bees present great ecological importance because they are the main pollinators of several ecosystems. Some species are threatened due to forest fragmentation and devastation; such human actions are decreasing directly the bee population in special the ones that nest in hollow of trees, like *Frieseomelitta varia*. This species is characterized by the production of honey quite viscous. Its distribution covers the Brazilian states of BA, MG and SP. The objective of this study was to verify the genetic variability of a small population of *F. varia* living at the campus of the University of São Paulo, Ribeirão Preto-SP with subsequent inferences about the colonization of new areas by this species and also test Kerr and Vencovsky's hypothesis, which postulates a minimum of 44 nests per area to prevent the loss of genetic variability in a population.

Methods: The DNA was extracted from workers collected in 22 nests. Five mitochondrial regions were amplified: [ND2/COI], [COII], [8 and ATPase 6/COIII], [ND1/16S], [16S/12S], and digested by the following restriction enzymes, *Eco*R I, Bcl I, *Dra* I, *Ase* I *Eco*R V, *Bgl* II, *Hind* III, *Pst* I, *Hinf* I, *Cla* I *Ssp* I and *Bam* HI.

Results: The results obtained so far, allow us to delineate mitochondrial regions that have accumulated more replacements of bases and the enzymes more effective in detecting them. Among the nest sampled only two haplotypes were identified. This fact indicates that this small population was presumably founded by at least two colonies, considering that the mtDNA has maternal inheritance.

POSTER PRESENTATION

Overwintering of *Culicoides* spp. in the western Mediterranean Basin

Miguel Angel Miranda[1], Ricardo Del RIo[1], Miriam Monerris[1], Marga Miquel[1], Carlos Calvete[3], Rosa Estrada[4], Javier Lucientes[4], David Borràs[2]

[1]University of Balearic Island, Palma de Mallorca, Baleares, Spain, [2]IBABSA, Palma de Mallorca, Baleares, Spain, [3]CITA, Aragón, Spain, [4]Universidad de Zaragoza, Zaragoza, Aragón, Spain

Since the declaration of an outbreak of Bluetongue (BT) in the Balearic Islands (Spain) in 2000 (BTV2) a survey, that was intensified in late 2003 (BTV4), was conduced for the *Culicoides* spp. species involved in the transmission of BTV. Collections were made every week in 21 farms distributed in Majorca, Minorca and Ibiza using 6V U.V. miniCDC light - traps. During the last four years (2004 - 2007) a total of 3.862 samples were analysed and 15.262 were identified as *C.imicola* Kieffer, 1913, 66.935 belonging to the Complex Obsoletus, 43 specimens as *C. pulicaris* Linnaeus, 1758, and 115.876 as other *Culiciodes* species. Annual capture of midges is required to better establish the seasonal vector free period in a given area. In the Balearics, the first detection of *C.imicola* occurs in April and remains active up to December, being the maximum period of risk during the vector population peak in late autumn. The introduction of BTV8 (2008) in the Iberian Peninsula and the presence of BTV4 and 1 has changed the situation. The *C. obsoletus* complex has been recently related with the transmission of BTV8 and BTV1 in northern Iberia. This species complex is active during the whole year and peaks in May-June. Tree species belonging to this complex are present in the Balearics: *C. obsoletus* “sensu stricto” Meigen, 1818, *C.scoticus* Downes and Kettle, 1952, and *C.dewulfi* Goetghebuer, 1936. The current epidemiological situation in Europe makes necessary to maintain a well developed entomological and virus surveillance system in an annual basis.

POSTER PRESENTATION

Cuticular hydrocarbons variability, as a potential taxonomic tool for *Anacroneuria* spp. (Perlidae: Plecoptera)

Maribet Gamboa, Jose Vicente Hernández, Jazzmín Arrivillaga

Universidad Simon Bolivar, Caracas, Miranda, Venezuela

Introduction: Cuticular hydrocarbons play a significant role in the regulation of permeability and the insect chemical communication system. We report here the variability in composition on the cuticular hydrocarbons in four Plecoptera species (*Anacroneuria chorrera*, *A. cacute*, *A. tachira* and *A. paleta)*, considered as bioindicators of the lotic system contamination.

Methods: Solid Sample of individual pronotum of naiads were prepared. Gas chromatography/mass spectroscopy was used to determine the presence or absence of cuticular hydrocarbons.

Results and conclusion: Cuticular composition indicate that four species represented two species groups, Group 1 (*A. chorrera* and *A. paleta)* and Group 2 (*A. tachira* and *A. cacute*). These results agreed with our naiads morphological revision performed previously.

POSTER PRESENTATION

Biology and behavior of the cocoa borer, *Carmenta foraseminis* (Eichlin, 1995) (Lepidoptera: Sesiidae)

Beatriz Herrera-Malaver[1], Carmen V. Liendo-Barandiaran[1], Cristina Sainz-Borgo[1], José Vicente Hernández[1], Franklin Morillo[2]

[1]Universidad Simón Bolívar, Caracas, Estado Miranda, Venezuela, [2]Instituto Nacional de Investigaciones Agrícolas, Estación Experimental Miranda, Calle El Placer, Caucagua, Estado Miranda, Venezuela

Introduction: In Venezuela, one of the most important cocoa pest insect is *C. foraseminis* Eichlin (1995). Larvae of this sesiid feed within the fruit and seed of *Theobroma cacao* L., cause serious damage on commercial products.

Methods: *C. foraseminis* larvae and pupae were collected from cocoa fruit in Choroní, Aragua State, Venezuela. Larvae were reared individually in clear plastic container, and feed with a small cocoa piece. Pupae were removed from their cocoons and kept on wed adsorbent paper until its emergence. Room conditions were 25℃, 63% relative humidity and 12:12 L/D. Male and female adult number of *C. foraseminis* that emerged during an hour intervals on different colect period were recorded by observers. Observation chambers wereprovided with a source of 10% sucrose solution and an unripe cocoa pod. Newly emerged female and male moth were place individually into the chamber. Female moth were observed for calling behavior by one hour intervals during ≥48h after emergence.

Result and Conclusions: Males and females of *C. foraseminis* moths showed an emergence peak within 14:00 to 15:00 hours. Pupal period was 15 ± 2 days and adult longevity was 7 ± 4 days. The onset of calling behavior occurs on the day after emergence and was observed during crepuscular period. Calling female of *C. foraseminis* assume a posture that includes abdominal hairs displayed and abdomen ventrally curved.

POSTER PRESENTATION

Phylogenetic relationships among Brazilian bumblebees (Hymenoptera: Apidae) inferred from mitochondrial DNA sequence data and gene organization

Elaine Françoso, Maria Cristina Arias

Universidade de São Paulo, São Paulo, SP, Brazil

Introduction: In Brazil, are found only six species from the genus *Bombus: Bombus morio, B. atratus*, *B. brevivillus*, *B. brasiliensis*, *B. transversalis and B. bellicosus,* a low number comparing to the Northern hemisphere. Molecular markers are widely used in biology, and molecular markers from mtDNA analyses were applied to stingless bee species and the data obtained has proving useful to infer hypotheses about phylogeny, population dynamics, species validity and evolution. The objectives of this research are: to understand the phylogenetic relationship among the Brazilian species through mitochondrial genes analysis; to correlate the present biogeography with past paleoclimatics and geological events; and to propose an alternative hypothesis for the evolution and speciation within the genus. To achieve our goals we analyzed sequences from three mitochondrial regions and also the gene order of two mitochondrial tRNAs clusters, which in previous studies showed translocations and presence of pseudogene in *Bombus morio.*

Methods: Mitochondrial DNA was extracted from ethanol preserved thoracic or dry leg from museum specimens. The genes 16S and COI, and tRNAs cluster 1 and 4 were amplified by PCR, cloned into vector and sequenced from both strands.

Results: A molecular phylogenetic relationships was inferred from mitochondrial DNA sequences data and the secondary tRNA structure was obtained showing the presence of $tRNA^{lys}$ pseudogene within cluster IV.

Conclusion: The six Brazilian bumblebee species consist a monophyletic group and the presence of the $tRNA^{lys}$ pseudogene seems to be a unique characteristic of this South American group.

POSTER PRESENTATION

Tephritide of economic importance in the Balearic Islands (Spain)

Miguel Angel Miranda, Marga Miquel, Jaume Terrassa, Maria del Mar Leza, Antònia Romero, Ricardo Del Rio, Miriam Monerris, Ana Alemany

University of Balearic Island, Palma de Mallorca, Baleares, Spain

The Balearic Islands are located in the western area of the Mediterranean Basin. Olive, citrus and stone orchards are the main crops in the islands. Several species of Tephritidae of economic importance are present in the Balearics. The Mediterranean fruit fly, *Ceratitis capitata* and the Olive fly, *Bactrocera oleae,* are well known species which cause important damages and losses to the agriculture. The current control strategies for these species are mainly based in the use of a wide range of insecticides. However, in the last year 10 years, a great effort in the use of alternatives, such as mass trapping and sterilization by chemical means, has been carried out in the Balearics. The combination of the three synthetic attractants Trimethylamine, Putrescine and Ammonium Acetate are the main lures used for the monitoring and mass trapping of the females of *C. capitata.* In the case of the Olive fly, the monitoring is still mainly based in the synthetic pheromones for capturing females and the use of ammonium phosphate for capturing females. Two news species of economic importance have been recently recorded in the Balearic. In August 2007 several specimens of *Carpomyia incompleta* and *Capparimyia savastani* were captured in traps that were deployed for capturing C. capitata and B. oleae respectively. The larvae of *C. incompleta* develop in the fruits of *Ziziphus* spp., meanwhile the larvae of *C. savastani* develop in the edible bud flowers of *Capparis spinosa*. Both species has been recorded as a potential pest species of their respective hosts.

POSTER PRESENTATION

Morphometric analysis of the antennal sensilla of the adult female blackfly, *S. chutteri* Lewis (Diptera: Simuliidae)

Vuyisile Hobololo[1], Alan Hall[3], Chris van der Merwe[3]

[1]ARC-Onderstepoort Veterinary Institute, Onderstepoort, Pretoria, South Africa, [2]University of Pretoria, Faculty of Veterinary Science, Onderstepoort, Pretoria, South Africa, [3]University of Pretoria,Laboratory for Microscopy and Microanalysis, Hatfield, Pretoria, South Africa

Introduction: A thorough understanding of blackfly behavioural patterns exhibited during host location cannot be fully understood unless detailed information on the structural dimensions, relative abundance and distribution of antennal sensilla of female *S.chutteri* is available.

Methods: Live populations of wild female *S. chutteri* were sweep-netted from sheep grazing in open fields in two localities of proven blackfly challenge along the Vaal River, South Africa. Specimens were prepared for scanning electron microscopy using standard techniques. The antennal hair-types were observed, micrographed and measured. All numerical measurements of all the antennal hair-types are averages of at least 20 observations. Statistical significance was determined using unpaired student's t-test at the 5% level.

Results: The antennal flagellum of female *S. chutteri* is divided into nine flagellomeres ranging from 183 to 311μm (average = 257 μm) in length. The overall length of the most prominent Type 1 sensilla chaetica (T1) ranges from 8.41 to 18.00 μm (average = 14 μm) with the mean basal diameter of 1.96 μm and 1.6 μm at midpoint. Type 2 sensilla chaetica (T2) have an average length of 9.38 μm (range = 7.75 – 9.80 μm) with the average base diameter of 1.45 μm and midpoint diameter of 1.05 μm. Sensilla trichodea (ST) have an average length of 15.9 μm (range = 12.90 – 20.42 μm), average basal diameter of 2.00 µm (1.92 – 2.17 μm). The elongate, cylindrical subtype of sensilla basiconica (SB) have an average length of 9.68 μm (range = 6.88 – 12.25 μm), while the club-shaped subtype have an average length of 3.9 μm, basal diameter of 1.58μm and midpoint diameter of 1.51μm. Grooved sensilla basiconica (GSB) average length is 5.90 μm (range = 4.81 – 7.00 μm), while basal diameter is 1.49 μm (range = 1.19 – 1.83 μm) and midpoint diameter of 1.05 μm (range = 0.75 – 1.13 μm).

Conclusions: The most numerous (>1000 sensilla), smooth-walled, olfactory ST are the longest sensilla occurring in all flagellomeres while the least abundant (2-5 sensilla) T1 are the most prominent contact chemoreceptors found only in the distal flagellomere. Although structurally similar to T1's, T2 are almost half the length of T1's, occurring in all flagellomeres. Club-shaped SB's are almost 2/5 the size of cylindrical SB's in length. GSB are the smallest sensilla in all dimensions.

POSTER PRESENTATION

Natural Products Based Pesticide Development Centre (BOPAM) in Turkey

Nezhun Goren[1], Neset Kilincer[2], M.Oktay Gurkan[2], Ayhan Gokce[3], Mark Wholan[4]

[1]Yildiz Teknik Univ., Istanbul, Turkey, [2]Ankara University, Ankara, Turkey, [3]Gaziosmanpasa Univ., Tokat, Turkey, [4]Michigan State Univ, Michigan, United States

This project aims to develop natural products that are compatible with other control strategies, are safe for non-target organisms and the environment, and will decrease residue issues at harvest. In order to achieve these aims, natural products extracted from plant species endemic to Turkey were tested against various important pest species e.g. *Spodoptera littoralis*, *Leptinotarsa decemlineata*, *Bemisia tabaci* under laboratory conditions.

Initial data has suggested that natural products are highly effective against insects, particularly those with a broad history of potential resistance. The unique mode of action of natural products e.g. antifeedant, repellent promises potential for their use in rotation with other pesticides with a decreased chance of development of resistance.

POSTER PRESENTATION

Ecological and biological investigations on emergent bluetongue vectors, the biting midges *Culicoides*, in Belgium

Jean-Yves Zimmer, Frederic Francis, Eric Haubruge

Gembloux Agricultural University, Functional and Evolutionary Entomology, Gembloux, Belgium

Introduction: Bluetongue is a non-contagious disease coming from South Africa that affects domestic and wild ruminants. This viral epizooty – of which there are 24 different serotypes – causes considerable economical losses on its passage. In 2006, bluetongue appeared in the North of Europe including Belgium. *Culicoides* are biting midges counting about 1400 species but only some of them seem to act in the transmission of the bluetongue virus. We aimed to identify the bluetongue adult vector species and determine the particular larval habitat.

Methods: A field study was performed in animal production farms in Belgium. A Culicoides adult trapping was realised using light trap to collect and identify the potential flying vector species. Also, knowing the ecological requirement of biting midge larvae, frequently observed in the upper layer of the wet and rich organic matter environment, an investigation of several potential ecological habitats of larvae were sampled and the larvae were reared in the laboratory until adult emergence to be identified.

Results: After adult Culicoides identifications, the relations between the characteristics of the investigated habitats, the presence of cattle, the distance to the farm and the identified biting midges species were studied. The survival and activity of adults were strongly influenced by the weather factors. Higher adult Culicoides populations were observed nearby farming than in the neighbouring meadows. The *C.obsoletus / scoticus* complex was the most abundant. The main potential bluetongue fly vectors privileged at the larval stage the anthropogenic areas close to livestock.

POSTER PRESENTATION

Effective sampling range of food-based attractants for pest Tephritidae

Nancy Epsky, Paul Kendra, Robert Heath

USDA/ARS, SHRS, Miami, Florida, United States

Introduction: Semiochemical-based detection and monitoring systems are critical components of tephritid fruit fly trapping programs. Trapping efficacy is dependent upon the attractant's effective sampling range, defined as the maximum distance from which an insect can reach an attractive source in a given period of time. Mark-release-recapture studies were conducted with sterile *Anastrepha suspensa* females to determine effective sampling range for a female-targeted synthetic food-based lure and for liquid protein bait.

Methods: Sexually immature and mature sterile females, marked with different pigments, were released from a centrally-located point source. 25 Multilure traps were placed in concentric circles between 9 and 46 m from the release point. Recapture was determined after 0.5, 1, 2, 3 and 6 d. Separate tests were conducted with Multilure traps baited with a two component synthetic lure (ammonium acetate and putrescine) or with liquid protein bait (torula yeast/borax).

Results: In all tests, recapture of immature females was higher than recapture of mature females. Most of the flies were recaptured within the first 24 h of release in traps located within 17-27 m of the release point. Results were similar for immature and mature flies, and for traps baited with synthetic lures or liquid protein. Few females were recaptured by 6 d of release.

Conclusions: Additional studies will be conducted to compare response of wild flies with sterile flies. This information is needed to determine coverage of traps used for population delimitation or for mass trapping control strategies, or to pin-point areas of infestation for precision targeting of control measures.

POSTER PRESENTATION

Fluctuations in abundance of green lacewings (Neuroptera: Chrysopidae) in guava orchards in southeastern Brazil

Jatinder Multani, Gilberto Albuquerque

Universidade Estadual do Norte Fluminense, Campos dos Goytacazes, RJ, Brazil

Introduction: Green lacewings are predominantly arboreal and play a key role in biological control. Despite the high diversity of these predators in the Neotropics (> 300 species), little is known about their population dynamics in this region. An understanding of their seasonal patterns of activity has implications for pest management in guava, an important cash crop in southeastern Brazil.

Methods: All stages of lacewings were sampled weekly, for two years, in three guava orchards in Campos dos Goytacazes, state of Rio de Janeiro. Tree branches were inspected thoroughly for immatures, whereas adults were collected with attractive traps. The influence of prey availability and climatic factors on the predators' abundance was evaluated.

Results: Adults of 17 species, from *Leucochrysa*, *Ceraeochrysa*, *Chrysopodes*, *Chrysoperla* and *Plesiochrysa*, were captured, with high abundance in July-August and a long period of low numbers between October and May. Six of these species, however, do not occur on guava trees, as demonstrated by their absence in the immature samplings, and were probably attracted from the surrounding vegetation. Of the 11 guava-inhabiting species, most individuals belonged to *Ceraeochrysa* spp. Considering only the species found in guava, there was no clear seasonality, i.e., all stages were present throughout the year, with alternating short periods of high and low numbers.

Conclusion: The year-round occurrence of green lacewings in guava orchards shows that there is no interruption in their life cycle in southeastern Brazil. Consequently, they show potential for use in conservative and augmentative programs to control guava pests during all seasons.

POSTER PRESENTATION

New developments in food-based synthetic attractants for pest Tephritidae

Robert Heath, Paul Kendra, Nancy Epsky

USDA/ARS, SHRS, Miami, Florida, United States

Introduction: Optimal capture of several species of *Anastrepha* and *Bactrocera* spp. tephritid fruit flies is in traps baited with the aqueous protein bait Nulure combined with borax. Nulure is produced by acid hydrolysis of corn and has an acidic pH. Addition of borax makes the solution more alkaline and more attractive to several fruit fly species. We report herein research on chemical modifications of Nulure to identify volatiles responsible for attraction and also to improve stability of Nulure-based baits for these species.

Methods: The pH of Nulure solutions was modified by addition of borax or sodium hydroxide (NaOH) at a range of pH4 to pH10. Stability was monitored and ammonia release rate was quantified over a 14 d period. Electroantenography (EAG) was used to determine antennal sensitivity for *Anastrepha suspensa* females, and field tests were conducted to determine effect on trapping efficacy.

Results: It was observed that the zwitter ion effect plays a critical and confounded role on pH stability in aqueous solutions. Stabilization of pH was noted when propylene glycol was added at a 10% (vol:vol) concentration. EAG analysis indicated that female antennal response to Nulure increased as pH shifted from acidic to neutral. Highest field capture of females was in traps baited with synthetic lures ammonium acetate and putrescine in combination with Nulure at pH7 with NaOH and 10% propylene glycol.

Conclusions: Chemical analysis will be used to identify additional attractant chemicals from modified Nulure bait solutions for use in food-based synthetic lures.

POSTER PRESENTATION

Decrease of vertical transmission rate of a spiroplasma in *Drosophila hydei* at low temperatures

Ryu Osaka[1], Masashi Nomura[1], Masayoshi Watada[2], Daisuke Kageyama[3]

[1]Graduate School of Horticulture, Chiba University, Matsudo, Chiba, Japan, [2]Faculty of Science, Ehime University, Matsuyama, Ehime, Japan, [3]National Institute of Agrobiological Sciences (NIAS), Tsukuba, Ibaraki, Japan

Introduction: In Japanese populations of *Drosophila hydei* infected endosymbionts belonging genus *Spiroplasma*. The infection rate of spiroplasma has been shown middle frequencies (23 to 66 %). But the spiroplasma did not cause male killing. In natural population of *D. hydei*, the frequency of spiroplasma is high in summer, but low in spring. Why the frequency is decrease with the approach of next spring?

Method: We used an iso-female line of spiroplasma–infected *D. hydei* that was established from collecting in Japan. New emerged adult flies were reared, and females were oviposited at various temperatures (28, 25, 18 and 15ºC). The frequency of infected spiroplasma in flies of next generation was investigated by using a diagnostic PCR method. Additionally, the titers of spiroplasma in flies of parental and next generation were quantified by using a real-time PCR method.

Results: In low temperatures (18 and 15ºC), the frequencies of infected spiroplasma in next generation were decreased dramatically. Especially at 15ºC, there was no transmission of infected spiroplasma. In parental generation, the titer of spiroplasma at 25ºC was higher than the titer at 18 and 15ºC, but the level of the titer of spiroplasma was equivalence. On the other hand, in next generation, the titer of spiroplasma at 18ºC was tithe as much as the titer at 28 and 25ºC.

Conclusion: Low temperatures restrict the frequency of spiroprasma in a natural population of *D. hydei*.

POSTER PRESENTATION

Mitochondrial gene order and the evolution of bees (Hymenoptera: Apidae)

Daniela Silvestre, Maria Arias

USP, São Paulo, SP, Brazil

Introduction: The classification of bees and their phylogenetic relationships are controversial questions still. Mitochondrial gene order is cited by several authors as a promising molecular marker to study the phylogeny of major groups, like Insecta orders. Thus comparative analyses of mtDNA may constitute a good character source to infer the phylogeny among tribes, subfamilies and families of bees.

Methods: mtDNA regions of 13 bee species from 11 different tribes were amplified with primers derived from other insects. All fragments were cloned and sequenced from both directions. Sequences were analyzed to determine gene order and compared among species.

Results: A large amount of rearrangements was found. Unfortunately, comparing all species of this work, gene translocations had not generated sufficient data to obtain a phylogenetic tree. It is common, in cases like that, to use a previous proposed phylogenetic tree to "apply" the rearrangements and try to get more data about them. Michener (2000) presents a tree to relate subfamilies and families of bees, splitting the group between short tongued and long-tongued taxa. Gene rearrangements of some clusters were plotted over that tree to infer some new hypotheses about the evolution of the group.

Conclusions: It is clear that bees have an accelerated rate of mitochondrial genome evolution, including base substitution and also gene order rearrangement. Data are congruent to previous studies on wasps. More investigations on that insect order can lead to a better understanding of molecular evolution.

POSTER PRESENTATION

Evolutionary and ecological events that influenced the population structure in *Plebeia remota*, a stingless bee from Brazil

Flavio O. Francisco, Maria C. Arias

Departamento de Genética e Biologia Evolutiva, Instituto de Biociências, Universidade de São Paulo, São Paulo, SP, Brazil

Introduction: Multidisciplinary studies have demonstrated that the stingless bee *Plebeia remota* have distinct behavior, morphometry, chemistry, and genetic characteristics according to the geographic distribution. In order to evaluate which evolutionary and ecological processes may have contributed to this scenario, the genetic structure of *P. remota*, from four distinct geographic areas in Brazil, was studied through mtDNA and microsatellite data.

Methods: Seventy nests were sampled and mtDNA was analyzed with 15 restriction enzymes. Microsatellite analysis was performed in 72 individuals from 72 nests, by screening 7 heterospecific loci.

Results: Fifteen composite haplotypes were found and a strong mtDNA population structure was detected among all populations. Analysis of microsatellite polymorphism indicated that the four populations are characterized by a low genetic diversity. We believe that vegetation shifts caused by climatic changes and uplift of Brazilian coastal ranges since Tertiary, and also female philopatry were responsible for population isolation. Recent habitat fragmentation caused by human occupation may be the reason for the low nuclear genetic diversity. Microsatellite and mtDNA data showed high genetic distance and isolation between one geographic distinct population and the other 3 ones.

Conclusions: Our work and the data already published in literature present evidences that one population might constitute a new species. This information plus the current habitat fragmentation between the populations studied constitute relevant data to conservation strategies.

POSTER PRESENTATION

Population analysis of *Partamona mulata* and *Partamona helleri* (Hymenoptera: Apidae: Meliponini) in Brazil

Rute M. Brito, Maria C. Arias

Departamento de Genética e Biologia Evolutiva, Instituto de Biociências, Universidade de São Paulo, São Paulo, SP, Brazil

Introduction: The *Partamona* genus comprises 33 species distributed from south Mexico to southern Brazil. Molecular approaches were developed to characterize populations of two species presenting a distinct geographic distribution: *P. mulata* has a small geographic range, found only in central Brazil (savanna); and *P. helleri*, which ranges largely in eastern Brazil (Atlantic forest).

Methods: Individuals of *P. mulata* and *P. helleri* were collected from 58 and 47 nests, respectively. Both samples were divided into 5 geographic sub-samples or populations following their endemic range. Four PCR amplified mtDNA regions were analyzed by 6 restriction enzymes, and 9 microsatellite loci were amplified by using heterospecific primers.

Results: *P. mulata* presented only 2 haplotypes which differed by presence/absence of one single restriction site. Analyses indicated no differentiation among the populations. Conversely, *P. helleri* presented 10 haplotypes, being some exclusive and others shared among populations. The microsatellite analysis showed low genetic variability in both species and discrete population structuring, not related to the geographic distribution.

Conclusions: The data indicates that *P. mulata* may have passed through a recent populational bottleneck or recent speciation process. However *P. helleri* seems to an ancient species that have suffered a recent isolation probably due Atlantic Forest fragmentation during the Pleistocene. In both species, the low nuclear variability is an evidence of migration of males, since the queens are highly phylopatric; also habitat fragmentation (degradation of savanna and Atlantic forest areas) should be taken in account to explain the current genetic scenario.

POSTER PRESENTATION

How much do eucalyptus leaf beetles eat?

Jane Elek, Natasha Beveridge

Forestry Tasmania, Hobart, Tasmania, Australia

Tasmanian leaf beetles, *Paropsisterna bimaculata* (formerly *Chrysophtharta* sp.; Coleoptera: Chrysomelidae), are native insects that cause economic loses of wood volume as a result of defoliation to commercial eucalypt plantations in Tasmania, Australia. The integrated pest management system used to prevent economic losses is based on damage thresholds from larval feeding alone. The amount of *Eucalyptus nitens* foliage lost due to feeding by adult beetles was assessed in a field trial during eight weeks at the end of summer, between eclosion and cessation of feeding prior to overwintering. Changes in area of matched control shoots were used to correct for leaf expansion of the treatment shoots on which feeding beetles were caged.

After eight weeks of feeding, half the beetles had changed elytra colour from green to red in preparation for overwintering and all had ceased feeding. During this period, each adult beetle caused an average loss (included potential expanded leaf area) of 16 $\pm$ 2.6 cm^2 of foliage, which was almost 9% of the total shoot leaf area. Feeding caused an average loss of 63 $\pm$ 17 mm^2 foliage per beetle per day.

Using data from this trial and other sources, the total amount of foliage lost due to one pair of beetles and one generation of their offspring during one summer was estimated to be about 13 leaves or almost 2 shoots. Adult beetles, both parent and first generation, would be expected to remove 195.5 cm^2 of foliage, which is 36% of the total estimated defoliation by both adults and larvae. One sixth of the damage was caused by the first generation adults at the end of summer. However, eucalypt trees are less able to refoliate at the end of summer so spend winter with lower crown volumes, resulting in greater relative growth impact on wood volume from late-summer defoliation.

These results demonstrate that it is important to incorporate both larval and adult defoliation into damage thresholds for IPM.

POSTER PRESENTATION

Reconstruction of Pterygota ancestral wing morphology

Diego Griffon

Universidad Bolivariana de Venezuela, Caracas, Venezuela

Introduction: The Devonian was likely the scenery where an insect flew for the first time. Unfortunately, there are no winged insects fossils found from this early time, so we have no direct information of the morphological characteristics of these ancient flying animals. This lack of information in the fossil record has led to the proposal of various hypothetical Pterygota archetypical wings. Between these proposals highlights the radically different models of Hamilton (1972) and Kukalova-Peck (1982)

Methods: In this work we use for the first time techniques of the Comparative Method (Harvey and Pagel, 1991) to build a hypothetical model of the wing morphology of the most recent common ancestor of Pterygota. These techniques allow the assignment of states to characters in ancestral nodes of a phylogenetic tree. In this case, we reconstruct the wing's longitudinal veins morphology for the node that represent the most recent common ancestor of all winged insects. We made the reconstructions based on morphological information of all extant insect's orders.

Results: The results of this work are consistent with the model of Hamilton (1972), differing only in our proposal of a basal union between Radius Posterior (RP) vein with Media Anterior (MA) vein.

Conclusions: We support the Hamilton archetypical model, in accordance with this author we name our wing type Archaeoptera, name that we propose as genus taxonomic rank name for the Pterygota most resent common ancestor.

POSTER PRESENTATION

Division of labor during the organization of open-air foraging of *Syntermes molestus* (Termitidae: Nasutitermitinae)

Dayaleth Alfonzo[1], Solange Issa[2]

[1]Universidad Bolivariana de Venezuela, Caracas, Dtto Capital, Venezuela, [2]Universidad Simón Bolívar, Caracas, Dtto Capital, Venezuela

Introduction: Foraging behavior is often a collective activity composed of integrated actions of individuals. The polytheism could be based upon sex, size, morphological characteristic, and age. The role of the castes in the division of labor on Isopteran is difficult to study because the majority of the termites foraging under covered galleries. *Syntermes* is a Neotropical genus distributed from Venezuela until Argentina. The specie, *S. molestus*, forms big epigeal nest and foraging on open air over grass.

Methods: By filming the foraging behavior, we determined if this specie present polytheism between castes. The data was analyzed by 2 x 2 Contingency Tables to establish the main activity of each caste involucres foraging behavior. In addition, a biometric study was made to establish differences between workers and soldiers (widest and longest head capsule, WH and LH, respectively); these were analyzed with ANOVA and Tukey Multiple Means.

Results: The observation over 9 nests show that *S. molestus* foragers caste has a sociometric trimorphism among workers and a monomorphic soldier. The three castes of workers can be distinguished as minor (LH:2.18±0.04cm; WH:1.94 ± 0.04cm), medium (LH:2.68±0.11cm; WH:2.15±0.04cm) and major (LH:3.17±0.14cm; WH:2.56±0.06cm). We, also observed three kind of basic tasks: Worker carrying soil particles from inside nest to outside; foragers looking and carrying grass to inside nest and soldiers as guardians of the foragers.

Conclusions: Polytheism between workers was clear, while minor and medium workers carrying soil particles; major workers were cutting and carrying grass from foraging site to the nest.

POSTER PRESENTATION

Behavior and chemical communication in *Carmenta theobromae* (Busck) (Lepidoptera: Sesiidae)

F Morillo[1], Beatriz Herrera[2], Carmen Virginia Liendo[2], Wilfredo Muñoz[2], Pedro Sánchez[2], Jose Vcente Hernández[2]

[1]Instituto Nacional de Investigaciones Agrícolas, Estación Experimental del Estado Miranda (INIA-Miranda), Caucagua, Miranda state, Venezuela, [2]Universidad Simón Bolívar (USB), Biología de Organismos, Laboratorio de Comportamiento, Caracas, Dtto. Capital, Venezuela

Introduction: *Carmenta theobromae* (Busck) is one of the main entomologic problems of cocoa plantations in Venezuela. In this work the behavior of adults was studied and the main compound involved as sexual pheromone in this insect was determined.

Methods: Larvae in the bark of perforated cocoa pods were collected, in Curiepe, Miranda State, Venezuela. They were individualized and placed in pieces of healthy pod bark, in containers of 350 ml. Each formed pupae was placed on plastic trays, on a piece foam rubber with humidified absorbent paper and covered with a container of 30 ml, under controlled environmental conditions. The emergence and the daily activity of adults were recorded in observation chambers. The chromatographic and spectrometric analyses were carried out on abdominal tip extracts of males and females.

Results: Adults emergences begin between 07:30-08:00 hours, and was extends from 14:00 to 15:30 hours, in females and males respectively. The emergence peaks occur in the first hour during the day for both sexes. The duration of the female calling behavior was 4 hours, with the calling peak at 17:30 hours. Female keep this behavior until the third day of life. The time of calling behaviour coincided with the higher flight activity, walk or flapping of the males. The female chromatograms showed an exclusive peak, not observed in males. It correspond to (*Z*,*E*)-3,13-octadecadienyl acetate.

Conclusion: *C. theobromae* females emit a sexual pheromone in sunset. Probably, the main component of the pheromone is the octadecadienil acetate or their isomeric ones.

POSTER PRESENTATION

High bluestain fungus (*Ophiostoma minus*) abundance negatively affects outbreaks of the southern pine beetle, *Dendroctonus frontalis*

Stephen Taerum[1], Kier Klepzig[2], Matt Ayres[1]

[1]Dartmouth College, Hanover, NH, United States, [2]Southern Research Station, USDA Forest Service, Pineville, LA, United States

Introduction: Feedbacks help shape multispecies interactions. One example is the southern pine beetle–mite–fungus symbiosis, which involves positive, negative, and commensal interactions between the southern pine beetle (*Dendroctonus frontalis*) and its symbionts. We examined how the abundance of the bluestain fungus (*Ophiostoma minus*), which depends on *D. frontalis* for transportation between pine trees and frequently outcompetes fungal mutualists of *D. frontalis* in trees, affects the population dynamics of *D. frontalis*.

Methods: Between 2001 and 2008, we estimated *O. minus* abundances at *D. frontalis* infestations, or "spots," in different forests in the United States (forests at different years are herein referred to as forest-years). Using USDA data on *D. frontalis* trap captures and spot formation, we determined how *O. minus* abundance affected *D. frontalis* populations in subsequent years.

Results: Forest-years with high *O. minus* abundances had significantly fewer *D. frontalis* infestations in subsequent years than forest-years with low *O. minus* abundances. In addition, forest-years with high *O. minus* abundances tended to have lower *D. frontalis* trap captures in following years than forest-years with low *O. minus* abundances.

Conclusions: High *O. minus* abundance had a negative effect on the number of *D. frontalis* infestations produced in following years, suggesting that *O. minus* abundance might predict *D. frontalis* outbreak dynamics.

POSTER PRESENTATION

Molecular intra-specific phylogeny of *Hylesia metabus* (Saturnidae: Hemileuciinae)

Cristina Sainz-Borgo, Maribet Gamboa, Beatriz Herrera-Malaver, Carmen V. Liendo-Barandiaran, José Vicente Hernández, Jazzmin Arrivillaga

Universidad Simón Bolívar, Caracas, Estado Miranda, Venezuela

Introduction: In Venezuela, *Hylesia metabus* has been reported as a "single species" with phenotypic differences based on adults coloration and female sexual pheromone composition that suggest genetic variability among populations with possible implications on the differentiation and divergence, if the female sexual pheromone produce partial or complete reproductive isolation.

Methods: The present work study the genetic variation on adults samples (males) from different geographical locations belong to Venezuela North east, and three different population peak cycles using molecular data (12S and COI mitochondrial regions) and cladistic analysis.

Results and Conclusions: The results indicate that *Hylesia metabus* is a single species without phylogenetic structure, which are not congruent with pheromone or coloration patterns based on the adults sampled.

POSTER PRESENTATION

Overexpression of c-type lysozyme from *Agrius convolvuli* using prokaryotic expression system

Sung Moon Yoe, Soon Ik Park, Jong-Wan Kim, Hong Sun An

Dankook University, Cheonan, Republic of Korea

We have isolated and characterized the *Agrius convolvuli* cDNA encoding a c-type lysozyme. The cDNA sequence encodes a processed protein of 139 amino acid residues with 19 signal sequence and 120 mature sequence.

Recombinant *A. convolvuli* lysozyme was expressed in *Escherichia coli* BL21 (DE3) pLysS cells for pGEX 4T-1 vector. Their optimal conditions for the fusion protein expression and purification were screened. Lysozyme gene amplified with primers ACLyz *Bam*HI and ACLyz *Xho*I was ligated into the pGEX 4T-1 vector, which contained the glutathione S-transferase (GST) gene for fusion partner. The anti sense primer has additional sequence (Gly) for protection of mature sequence from various stressful circumstances and increasing solubility.

After transformation, the bacteria cell was incubated and inoculated IPTG for 2h. The cell lysate was analyzed by SDS-PAGE, where the appearance of a ~45kDa band indicates the synthesis of GST fused lysozyme. Recombinant lysozyme, fused to GST, was purified by glutathion-Sepharose 4B affinity chromatography.

Western blot analysis of this protein revealed an immunoreactivity with the anti-*Agrius* lysozyme. Thrombin digestion of GST-lysozyme fusion protein, 15, 29 and 45 kDa fragments were detected by SDS-PAGE. From the size of fragments, it seems that 29 kDa fragment represents the GST fusion partner and 15 kDa fragment represents the recombinant lysozyme while 45 kDa fragment represents uncut GST-lysozyme.

POSTER PRESENTATION

Overexpression of a cecropin-like peptide from *Agrius convolvuli* in *Escherichia coli*

Sung Moon Yoe, Hong Sun An, Soon Ik Park, Jong-Wan Kim

Dankook University, Cheonan, Republic of Korea

Insects have developed efficient immune responses that protect them against the damaging effects of microbial and eukaryotic invader. Antibacterial peptides are one of the most important humoral immune system in insects. Cecropin is a well-studied group of insects antibacterial peptides and widespread in a variety of organisms.

A cDNA encoding cecropin like peptide from *Agrius convolvuli* (named ACcec) was isolated from total RNA using RT-PCR and was expressed in *Escherichia coli.* The DNA fragment encoding mature ACcec was amplified with primers ACcec *Eco*RI and ACcec *Xho*I was ligated into the pGEX 4T-1 expression vector. These recombinant ACcec was highly expressed in *E.coli* BL21 (DE3) pLysS by fusing glutathione S-transferase (GST) and optimal induction concentration of IPTG. The expressed proteins, fused to GST, were purified by glutathione-Sepharose 4B affinity chromatography. After purification, the GST fusion partner was cleaved by thrombin. After thrombin digestion of GST-ACcec fusion protein were detected by SDS-PAGE.

POSTER PRESENTATION

A molecular phylogeny of the tribe Aphidini (Insecta: Hemiptera: Aphididae) based on the mitochondrial tRNA/COII, 12S/16S, and the nuclear EF1α genes

Hyojoong Kim, Seunghwan Lee

Seoul National University, Seoul, Republic of Korea

A phylogeny of the tribe Aphidini (Hemiptera: Aphididae) was reconstructed from three gene fragments: two mitochondrial regions, partial tRNA-leucine + cytochrome oxidase II (tRNA/COII), partial 12S rRNA + tRNA-valine + 16S rRNA (12S/16S), and one nuclear gene, the elongation factor-1 alpha (EF1α). Three minimum evolution phylogenetic analyses were performed on each individual dataset of tRNA/COII, 12S/16S, and EF1α, and maximum parsimony, Bremer support test, maximum likelihood, and Bayesian phylogenetic analyses were performed on the combined dataset. After comparing our molecular phylogenetic results with the classical classification based on morphological and ecological data, we analyzed three main issues: the monophyletic relationships among tribes and subtribes, the validities of the latest taxonomic positions of genera and species, and the status of certain *Aphis* species groups. Our results indicate that 36 of the species analyzed, with the exception of *Cryptosiphum artemisiae*, are clustered within the monophyletic clade of Aphidini. Also, the 28 species selected in the subtribe Aphidina were separated from the 8 species selected in Rhopalosiphina; each monophyletic subtribe was supported by significant *P* values in the combined analysis. According to our results, *Cryptosiphum* should be moved to Macrosiphini because it is more closely related to the genera *Lipaphis* and *Brevicoryne*. The genus *Toxoptera* was recovered as non-monophyletic. In Rhopalosiphina, three genera, *Hyalopterus*, *Rhopalosiphum*, and *Schizaphis* were relatively closer to each other and than to the genus *Melanaphis*. In the relationships between species-groups among *Aphis*, most species were separated to the two main lineages; the *fabae* group seemed to be more closely related to the *spiraecola* and *craccivora* group rather than to the *gossypii* group.

POSTER PRESENTATION

Difference in aphid and fly host-driven divergence of *Entomophthora*

Annette Bruun Jensen[1], Jørgen Eilenberg[1], Claudia Lopéz Lastra[2]

[1]University of Copenhagen, Copenhagen, Denmark, [2]Universidad Nacional de La Plata, La Plata, Argentina

Several species of the fungal genus *Entomophthora* infect higher dipterans (Cyclorrhapha): *E. fernandii*, *E. grandis*, *E. muscae*, *E. scathophagae*, *E. schizophorae* and *E. syrphi*. In comparison, only two aphid pathogenic *Entomophthora* species, *E. chromaphidis* and *E. planchoniana* have been described. Recently molecular analyses have confirmed the species status of most of the fly pathogenic *Entomophthora*, while it has been questioned whether the two aphid pathogenic *Entomophthora* species are distinct species, since they cannot be distinguished molecularly. In addition, molecular analyses have revealed high intra-specific variation within *E. muscae* showing that each host species harbor its own fungus genotype.

In the current study we sequenced several DNA regions of *Entomophthora* originating from different fly and aphid host taxa. The results documented a huge genetic divergence of the fly pathogenic *Entomophthora* in comparison to the aphid pathogenic *Entomophthora*, where only minor differences in the sequences where detected. The evolutionary time of divergence of the fly and the aphis host taxa included in this study cannot account for this difference. The host driven divergence of *Entomophthora*, therefore, is much higher in flies compared to aphids. A recent host shift of *Entomophthora* to become pathogens of aphids is an alternative hypothesis explaining the lack of differentiation seen in aphid pathogenic *Entomophthora*.

POSTER PRESENTATION

Novel insecticidal alkaloids from *Alstonia boonei* De Wild (Apocynaceae)

Nathaniel Oigiangbe, Benjamin Igbinosa, Manuele Tamo, Osayande Eguavoen

Ambrose Alli University, Ekpoma, Edo State, Nigeria

Alstonia boonei De Wild (Apocynaceae) is an important medicinal plant in the rain forest regions of West and Central Africa. Bioactive compounds found in this plant include alkaloids, saponins, tannins, cardiac glycosides and flavonoids. In some preliminary bioassays, the crude water and methanol extracts of the leaves and stem bark were effective against *Maruca vitrata* Fabricius and *Sesamia calamistis* Hampson. Several indole alkaloids have been reported from *A. boonei*. We tested the mixture of crude alkaloids from *A. boonei* against *M. vitrata* in a bioassay. There were significant differences in the survival, growth, and duration of development of the insect when reared on artificial diet incorporated with 0.0 ppm (control), 1.0 ppm, 2.5 ppm and 5.0 ppm of the alkaloids. At ten days after introduction (10 DAI) the survival of the larvae ranged from 70.83 % in the 5.0 ppm treatment to 91.67 % in the control. Similarly, larval weight ranged from 18.59 mg in the 5.0 ppm treatment to 40.09 mg in the control. Fifteen days after introduction, 62.5 % of the larvae in the control diet were at the pupal stage and 20.83 % at the pre-pupa stage. The percentage pupation was 0.0, 25.00 and 33.33 in the 5.0 ppm, 2.5 ppm and 1.0 ppm treatments, respectively at 15 DAI. The bioactivity of each of the individual alkaloids against *M. vitrata* and *S. calamistis* will be evaluated within the next four months. The potential of each alkaloid in the management of these insects will be discussed.

POSTER PRESENTATION

Early Jurassic trace fossils of possible termite origin

Adam Bumby[1], Emese Bordy[2], Christian Pirk[3], PW (Bill) Bateman[3]

[1]Department of Geology, University of Pretoria, Pretoria 0002, South Africa, [2]Department of Geology, Rhodes University, Grahamstown 6140, South Africa, [3]Department of Zoology and Entomology, University of Pretoria, Pretoria 0002, South Africa

Bioturbated sandstone pillars at Mapungubwe (South Africa), at the confluence of the Limpopo and Shashe rivers, and in western Lesotho are preserved in aeolian sandstone of the Lower Jurassic Clarens Formation. Preserved pillars are up to 3.3 m high, often elliptical in plan, and are orientated N-S. Typically the pillars have bent apices, and are inclined towards the east. Pillar walls are characterised by an anastomosing network of approximately 5 mm diameter sandstone tubes, some of which have preserved meniscate back-filling. Other pillars have smooth outer walls, which may surround an empty space.

The pillars resemble termite nests, which were coeval with the Clarens Formation. The eastward-inclined apices are thought to reflect nest construction within dominantly westerly palaeowinds, derived from the dip-direction of aeolian dune foresets. Tube networks with rare backfilling are interpreted as galleries within the termite nest, and empty spaces are thought to be preserved paracaie structures. The elliptical shapes of nests may be to enhance diurnal cooling of nests, or to enhance nest respiration by build-up of a pressure gradient, as nests appear to be constructed perpendicular to the prevailing palaeowind.

Although the state of preservation of the pillars does not allow for a fully conclusive interpretation, the similarity of these trace fossils to structures constructed by modern-day termites is striking, and the possibility of eusocial termite-like colonies having evolved in semi-arid environments by the Early Jurassic should be bourn in mind.

POSTER PRESENTATION

Altitudinal variation of dung beetle communities in Sierra Nevada Mountains (Southeast Spain)

Rocío Márquez-Ferrando[1], Adela González-Megías[1], Rosa Menéndez[2]

[1]Universidad de Granada, Granada, Spain, [2]Lancaster University, Lancaster, United Kingdom

We studied dung beetle communities of the Sierra Nevada Mountains (southeast of Spain) a region of high animal and plant diversity in Europe. We examined changes in species richness, abundances and community composition along altitudinal gradients (from 800m to 2500m) on both northern and southern facing slopes. Beetles were collected using dung-baited pitfall traps during three months (May to July) and in two consecutive year (2006 & 2007). We recorded 47 dung beetles species (21 Scarabaeidae, 2 Geotrupidae and 24 Aphodiidae). Total species richness increased with altitude as well as the species richness of the two dominant families (Scarabaeidae and Aphodiidae). Although Scarabaeidae was the richest taxa at all altitudes, the proportion Scarabaeidae species decreased with altitude and the opposite was observed for Aphodiidae. The number of individuals collected was not significantly related to altitude when considering all species together or when considering only Scarabaeidae species, but did increase with altitude for Aphodiidae species. Aspect did not have an effect on the relationship between species richness and altitude for any of the studied groups but it affected the relationship between altitude and number of individuals. Species composition was also related to both aspect and altitude. We discuss our results in relation to those found in other mountain areas in Europe and the implications of our findings for the conservation of mountain dung beetle communities in view of future climate change.

POSTER PRESENTATION

Inhibition of esterases by synergists in the western flower thrips, *Frankliniella occidentalis* (Pergande)

Neus López-Soler, Amelia Cervera, Ana C. Maymó, Rafael Martínez-Pardo, María Dolores Garcerá

Universitat de València, Burjassot, Valencia, Spain

Introduction: Synergists are frequently utilized as indicators of the possible biochemical mechanisms involved in insecticide resistance. The fact that piperonyl butoxide (PBO), a known inhibitor of oxidases, also inhibits esterase activity, and that some insecticides act as synergists, points out the necessity to investigate the direct effect of synergists on enzyme activity, in order to corroborate the resistance mechanisms of insects to insecticides. In this sense, we have investigated the effects, both *in vivo* and *in vitro*, of two synergists (PBO and *S*,*S*,*S*-tributyl phosphorotrithioate (DEF)) and one insecticide (metiocarb) on total esterase activity of one susceptible and three laboratory selected resistant strains to acrinathrin, formetanate and metiocarb of the western flower thrips *Frankliniella occidentalis* (Pergande). At the same time *in vitro* inhibition of esterase isoenzymes by sinergysts has been analyzed.

Methods: α-naphthyl acetate esterase activity was measured with a Tecan Spectrafluor microplate reader. *In vitro* determinations were performed incubating homogenates from each individual strain with the synergists. For *in vivo* bioassays insects were treated with the synergists and after 10, 20, 30, 60 or 90 min, freeze at -80ºC until use. *In vitro* inhibition of esterase isoenzymes was performed in native conditions polyacrilamide gel electrophoresis.

Results: DEF is the compound with major esterase inhibitory capability independently of the studied strain. On the other hand electrophoretic study of esterase isoenzymes reveals that DEF inhibition points to a specific group of three isoenzymes previously described by our group as related to insecticide resistance. PBO inhibition was greater after 90 min of treatment.

POSTER PRESENTATION

P450 activity in *F. occidentalis* (Pergande)susceptible and resistant strains strains

Ana C. Maymó, Amelia Cervera, Neus López-Soler, Rafael Martínez-Pardo, María Dolores Garcerá

Universitat de València, Burjassot, Valencia, Spain

Introduction: The western flower thrips (WFT), *Frankliniella occidentalis* is one of the main pests of horticultural crops in Southern Spain and has become an economic problem. Recently this species has been reported with the highest number of control failures in Spain, due to its ability to develop resistance under high insecticide pressure, as is the case of greenhouse cultures of the SE of Spain. MFOs have been reported as enzymes responsible for resistance mainly based in bioassays with synergists (PBO). On the other hand, it has been indicated the difficulty to measure directly P450 oxidase related activities in *F. occidentalis* extracts. So, we have tried to quantify and to compare P450 activity in one susceptible and three laboratory selected resistant strains to acrinathrin, formetanate and metiocarb of the western flower thrips *Frankliniella occidentalis* (Pergande).

Methods: 7-ethoxycoumarin (ECOD) P450 activity was measured with a Victor 1420 multilabel HTS counter (Wallac) using the kinetic mode for 10 min. An aliquot of 20µL of extract from a pool of insects was used as enzyme source.

Results: Preliminary results indicate that selected resistant strains have higher ECOD activity than the susceptible one. The study of the Michaelis Menten constant calculated for each strain seems to indicate that the higher activities found in the resistant strains are due to a higher proportion of enzyme present in the sample, rather than to a better efficiency of it.

POSTER PRESENTATION

Biological control of *Oligonychus perseae* (Acari: Tetranychidae) on avocado in the Canary Islands (Spain)

Estrella Hernandez-Suarez, Eduardo Torres, Yiselle Velazquez, Aurelio Carnero, Francisco Ferragut

ICIA, La Laguna, Canary Islands, Spain

Introduction: *Oligonychus perseae* Tuttle, Baker and Abbatiello is a pest of avocado that has reached the Mediterranean Basin and the Canary Islands in recent years. This species has become a major pest of avocados in the Canarian archipelago, causing defoliation of trees that indirectly produce important yield looses due to sunburn damage and premature fruit drop. The aims of this study were to (1) identify the indigenous predatory fauna on avocado, (2) understand the population dynamics of *O. perseae* and their main predators and (3) study the effect of inundative releases of *Neoseiulus californicus* (McGregor) to improve biological control.

Methods: In 2006-2007, avocado production areas were surveyed to identify the predatory fauna of *O.perseae* and two commercial avocado orchards were selected to study fluctuations in mite populations. Two field trials were conducted in early spring and late summer 2007 to evaluate the effects on *O.perseae* populations of releases of *N. californicus* at two rates of 1000 and 2000 per tree.

Results: Ten phytoseiid species were found associated with *O.perseae*, being *Euseius stipulatus* (Athias-Henriot) the dominant species, followed by *Iphiseius degenerans* (Berlese) and *N. californicus*. Two population peaks of the persea mite occurred in summer (June-July) and autumn (October-November). Phytoseiid mite populations (mostly *E. stipulatus*) peaked in summer (August) and autumn (November), following spider mite increases, but *O. persea* leaf damage still not admissible by growers. *N. californicus* releases did not improve *O. persea*e control in any of both field trials.

POSTER PRESENTATION

Scale-dependent responses in cabbage herbivores affect attack rates in spatially heterogenous systems

Peter Hambäck[1], Maria Björkman[1], Birgitta Rämert[2]

[1]Dept Botany, Stockholm University, Stockholm, Sweden, [2]Dept of Plant Protection Biology, Swedish University of Agricultural Sciences, Alnarp, Sweden, [3]Dept of Ecology, Swedish University of Agricultural Sciences, Uppsala, Sweden

Herbivorous insects face a dilemma when selecting suitable hosts in a complex environment, and their sensory capability may often reduce the female capacity for proper selection. This has the consequence that eggs are often deposited on inferior hosts, affecting both on insect and host plant fitness. We examined the attack rates of three cabbage herbivores in monocultures and bicultures plots, of different *Brassica oleracea* genotypes, with different spatial heterogeneity. The main goals of the study were to improve our understanding of the spatial scales involved in herbivore search processes and to examine the possibility of using spatial heterogeneity for manipulating pest attack rates in cabbage cropping systems. The results showed that the host selection behavior of the small white butterfly (*Pieris rapae*) was strongly dependent on spatial heterogeneity. The difference in egg density between plant genotypes was larger when contrasting plants were growing in close proximity than among monoculture plots This suggests that *P. rapae* is able to compare among genotypes from a small distance, while selection is compromised at larger spatial scales. The two other herbivores in the study (*Mamestra brassicae* and *Delia radicum*) did not respond to heterogeneity at any spatial scale, but showed a constant preference hierarchy. This suggests that host selection for these species occurs on direct plant contact. The difference in species responses to spatial heterogeneity has consequences both for selection gradients in natural communities and for the potential to reduce pest attack in polyculture systems.

POSTER PRESENTATION

Diocalandra frumentii (Coleoptera: Curculionidae), a new pest for palms in the Canary Islands

Aurelio Carnero, Antonio Gonzalez, Jose Esteban, Nuria Casañas, Angeles Padilla

ICIA, La Laguna, Canary Islands, Spain

Introduction: This species is a plague known only in the islands located in the Pacific and Indian oceans, introduced into the Canary Islands in an unknown way. Now it strongly attacks Canarian palms and palm-like species in Tenerife and Gran Canaria. *D. frumentii* is a small curculionid. During its larval stage it digs in the base of the leaves and in the crown, producing desiccation and plant death. The pest is a problem very difficult to control. Furthermore it could spread to the European mainland. There are no known natural enemies, and its vital cycle in the field is poorly known.

Methods: At present, breeding is taking place in chambers, under artificial conditions. Improved artificial diet or natural (based on sugarcane) are taking place, in order to know the biology and development of *D. frumentii*, and also to compare with results obtained by other authors (González-Nuñez et al, 2002). Then, the biology in field and semi-field conditions are going to be studied. Also, control assays using native strains of entomopathogenic nematodes and fungi from our collections will be developed.

Results: It is known that, with sugarcane, it takes 7,8 days for eggs, 76,2 days for the larval stage and 10,2 for the pupa (González-Nuñez el al, 2002). Survival was very low in normal artificial diet conditions. Results regarding to entomopathogenic organisms are not finished.

POSTER PRESENTATION

Semi-field assay using a strain of *Metarhizium anisopliae* (Metschn.) for the control of *Cosmopolites sordidus* (Germar, 1824) (Coleoptera: Dryophthoridae)

Angeles Padilla, Aurelio Carnero, Dulce Molina, Luis Lopez, Carolina Fernandez

ICIA, La Laguna, Canary Islands, Spain

Introduction: The potential use of a strain of *M. anisopliae* isolated in the Canary Islands was assayed in semi-field conditions. The bioformulation of this organism was developed by FuturEco S.L.

Methods: The assay was performed in greenhouse conditions, using Nemacur® 10G, a commercial bioformulated bioformulation (Botanigard®) based on *Beauveria bassiana*, the strain of *M. anisopliae*, and the control. The plague development was tested 35, 77 and 120 days after transplanting. Along the experiments, the following variables were taken in account: situation and number of *C. sordidus*, abundance and stages of *C. sordidus*, infestation coefficient at the border level, base and transversal cut. Two methods (Guzmán, 1994 y Vilardebó, 1973) were used to evaluate damage produced by larvae in the rhizome.

Results: According to the obtained results, both the commercial formula and the strain of *M. anisopliae*, act as control agents against adult *C. sordidus*. *M. anisopliae* can be an effective alternative to the chemical control of this insect.

POSTER PRESENTATION

Elucidation of defence pathways activated in Betta near isogenic wheat lines upon infestation by *Diuraphis noxia*

Thia Schultz, Anna-Maria Botah-Oberholster

Department of Genetics & FABI, University of Pretoria, Hillcrest, Pretoria, Gauteng, South Africa

Russian Wheat Aphid (*Diuraphis noxia*, Kurdjumov) has yet again become a focal point to research and commercial fields after the recent development of new RWA biotypes. The mechanism of defense, conveyed by each *Diuraphis noxia* (*Dn*) gene differ i.e. *Dn1* confers an antibiotic resistance, while *Dn2* confers a tolerance for aphid infestation. We aimed to investigate the systemic changes and biological pathways activated due to systemic acquired resistance (SAR) conferred by *Dn1* and *Dn2*. For this propose, we used susceptible 'Betta' and two resistant near isogenic lines 'BettaDN' and Betta *Dn2*, in cDNA-AFLPs to identify transcripts affected by RWA infestation. 146 transcript derived fragments (TDFs) where sequenced characterized for putative identification with BLASTn and BLASTx. Transcripts where grouped into the following cellular processes: Amino acid metabolism, nucleic acid processing, fatty acid and lipid metabolism, starch and sucrose metabolism, protein folding, cell cycle, cell maintenance, membrane proteins, chloroplast or photosynthesis related, defense or stress related, unknown proteins and proteins with no homology. TDFs carrying material from 'BettaDN' had identities such as; defence F-box protein, Zinc finger-like protein, chaperone proteins, annexin-like protein, WAP2 kinase, Zn-dependant protease and ubiquitin specific protease; while TDFs from material from Betta *Dn2* showed; Na+/H+ antiporters, P-type ATPase transporter, Zinc transporter, Integral membrane protein NRAMP, Cytochrome p450, ATP dependent Clp protease- chloroplast precursor and non-phototrophic hypocotyls 1b.

POSTER PRESENTATION

How sensitive are insects compared to other aquatic organisms for the presence of cyanobacterial biotoxins in drinking water?

Paul Johan Oberholster, Bongiwe LS Mthethwa, M Callies Selala

Department of Genetics & FABI, University of Pretoria, Hillcrest Pretoria, South Africa

Bloom-forming cyanobacteria in eutrophic surface waters have caused increasing concern over the last decade in South Africa due to their toxic potential. Due to a lack of toxin standards and resource limitations for wide scale use of analytical methods (i.e. high-performance liquid chromatography and enzyme-linked immunosorbent assay) in cyanobacterial toxin monitoring, it is necessary to assess and develop additional methods that is rapid yet realistic and cheap for the detection of cyanobacterial toxins in rural water treatment plants of South Africa. A well-known cyanobacterial secondary metabolite, microcystin-LR and dominant cyanotoxin in South Africa, was tested for its effect on insects, i.e. *Periplaneta americana* (American cockroach); *Tenebrio molitar* (yellow mealworm) and *Gryllus bimaculatus* (common cricket) and the macrophyte *Spirodela punctata* (duckweed); as well as the crustacean zooplankton (*Artemia salina*). LD_{50} values calculated for *Gryllus bimaculatus* and *Artemia salina* body weight were respectively 0.45 µg/animal and 0.1 µg/animal within 48 h, making these organisms as sensitive to low concentrations of microcystin-LR as the mouse bioassay. No 48 h LD_{50} was established for any of the pure microcystin-LR (0.5, 1.0, 5.0 $\mu g l^{-1}$) concentrations in the conducted *Periplaneta americana* and *Tenebrio molitar* bioassays. DNA laddering was also detected in *Periplaneta americana*, *Tenebrio molitar*, *Artemia salina* and *Gryllus bimaculatus* within the first 48 hours. Although ease of culturing the American cockroach and yellow mealworm make them the ideal organisms to include in a battery of bioassays, their 48h LD_{50} non response to low levels of microcystin exclude them from a rapid sensitive bioassay.

POSTER PRESENTATION

Understanding potential effects of climate change on dung beetle communities in subtropical rainforests of Australia

Rosa Menéndez[1], Geoff Monteith[2]

[1]Lancaster University, Lancaster, United Kingdom, [2]Queensland Museum, Brisbane, Australia

We investigated changes in dung beetle communities along an altitudinal gradient in a subtropical rainforest in order to asses the sensitivity of different species to changes in temperature and to identify potential bio-indicators for future climate change. The work took place in Lamington National Park, Queensland, Australia. The sampling protocol consisted of using four baited pitfall traps and one flight intercept trap to collect the dung beetles in four replicate (1ha plots) positioned at five altitudes: 300m, 500m, 700m, 900m and 1100m. A total of 33 species of native dung beetles (Coleoptera, Scarabaeinae) were collected along the altitudinal gradient; all of them exclusives to the rainforest. Examination of individual species distributions along the altitudinal transect showed a highly stratified fauna, and that no single species occurs at all elevations. The lowest zone (300m) has not only the most diverse fauna (22 species), but also 41% of species which occur there do not occur any higher than 500m. The highest zone (1100m) has a small fauna of 9 species but 78% of those are restricted to high elevations extending downwards only as far as the 900m. These results suggest that species altitudinal distributions are probably constrained by climatic conditions, and they are likely to be affected by global warming. We discuss the potential effects of climate change on individual species based on their occurrence along the altitudinal gradient as well as their geographic distribution in Australia.

POSTER PRESENTATION

How persistent are the dorsal abdominal scent glands in the Heteroptera adults?

Jitka Vilimova, Katka Kutalova

Charles University, Faculty of Science, Department of Zoology, Prague, Czech Republic

Introduction: The specific scent gland system represents the autapomorphy of the Heteroptera. The dorsal abdominal scent glands (DAGs) were originally supposed to be the unique nymphal structure. However, recently the persistence of DAGs in adult stage has been proved for more and more heteropteran taxa.

Methods: The material of Central European representatives was analysed. The dissected heteropteran adults were studied using standard optical and scanning electron microscopes.

Results: The following diversity of morphological traces of DAGs in heteropteran adults was found: Neither any part of scent system, nor its remnant maintained (e.g., representatives of Notonectidae, Nepidae, Naucoridae, most of Gerridae, Cimicidae). Differently conspicuous scars in location of nymphal DAGs developed (e.g., representatives of Lygaeidae, numerous Pentatomoidea). Small, probably partly full, variable conspicuous gland reservoirs developed (e.g., Corixidae, Aphelocheiridae, Saldidae, Tingidae, Aradidae, numerous Pentatomoidea). Apparently full, one to three reservoirs developed, sometime sexually dimorphic (e.g., Pyrrhocoridae, Rhopalidae, many Pentatomoidea - most frequently predacious Asopinae). The largest number of full reservoirs, four, developed in representatives of Dipsocoromorpha.

Conclusions: DAGs are very probably persistent, and functional?, in heteropteran adults in larger extent than was believed. DAGs are not almost generally maintained in the adults of Nepomorpha and Gerromorpha. On the contrary, DAGs are very often persistent in all the other heteropteran infraorders. The only one conclusive evidence for the adult functional DAG is the full gland reservoir and functional ostiole.

POSTER PRESENTATION

Mate number and paternity in *Plebeia remota*

André Ramos Vaquero, Maria Cristina Arias

São Paulo University, São Paulo/São Paulo, Brazil

Introduction: The stingless bees present large distribution, great diversity, very significant contribution as pollinator agents, and economic and medical value. Despite their biological and economic importance, basic aspects about their biology and evolution are still not elucidated. The multiple mate in Hymenoptera is relatively common, however in stingless bees only few studies on this subject have been published. To increase our understanding on this behavior the species *Plebeia remota* was choosen as experimental model. This species has a small body size and small number of individuals per nest. The literature has postulated that queens of *P. remota* mate once, However all these studies are based on just one temporal sample and one nest. The knowledge of queen mate number and the relationship degree among workers allows inferences on social evolution and conflict between queen and workers in the male production.

Methods: Workers and males from two colonies were collected monthly during one year, totalizing 123 individuals. Total DNA was extracted and used to PCR amplify microsatellite loci. Four loci were screening by using heterologous primers derived from *Melipona bicolor* (Mbi33, Mbi 215, Mbi 259 and Mbi278).

Results: The loci Mbi215, Mbi259 and Mbi278 presented two alleles each. By analyzing the males we could infer the queens genotypes, which were heterozygous for the three loci. Also most of the workers were heterozygous, however in different temporal samples we found workers homozygous for either alleles.

Conclusion: The data indicated that the queens likely were mated by at least two males.

POSTER PRESENTATION

The effect of nematicide vapors on the spiraling whitefly, *Aleurodicus dispersus* Russell (Homoptera: Aleyrodidae) population and its natural enemies.

Helga Blanco-Metzler[1], Sergio Laparade Coto[2]

[1]University of Costa Rica, San Jose, Costa Rica, [2]CORBANA, San Jose, Costa Rica

Introduction: Side effect of pesticides on natural enemies has been widely documented; phytophagous organisms previously innocuous can become frequent and serious pests due to beneficial organism destruction. This study was conducted to determine if nematicide vapors were responsible for the spiraling whitefly outbreaks and the reduction of their natural enemies in banana plantations of Costa Rica.

Methods: The effect of terbufos (Counter®), terbufos (Bioquím®), carbofuran (Furadan®), cadusafos (Rugby®) and fenamifos (Nemacur®) on the spiralling whitefly and its parasitoid, *Encarsiella* spp. population was evaluated. The number of live and parasityzed nymphs of *A. dispersus* were evaluated prior to nematicide application as at 15, 30, 45 and 60 days after pesticide application.

Results: The total number of nymphs was greater when Counter and Bioquim were applied, while parasitoid population was greater in the control and the lesser *Encarsiella* population was found when Bioquim was applied. The study showed that organophosphates affected the pest-parasitoid equilibrium. Since nematicides are of obligatory use in banana production, there is a need to understand the timing of pesticide application.

POSTER PRESENTATION

Phoretic behavior of a scelionid egg parasitoid on its reduviid host

Walker Jones[1], William Warfield[2]

[1]*European Biological Control Laboratory, ARS, USDA, CS90013 Montferrier sur Lez, France,*
[2]*Beneficial Insects Research Unit, ARS, USDA, Weslaco, TX, United States*

Introduction: Although telenomine parasitoids of Heteroptera eggs may use adult-produced cues to locate host eggs, few are known to search for and mount adult female hosts to await an oviposition bout. A new such association has been discovered between an undescribed *Telenomus* sp. and the assassin bug, *Sinea coronata* (Reduviidae) in Texas.

Methods: A field survey was conducted to record the frequency of male and female hosts bearing *Telenomus* sp. individuals. Laboratory observations were recorded on Host defensive behaviors, and parasitoid mounting and positioning behaviors were recorded in the laboratory.

Results: Twenty-three of 33 mating pairs observed in the field had at least one parasitoid mounted; only once was a parasitoid observed on the male. Of 113 solitary males observed, 33 (29%) had at least one parasitoid mounted; 14 had more than one parasitoid (2-4). Of 115 females observed, 67 (58%) possessed phoretic parasitoids; 40 were carrying from 2 up to 13 individual parasitoids. All parasitoids observed on adult hosts were female. Host females resisted mounting of stalking parasitoids by kicking. Immediately upon mounting, the host frequently released its grip on the substrate. Other defensive behaviors included wing-buzzing and leg-rubbing. Solitary parasitoids preferred to position themselves on the dorsum of host females along the midline of the pronotum, mesonotum or scutellum, sometimes with movement among these sites during the day. Multiple parasitoids on a single host usually distributed themselves over the same areas that solitary parasitoids preferred. No evident competition was observed among parasitoid individuals.

Conclusions: A new phoretic relationship is described between an egg parasitoid and its predaceous host. It is unclear what the attractant cues may be, but are clearly different from the *Telenomus calvus* - *Podisus maculiventris* (Pentatomidae) system.

POSTER PRESENTATION

The French Quarter program: A pilot program for area-wide integrated pest management of formosan subterranean termites in New Orleans, Louisiana, USA

Dennis Ring[1], Alan Morgan[1], Frank Guillot[2], Alan Lax[2]

[1]LSU agCenter, Baton Rouge, Louisiana, United States, [2]USDA, ARS, Southern Regional Research Center, New Orleans, Louisiana, United States

The Formosan subterranean termite, *Coptotermes formosanus*, is a serious pest where it has become established and is one of the most destructive insects in Louisiana. A pilot test was begun in 1998 in the French Quarter to demonstrate the effectiveness of using area-wide management. All properties in a contiguous 15 block area were treated using commercially available baits or non-repellent termiticides. The treatment zone was expanded in 2002, 2003, 2006, and 2007. Glue boards were used to estimate alate numbers and in-ground monitors for foraging activity. Alates were sampled once a week in April and two to three times weekly from May to July 15 in 1998 through 2008. Monthly monitoring of foraging activity began in January, 1999. These data showed that area-wide management reduced termite activity by 50 % within two years after initial treatment and overall by 75 % in the first area treated. Isolated areas of "high" termite activity remain inside the test area. Thorough inspections of properties assisted by infrared videography are being conducted to allow discovery and treatment of colonies which have, so far, escaped treatment. Such treatments are expected to further reduce termite numbers. Continued treatment, expansion, and monitoring are required to assess the long-term effects of the area-wide management program.

POSTER PRESENTATION

Effect of habitat and trap depth on pitfall trap catches of ground dwelling invertebrates

Colin Bergeron, Evan Esch, Jaime Pinzon, John Spence

University of Alberta, Edmonton,Alberta, Canada

Introduction: Biases of the long used pitfall trap sampling method in assessing ground dwelling invertebrate communities are well acknowledged. However, the effects of the depth at which the opening of the trap is located in the ground profile (potentially arising from installation irregularity) remains unknown. The goal is to quantify the combined effect of trap depth and habitat on pitfall trap catches of Coleoptera (Carabidae and Staphylinidae) and Araneae.

Methods: Three nested replicate of six pitfall traps were installed in White spruce dominated, Aspen dominated and Black spruce dominated habitats of the Boreal Mixedwood forest of Western Canada. In each site, three randomly selected traps were installed with the opening at the level of mineral soil (15 to 25 cm below the forest floor) and three other with the opening at the level of the forest floor.

Results: More specimens and species were caught in the surface traps than in the deep traps. Few species characteristic of deep traps are known to be underestimated when comparing pitfall traps to litter washing. The effect of trap depth and habitat is more obvious on beetles than on spiders. Habitat overrides the effect of trap depth in multivariate analysis.

Conclusions: The trap to trap depth variation in pitfall trap studies is of minimal importance when analyzing composition data using multivariate analysis. However, the use of pitfall traps by itself to evaluate the density of certain species is erroneous as some species crawl in the litter and their density is not adequately estimated.

POSTER PRESENTATION

Efficacy of YieldGard® corn borer and VT PROTM Bt corn hybrids against key lepidopteran insect pests in the United States and South America: The reduction of Aflatoxin in grain produced from Bt corn hybrids under insect infestation

Isaac Oyediran, Oscar Heredia, Guillermo Videla, Claudio Robredo, Juan De Santa Eduviges, Paula Bodrone, Ricardo Miranda

Monsanto Company, St. Louis, MO, United States

Introduction: Monsanto developed YieldGard® Corn Borer hybrids expressing the Cry1Ab protein. These hybrids have provided excellent control of corn borers; European corn borer (*Ostrinia nubilalis*), southwestern corn borer (*Diatraea grandiosella*), and sugarcane borer (*Diatraea saccharalis*). New corn hybrids, YieldGard VT PRO™ expressing Cry1A.105 and Cry2Ab2, two lepidopteran insecticidal proteins, are effective for controlling these key lepidopteran stalk-borers, as well as corn earworm (*Helicoverpa zea*), and fall armyworm (*Spodoptera frugiperda*). These lepidopteran insects can cause significant damage to corn resulting in grain and yield reduction. Damaged grains have high fungal infestation, leading to unacceptably high levels of aflatoxin in the grains.

Methods: Trials were conducted in the United States and South America to test the efficacy of YieldGard®, YieldGard VT PRO™ and Non-Bt corn against key lepidopteran pests. Aflotoxin concentration in grains under insect infestation was determined only in the U S.

Experimental design was randomized complete block (RCB) with four replications. Data were collected on leaf feeding, stalk tunneling, ear damage, and aflatoxin concentrations in grains. Data were analyzed using SAS statistical software (SAS Institute Inc. 2003) and subjected to analysis of variance (ANOVA). Means were separated by LSD test at $\alpha = 0.05$.

Results: Insect damage and aflatoxin concentrations varied significantly. Compared to the YieldGard® and YieldGard VT PRO™ hybrids, insect damage and aflatoxin concentrations in the Non-Bt hybrids was significantly higher.

Conclusion: YieldGard® and YieldGard VT PRO™ hybrids provided excellent control against key lepidopteran insect pests. Aflatoxin levels were very low in the grains of these hybrids under insect infestation.

POSTER PRESENTATION

Evaluation of bagging materials for the control of the fruit fly *Anastrepha* sp. (Diptera:Tephritidae) in Taiwaneese guava fruits (*Psidium guajava* L.) variety Tai-kuo bar in Carrillos Bajos de Alajuela, Costa Rica.

Helga Blanco-Betzler[1], Rossy Morera[1], Carlos Loria[2]

[1]University of Costa Rica, San Jose, Costa Rica, [2]University of Costa Rica, Alajuela, Costa Rica

Introduction: The main problem in guava production is fruit fly damage; this insect feeds inside the fruit and facilitates the entrance of pathogens and fruit drop.

Methods: This study evaluated different materials used for making protective bags for guava fruits in order to reduce fruit fly damage and pathogen presence, as well as to extend their life expectancy in the field. The study took place during the dry and rainy seasons. During the first phase four different bagging materials were evaluated: waxed paper, nylon fabric, Taiwan bag and telephone guide paper, the latter normally used by local farmers; for the second phase only Taiwan and nylon bags were used.

Results: Highly significant differences were found during the first bagging period in terms of percentage of protected fruit where nylon > Taiwan > waxed paper > telephone guide paper. For the second period nylon bags protected more fruits than Taiwan bags. The longest duration of the bag in the field was obtained with nylon followed by telephone guide paper, Taiwan and waxed paper bags. For the second phase Taiwan outlasted nylon. Telephone guide paper and nylon yielded the highest amount of infected fruit during the first and second periods respectively. The highest number of fallen fruit was obtained in the control during the first phase. The results of this research show that the use of the nylon bag offers the highest protection against the fruit fly; however it doesn't protect against pathogens which also affect guava production.

POSTER PRESENTATION

Durivo (Thiamethoxam plus Clorantraniliprole) to control Asian citrus psyllid *Diaphorina citri*, citrus leafminer *Phyllocnistis citrella* and brown citrus aphid *Toxoptera citricida* in citrus drench application

Santin Gravena[1], Renan Gravena[1], Sergio Benvenga[1], Jose Silva[1], Adriana Gravena[1], Paulo Aramaki[2]

[1]Gravena Ltd., Jaboticabal, SP, Brazil, [2]Syngenta Crop Protection, São Paulo, SP, Brazil

Introduction: *Diaphorina citri* (Hemiptera: Psyllidae), *Phyllocnistis citrella* (Lepidoptera: Gracillariidae), *Toxoptera citricida* (Hemiptera: Aphididae) are associated to important diseases in Brazilian citriculture. This research was to test the ecological selective use of a new formulation mixture of Thiamethoxam + Clorantraniliprole, in drench application, to control those pests.

Methods: The trial was conducted in a citrus orchard, Matão, São Paulo, Brazil, var. Valencia, rootstock of lemon volkameriano, 2 years old and height of 2.0 m. The statistical design was the complete randomized blocks with 7 treatments, 4 repplications and the mean comparison was made under Tukey's test. The application of Durivo at dosages of 1.0, 1.5, 2.0, and 3.0 mL/plant were done in November 26, 2007, being Thiamethoxam in drench (Actara 250WG) and Imidacloprid on trunck spray (Winner) as standards treatments. The evaluations were made at 0, 7, 10, 14, 17, 21, 25 and 30 days after the applications. The number of nymphs anda adults of psyllids and aphids, and number of leafminer larvae were counted in 15 young terminals as well as the percet of presence on terminals was calculated.

Results: The directly application of systemic insecticides in soil or on trunk is a way to preserve natural enemies in citriculture as found by the results. Leafminers and sucking insects like aphids and psyllids are controlled by thiamethoxam, clorantraniliprole, as compared with imidacloprid and thiamethoxam sprayed on the citrus canopy.

Conclusions: Durivo was efficient at all dosages in drench application to control the psyllid, the leafminer and the aphid.

POSTER PRESENTATION

Mass production of entomopathogenic fungi for aerial use as mycoinsecticide

Buba Ahmed, Tariq Butt

Abubakar Tafawa Balewa University, Bauchi, Bauchi, Bauchi State, Nigeria

The development of resistance to chemical pesticides by insect pests as well as the public concern over their high cost and deleterious effects on environmental and human safety is at increasing rate. These concerns which are today compounded by perceived risks associated with genetic modification of plants have provided strong impetus and desire for the development of sustainable and environmentally friendly strategies for the control of insect pests. Interestingly, there have been increasing interests in exploitation of naturally occurring microorganisms (Bacteria, Fungi, Protozoa and Viruses) for use in the control of insect pests. Of the entire microorganisms, fungi have demonstrated high considerable potentials in providing environmentally friendly alternative to the use of chemical pesticides. Normally, the fungus will come into contact with the cuticle/body of the insect. The spore will germinate and penetrate into the body of the insect as a result of physical pressure and enzymatic degradation of the cuticle. The fungus will then invade the internal organs of the insects and starts to feed on the liquid content and at the same time secreting toxin until the insect finally died. The technology for the mass production of the fungus is accomplished by producing conidia of *Metarhizium anisopilae* on rice substrate. The first step was the preparation of a Sabouraud Dextrose Agar (SDA) broth media followed by formation of 3-day-old mycelium as shown in the figures. Thereafter, about 500g of rice was prepared (step 3) and transferred into an autoclaving bag (step 4) and autoclaved at 120 ºC for 20 minutes. After cooling, the rice was inoculated with 15ml of 3-day mycelium as shown in step 6. They were then inflated with sterile air, tied at the top and incubated at 25 ºC for 14 days (step7). Rice grains highly and fully colonized by fungus (inoculum) capable of controlling insect pests were harvested and obtained as shown in step 8. This was later transferred into commercial containers for distribution to farmers at a price lower than the conventional insecticides with a view to reduce poverty among our local farmers (step 9).

POSTER PRESENTATION

Occurrence of Mediterranean and Natal fruit flies (Diptera: Tephritidae) in the Western Cape Province, South Africa: Differences between orchards and home gardens

Nonto Mfeka, Aruna Manrakhan, Pia Addison

University of Stellenbosch, Stellenbosch,Western Cape, South Africa

Introduction: Mediterannean fruit fly, *Ceratitis capitata* (Wiedemann) and Natal fruit fly *C. rosa* Karsch are important pests of commercial fruits in the Western Cape Province of South Africa. Homegardens that contain multiple host species throughout the year are claimed to be potential breeding grounds for these pests and could be sources of infestation in orchards for the first ripening fruits. The aim of this study was to compare the abundance of these two species in orchards and homegardens and to determine the patterns of host use for each species.

Methods: Traps baited with a food attractant (Biolure, 3 component lure) were placed in commercial orchards and homegardens in five localities in Western Cape to monitor for adult fly activities. Various fruit species were sampled in orchards and homegardens on a monthly basis. Fruits were collected, brought to laboratory and incubated in plastic containers filled with sand for 6 weeks. Emerged flies were fed on protein and sugar for four days before being killed for identification.

Results & Discussion: In most of the study areas, adult fly activity was observed in homegardens throughout the year whilst in orchards very few or zero fly catch was recorded during winter, Fruit fly population in homegardens tended to be higher compared to orchards. Relative abundance of the two species was a function of locality and host species. Both Medfly and Natal fly were found to have a number of bridging hosts across the year. Practical implications of these results are discussed.

POSTER PRESENTATION

Sarcopromusca pruna (Shannon & Del Ponte, 1926): Not only a cattle dung breeding muscid fly

Thiago Moretti[1], Patrícia Thyssen[1], Daniel Solis[2]

[1]*São Paulo State University; Júlio de Mesquita Filhot; - UNESP, Botucatu, São Paulo, Brazil,*
[2]*São Paulo State University; Júlio de Mesquita Filhot; - UNESP, Rio Claro, São Paulo, Brazil*

Introduction: Despite taxonomic and morphological studies, and also investigations regarding to the adult development and to the role of the muscid fly *Sarcopromusca pruna* as the most important egg vector of *Dermatobia hominis* (Linnaeus Jr., 1781) in the Neotropical region, life history studies of *S. pruna* are still very scarce, particularly considering its immature stages.

Methods: During a field investigation conducted in a secondary forest (ca. 3,500 m^2) in the city of Campinas, Brazil (22°49'15''S, 47°04'08''W), from August 2003 to June 2004, aiming to analyze the composition of the local carrion invertebrate fauna, four carcasses were left inside iron cages in sunlit and shady areas twice a season for four seasons (n=16 carcasses of mouse and n=16 carcasses of rat). The visiting invertebrates were collected daily and identified. Immature forms were also collected and grown in laboratory for further identification.

Results: During the spring trial, we collected 2,749 dipteran larvae, belonging to the families Muscidae, Sarcophagidae, Calliphoridae and Fanniidae. From these, 20 larvae of *S. pruna* were collected from one mouse carcass (45,31 grams) exposed in the shady area.

Conclusions: The unexpected finding of juvenile forms of *S. pruna*, which has rarely been observed displaying a necrophagous behavior, may contribute to a better understanding of the biology of *S. pruna* immature stages. Moreover, due to its breeding in vertebrate carrion, we understand that this species can now be considered of potential forensic interest, and should not only be regarded as a cattle dung breeding dipteran.

POSTER PRESENTATION

A preliminary checklist of necrophagous insects associated to different environments in Southeastern Brazil: implications for forensic entomology

Thiago Moretti, Patrícia Thyssen, Wesley Godoy

São Paulo State University; Júlio de Mesquita Filho; - UNESP, Botucatu, São Paulo, Brazil

Introduction: Forensic entomology investigations have shown that the post mortem interval (PMI) may be estimated in two ways: by the age of the insect or by analyzing the succession and faunistic composition of the insects associated to carcasses.

Methods: The collections of insects were carried out monthly from September 2006 to March 2007 using as baits fish, cow liver and poultry viscera in appropriate bottle-traps in three different environments (rural, urban and forest area) in five municipalities in Southeastern Brazil.

Results: We collected adult members of the following species: Diptera: Calliphoridae: *Lucilia eximia* (n=110), *Lucilia cuprina* (n=4), *Chrysomya albiceps* (n=34), *Chrysomya megacephala* (n=22), *Chrysomya putoria* (n=9), *Mesembrinella bellardiana* (n=5) and *Cochliomyia macellaria* (n=16); Muscidae: *Musca domestica* (n=4); Otitidae: *Euxesta* sp. (n=4); Phoridae: *Megaselia scalaris* (n=16); Drosophilidae: *Drosophila* sp. (n=1); Piophilidae: *Piophila casei* (n=1); Lepidoptera: Nymphalidae: *Paryphthimoides poltys* (n=3), *Paryphthimoides prhonius* (n=1), *Fountainea ryphea* (n=3) and *Hermeuptychia hermes* (n=2); Riodinidae**:** *Cremna thasus* (n=1); Hymenoptera: Vespidae: *Agelaia pallipes* (n=62); Orthoptera: Tettigoniidae: Copiphorinae (n=1); Gryllidae: Nemobiinae (n=2). Interestingly, all the lepidopterans and all the specimens of *M. bellardiana* were caught in the forest area of the analized cities, which may be important to analize possible forensic indicators for this specific environment.

Conclusions: Information on the presence of insects from groups that are usually neglected as cadaveric fauna, associated to the knowledge on their biology and ecology, may provide important tools to increase the accuracy in the estimation of the post-mortem interval, when it is based on the succession patterns or faunistic composition.

POSTER PRESENTATION

Female sex pheromone of the sorghum plant bug, S*tenotus rubrovittatus* (Miridae)

Msasashi Kakizaki, Takeshi Teramoto

Hokkaido Dohnan Agricultural Experiment Station, Hokuto, Hokkaido, Japan

The sorghum plant bug, *Stenotus rubrovittatus* (Matsumura), is distributed in Japan, Korea, China, and eastern part of Russia and injures various gramineous crops and forage grasses, is one of important species causing a pecky rice in Japan. The female sex pheromone of this bug was analyzed by the GC-EAD method and GC-MS. Eleven EAD-active peaks by male antennae were found in hexane extracts of the female whole body. *n*-Hexyl *n*-butyrate were major components in female extracts. *n*-Hexyl *n*-butyrate, (*E*)-2-hexenyl *n*-butyrate, *n*-hexyl acetate, *n*-hexyl *n*-hexanoate, and *n*-hexyl (*E*)-2-hexenoate, and (*E*)-2-hexenyl acetate in the ratio of 1000 : 76-136 : trace–3.2: 21–35 : 6.3 : trace were contained in the female extracts, esters of *n*-hexan-1-ol were dominated in female extracts. On the other hand, esters of (*E*)-2-hexen-1-ol were dominated in male extracts, the relation of amounts of *n*-hexyl esters and (*E*)-2-hexenyl esters in the extracts were contrary between female and male. Field trapping tests using these synthetic compounds indicated that a mixture of *n*-hexyl *n*-butyrate, (*E*)-2-hexenyl *n*-butyrate, *n*-hexyl acetate, *n*-hexyl *n*-hexanoate, and (*E*)-2-hexenyl acetate are sex pheromone components. Optimum ratio of the 5-components for male attraction is narrow range, males were attracted to the mixtures of *n*-hexyl *n*-butyrate, (*E*)-2-hexenyl *n*-butyrate, *n*-hexyl acetate, *n*-hexyl *n*-hexanoate, and (*E*)-2-hexenyl acetate in the ratio of 100 : 10 : 1.5 : 2.5 : 0.03–1.0. The optimum doses on gray rubber septum are ranging from 100 μg to 300 μg *n*-hexyl *n*-butyrate in the 5-component mixture in this ratio for male attraction.

POSTER PRESENTATION

A preliminary screening of candidacy materials for development of monitoring tools of pumpkin fruit fly, *Bactrocera depressus* (Tephritidae: Diptera)

Kim Dong-Soon, Seo Yon- Dong, Choi Kyung San, Kang Taek Joon, Jeon Heung-Yong

Cheju National University, Jeju-si, Republic of Korea

Introduction: In Korea, total 85 species of Tephritid fly in 45 genera are recorded. Among them, the pumpkin fruit fly, *Bactrocera depressus*, is one of the most important pests in Cucurbitaceae plants, and this fly is considered a serious quarantine pest in foreign countries. Development of a monitoring tool is needed to control the flies successfully.

Methods: The attraction ability of various candidacy materials for *B. depressus* were evaluated in the field and laboratory. Materials included were methyl eugenol, cue-lure, protein sources, and volatiles from pumpkin fruits. Also, GC-EAD analysis was conducted for Orbo trap extracts of pumpkin odors.

Results: *B. depressus* showed no response to methyl eugenol and cue-lure in the field and laboratory. The protein sources of brewer hydrolysate and torula yeast attracted well *B. depressus* in the laboratory. However, a few adult flies were caught in the protein-baited traps in the field. The crude extracts from three varieties of pumpkin induced a behavioral response to *B. depressus* adults such as highly attraction and oviposition. Orbo trap extracts of the pumpkin odors had 8 to 10 common components. Some of them elicited significant EAG response from antennae of female flies.

Conclusions: Methyl eugenol, cue-lure, protein-baited traps were not appropriate as a monitoring tools of *B. depressus.* Adult flies showed significant behavioral and EAG responses to the crude extracts or odors of pumpkins. The odors of pumpkin should be useful for attraction chemicals of *B. depressus*, and further studies were required.

POSTER PRESENTATION

Effects of saline intake until the second mating on the spermatophore mass and sperm number in male swallowtail butterfly, *Papilio xuthus*

Sunao Niihara, Mamoru Watanabe

University of Tsukuba, Tsukuba city, Ibaraki prefecture, Japan

Introduction: Although sodium ions induce puddling behavior in males of some butterfly species, the role of sodium ions in male life history is unclear.

Materials and Methods: Effects of saline intake until the second mating on the spermatophore mass and sperm number were examined in male swallowtail butterfly, *Papilio xuthus*.

Results and Discussion: A virgin male transferred a spermatophore of 6mg with 40 eupyrene sperm bundles to a virgin female during the copulation. Although every spermatophore of the second mating of the mated males the day after the first copulation was too small, the mated males that fed on 0.01mol/L saline solution for the day produced a relatively large one than the mated males fed on the distilled water. The mated males fed on 0.01mol/L saline solution during five days until the second copulation increased the spermatophore size rather than that fed on distilled water. However, It was not a full size. The number of eupyrene sperm bundles included in the second spermatophore transferred by the mated males fed on 0.01mol/L saline solution for a day was around 45, which was greater than that in the first spermatophore. Thus, saline intake affected the number of eupyrene sperm bundles rather than the spermatophore size.

POSTER PRESENTATION

Synergistic behavioral responses of female moths to synthetic plant-derived mixtures are mirrored by odor-evoked calcium activity in their antennal lobes

Jaime Pinero[2], Giovanni Galizia[1], Silvia Dorn[2]

[1]University of Konstanz, Konstanz, Germany, [2]ETH-Zurich, Zurich, Switzerland, [3]University of Hawaii at Manoa, Honolulu, United States

Introduction: Synergism among constituents of odor mixtures can underlie attraction of insect herbivores to their host plants. Yet, practically nothing is known about the representation of synergistic odor-mixture effects in the antennal lobes. We combined behavior with optical imaging to characterize the response of female Oriental fruit moths, *Cydia (Grapholita) molesta* (Lepidoptera: Tortricidae), to synergistic odor mixtures.

Material. Behavioral and neurophysiological experiments were conducted to (1) quantify, in dual choice bioassays, the olfactory response of females to synthetic mixtures, and (2) characterize, using calcium imaging, the pattern of glomeruli activated by odor mixtures and their individual constituents in the antennal lobes of the female moths.

Results Behaviorally, trace amounts of benzonitrile synergized the behavioral response of female moths to a synthetic mixture. Physiologically, the addition of trace amounts of benzonitrile to an unattractive mixture led to more complex patterns of activated glomeruli in the antennal lobes. A new type of olfactory receptor functioning as a mixture detector was discovered.

Conclusions: Synergistic interactions documented at the level of behavior were mirrored by calcium activity in the antennal lobes of female moths. The mixture-sensitive glomerulus discovered offers excellent physiological evidence for a complex pattern extractor of behaviorally relevant mixtures already occurring at the level of odor representation in the antennal lobes of this moth species. The synergistic effect elicited by benzonitrile seems to be central, when present in a mixture that contains other key constituents, for adequate coding (at the physiological level) and discrimination (at the behavioral level) of odor mixtures.

POSTER PRESENTATION

Managing Oriental fruit fly, *Bactrocera dorsalis* (Diptera: Tephritidae) using Spinosad-based protein sprays in papaya orchards in Hawai'i

Jaime Piñero[1], Ronald Mau[1], Roger Vargas[2]

[1]University of Hawaii at Manoa, Honolulu, Hawaii, United States, [2]USDA-ARS, Hilo, Hawaii, United States

Introduction: Management of tephritid flies in many areas of the world has traditionally relied on frequent applications of broad spectrum insecticides. We evaluated the efficacy of sprays of GF-120 Fruit Fly Bait, in combination with two additional environmentally friendly fruit fly management methods, in reducing populations of oriental fruit fly in papaya orchards in Hawai'i. Our main goal is to develop and implement environmentally acceptable and sustainable pest management strategies that reduce use of broad spectrum insecticides while suppressing fruit flies to economically manageable levels.

Material Study was conducted in the Puna district of the island of Hawai'i in an area comprising 60 hectares currently in production. Fruit fly management tactics used included field sanitation (by growers), use of the highly attractive male-specific lure methyl eugenol and weekly sprays of GF-120 Fruit Fly Bait to papaya tree foliage and bordering plants. Results were assessed weekly using traps that monitored local populations of females and every 6 week by sampling fruit to determine level of infestation.

Results Weekly applications of GF-120 Fruit Fly Bait, when combined with field sanitation and mass trapping of males, led to a significant reduction in the number of females captured in monitoring traps in the treated plots compared to the control plots and a substantial reduction in levels of fruit infestation of papaya fruit.

Conclusions: An environmentally-friendly approach to managing oriental fruit flies was evaluated with high success. With additional research currently being conducted, this technology will be transferred shortly to papaya growers in Hawai'i.

POSTER PRESENTATION

Effects of cold winter microenvironments on overwintering survival and potential fecundity of sunn bug pest (*Eurygaster integriceps* Put.)

Ahmad Baghdadi, Sedigheh Salemimoez

Tehran university, Tehran, Islamic Republic of Iran

The effects of two overwintering microenvironments on survival and potential fecundity of sunn bug pest (*E. integriceps* put.) was studied during 2006-2007 in ghara-aghaj altitudes of Varamin located in central part of Iran. Freeze-tolerant adults overwinter on dry or moist microenvironments under different plants on mountains. When plant covered by snow, adults insect and plants freeze together. There is some dry microenvironment too. By winter's end, the mortality rate in the dry and moist microenvironments were 68% and 23% respectively that showed significant difference and reduced potential fecundity of pest (21±2 eggs/female for dry microenvironment and 37±3 eggs/female for moist microenvironments), probably due higher metabolic rates in dry microenvironment which reduced the energy available for development and egg production in spring.

We conclude that, freezing winter microenvironments, had a positive effect on survival and potential fecundity of sunn bug pest, particularly those that stored his energy for produce eggs in future spring. The enhanced reproductive output of insects overwintering in freeze microenvironments may be a selective effect promoting the evolution of increased cold-hardiness.

POSTER PRESENTATION

Improved performance of Abamectin insecticide by Volk oil for chemical control of the leaf miner, *Liriomyza trifolii* (Burgess)

Ahmad Baghdadi, Fatemeh zeshti, Aziz Sheikhi

Tehran University, Tehran, Islamic Republic of Iran

The leaf miner, *Liriomyza trifolii* (Burgess), has become the most serious pest in greenhouses of vegetable crops through out the world because of its short generation time, high reproductive rate, conspicuous damage, and ability to develop resistance to currently registered insecticides. Abamectin recommend to control *L. trifolii* ,the use of plant oil might help to reduce the required rate to achieve acceptable control of this pest. In conclusion, the effectiveness of Abamectin applied alone or mixed with plant oil on leaf miner fly (LMF) *L. trifolii* , was evaluated on cucumber plants under laboratory conditions The addition of plant oil (25%) to Abamectin concentration increased the effectiveness of the insecticide to the extent that the active ingredient of the insecticide could be reduced of the normal dosage. The synergistic effect shown by the mixture of Abamectin and plant oil allows a reduction in the commercially recommended concentration of Abamectin without any loss in effectiveness. For determine the relationship of different affective of Abamectin alone and the mixture of plant oil a randomized complete design with six treatment and three replication in each experimental, for determine to the LC_{50}. In the laboratory to evaluate the effects of various concentrations of insecticide and determine LC_{50}, leaf miner (*L. trifolii*) were collected from cucumber greenhouse in the Varamin area and rearing. A leaf dip bioassay of leaves of *cucumber sp.* infested with different extract solutions Abamectin applied singly or in combination with plant oil. Analysis data was calculated with POLO-PC , SAS software indicate significantly different characterization were found on the mixture of Abamectin produced lower LC_{50} in the compared to the mixture and plant oil. (LC_{50} of Abamectin alone = 82/31ml , LC_{50} of Abamectin and oil = 32/3 ml). Laboratory bioassay showed that, residual efficacy was significantly reduced when Abamectin was applied in an oil spray environment.

POSTER PRESENTATION

Below and aboveground multitrophic interactions in tropical and temperate regions

Hironori Yasuda[1], Keitaro Tawaraya[1], Hideki Murayama[1], Satoru Sato[1], Takashi Nisizawa[1], Testuya Murayama[1], Tomonobu Tomoyasu[1], S Suhardi[2], Andi Trisyono[3], Erry Purnomo[4], S Suputa[3], W Witjaksono[3]

[1]Faculty of Agriculture, Yamagata University, Tsuruoka, Japan, [2]Faculty of Forestry, Gadjah Mada University, Yogyakarta, Indonesia, [3]Faculty of Agriculture, Gadjah Mada University, Yogyakarta, Indonesia, [4]Faculty of Agriculture, Lambung Mangkurat University, Banjarbaru, Indonesia

Introduction: Understanding of the linkages between below and aboveground organisms is important issue in ecology since they influence each other, which in turn would produce biological diversity, although our understanding of the interactions is still incomplete, tropical regions in particular. Here, we reveal that the effect of arbuscular mycorrhizal (AM) colonization on diversity of arthropods through plant diversity at Java islands in Indonesia in addition to at Tsuruoka in Japan.

Methods: Vegetation at the experimental plot (5 m x 5 m) was removed by herbicide, then fungicide (benomyl) was applied on soil surface at each plot every two weeks as a treatment, while water was applied to the plot as a control through a year in 2004 at the three sites mentioned above. In general, plant and insect samplings were obtained every two months except for the sampling in Japan, while AM colonization was measured twice through the year.

Results: Fungicide application decreased the AM colonization of three plant species, while the effect of fungicide application tended to be smaller in other species. In contrast, in general, plant biomass tended to increase after fungicide application.

Conclusions: Belowground organisms are likely to influence differently on the functional groups of arthropods through plant diversity across spatial and temporal scales, and possible mechanism of this will be discussed.

POSTER PRESENTATION

Genetic variation and prevalence rule of *Bursaphelenchus xylophilus* in China

Hong Yang Pan

General Station of Forest Pest Management, State Forest Administration, Shenyang, China

Genetic diversities existed in not only inter-population but also inner-population between *B. xylophilus* and *B. mucronatus*. Genetic diversities of inter-population (86.6%) were higher than that of inner-population (13.4%). Under the condition of genetic distance <0.01, 173 strains of *B. xylophilus* from 13 provinces could be divided into 86 colonies. Relationship between Chinese and Japanese populations was closer than that of Chinese and American. Under the condition of genetic distance <0.197, 173 strains were divided into 3 groups.
In temporal pattern, development of pine wilt disease in local area could be divided into 3 phases. According to occurrence area, temporal phases were 1^{st}~3^{rd} y, 4^{th}~7^{th} y and time after 7 years. According to quantity of dead trees, temporal phases were 1^{st}~4^{th} y, 5^{th}~8^{th} y and time after 8 years. In whole China, damage process of pine wilt disease could be divided into 4 phases.

The spatial pattern and distribution of pine wilt disease were conducted with geostatistics. The results indicated that semivariogram of pine wilt disease could be described by spherical model in the whole country and provinces of Jiangsu, Anhui, Guangdong and Zhejiang, showing an aggregated spatial arrangement. Ranges of spatial dependence were 10.19°, 3.45°, 2.16°, 3.08° and 2.44°, and degrees of spatial dependence were 79.60%, 87.43%, 95.88%, 94.98% and 94.54% respectively. There were two main aggregated areas of pine wilt disease in China, the first one was E113°~114.5°, N22.5°~24° in Guangdong area. The second one was E22.5°~24°, N30.5°~32.5°, which centered with Nanjing.

POSTER PRESENTATION

Interspecific variation of male ejaculates on monandrous and polyandrous swallowtail butterflies (Lepidoptera: Papilionidae) in successive copulation

Nayuta Sasaki, Mamoru Watanabe

University of Tsukuba, Tsukuba, Ibaraki, Japan

Introduction: In Japanese swallowtail butterflies, lifetime mating frequency of females in *Papilio xuthus*, *P. protenor* and *P. machaon* has been reported to 3, 2.5 and 1.2, respectively. To clarify the quantity and quality of male ejaculate in relation to the mating frequency, laboratory reared butterflies were mated by hand-pairing method.

Results and Discussion: For *P. xuthus*, copula duration was 1 hour and the weight of a spermatophore transferred was 6 mg, including 40 eupyrene sperm bundles and 170,000 apyrene spermatozoa. The length of an eupyrene and an apyrene spermatozoon was 0.7 mm and 0.4 mm, respectively. On the second day after the first mating, the mated males transferred a smaller spermatophore (3.6 mg) with significantly more eupyrene sperm bundles (60), but not significantly different number of apyrene spermatozoa (180,000) than those in the first mating. For *P. protenor* and *P. machaon*, the copula duration, the spermatophore weight and the number of apyrene spermatozoa at the first mating were similar to those of *P. xuthus*. However, the number of eupyrene sperm bundles in both species was higher than that of *P. xuthus*. The eupyrene and apyrene spermatozoon sizes in *P. protenor* were as half as those of *P. xuthus*. A smaller spermatophore in the second mating with the same number of apyrene spermatozoa was also found in the mated males of both species, though no increase in the number of eupyrene sperm bundles at the second mating was found. The lifetime mating strategy of male swallowtail butterflies was discussed in relation to female polyandry.

POSTER PRESENTATION

Electron beam treatment as a phytosanitary measure for stored product pests

Nouraddin Shayesteh, Abbas Hosseinzadeh, Mohammad Reza Ardakani, Hamid Reza Zolfagharieh, Mohammad Babaii, Hadi Fatollahi, Hasan Zareshahi, Shahram Aramideh

Islamic Azad University, Branch of Mahabad, Mahabad, Islamic Republic of Iran

Introduction: Grains and pulses infested with insects such as *Tribolum castaneum* and *Plodia interponctella* may be disinfested with methyl bromide. Despite low residues, however, fumigation with MeBr may not to be desirable from the viewpoint of human health. More importantly, MeBr can deplet the ozon layer and on this basis it will be phased out for most uses. Development of an alternative treatment is urgently needed.

Methods: Developmental stages of two stored-product insect pests **viz.** *Tribolum castaneum* and *Plodia interponctella* were exposed directly to electrons using Rhodetron accelerator(tt200). Exposure doses on all stages were 0, 270, 380, 520, 700, 840, 1640, 2020, 2400, 2750 and 3130 Gy.

Results: The results of these studies indicate that inhibiting doses for eggs, larval, pupal and adults of *Tribolum castaneum* were 840, 380, 2020 and 3130Gy respectively. These criteria for *Plodia interponctella* were 840, 520, 1640 and 3130 respectively. Due to results eggs, larval and adults of *Tribolum castaneum* were sensitive than *Plodia interponctella*.

Conclusions: We suggest that it is possible to disinfest grains contaminated with these insects using high energy electrons at 3130Gy.

POSTER PRESENTATION

Programmed cell death in intestinal cells of *Bombyx mori* during the metamorphosis: morphological observation of autophagy and apoptosis and expression of the ecdysone-regulated genes

Zhi-Jun Huang[1], Qing-Rong Li[1], Yan-Xia Shi[1], Xiao-Juan Deng[1], Wan-Ying Yang[1], Ya-dong Huang[2], Qili Feng[3], Yang Cao[1]

[1]Department of Sericulture science, College of Animal Science, South China Agricultural University, Guangzhou, Guangdong, China, [2]Biopharmaceutical Research and Development Center, Jinan University, Guangzhou, Guangdong, China, [3]Guangdong Provincial Key Lab of Biotechnology for Plant Development, School of Life Sciences, South China Normal University, Guangzhou, Guangdong, China

During metamorphosis in insect, degeneration and dissolution of the larval tissues, which is triggered by ecdysone hormone (EH), require programmed cell death, such as autophagy and apoptosis. Morphological observation on autophagy and apoptosis and analysis of ecdysone-regulated gene expression in the epithelium cells of *Bombyx mori* gut indicated that the Cvt, autophagy, mitophagy and reticulophagy pathwayes of autophagy occurred in intestinal epithelium cells during the larval to pupal metamorphosis. The typical DNA ladder of apoptosis was also detected in the degenerating epithelium cells. The expression peaks of transcripts of the EH receptor gene BmEcR and earlier transcriptional genes BmHR39□BmE74A appeared before pupation, but BmFTZ-F 1 expressed later. All the data together suggested that the early expression of BmEcR□BmHR39□BmE74A might initiate autophagy and apoptosis, and autophagy pathway occurred dominantly and earlier than apoptosis pathway. This work was supported by the “863 project” (2006AA10A119), the “973 Project) (2005CB121000), NNSF (30370716, 30570938) of China.

POSTER PRESENTATION

Functional divergence and inductive expression patterns of three multi-gene families of antimicrobial peptides in *Bombyx mori*

Ming-qiang Ye[1], Wan-ying Yang[1], Ya-dong Huang[2], Xiao-juan Deng[1], Shuo-yang Wen[3], Qing-you Xia[4], Yang Cao[1]

[1]Department of Sericulture Science, College of Animal Science, South China Agricultural University, Guangzhou, Guangdong, China, [2]Biopharmaceutical Research and Development Center, Jinan University, Guangzhou, Guangdong, China, [3]Department of Entomology, College of Natural Resource of Environment, SCAU, Guangzhou, Guangdong, China, [4]The Key Sericultural Laboratory of Agricultural Ministry, College of Sericulture and Biotechnology, Southwest University, Chongqing, China

Three multi-gene families of the antimicrobial peptides, Cecropins, Moricins and Attacins, in *Bombyx mori* were investigated for their inductive expression and functional divergence. Fifteen genes were cloned and expressed *in vitro*. Antimicrobial activity of the peptides was assayed by agar diffusion and minimum inhibitory concentration. Gene expression of the four Cecropin subfamilies was examined by quantitative RT-PCR. Strong antibacterial activity in Cecropin D and BmcecB1 and high transcriptional levels in Cecropin D and BmcecB1-B5 were found, whereas BmcecD1 transcripts were not detected, indicating that dominant inducible genes are present in this family. Antibacterial activity and high transcription levels were detected in the Moricins A, but not Moricins B subfamily, suggesting that Moricins A subfamily is dominant in the Moricins family. Antibacterial activity of Bmatt1 and Nuecin in the Attacins family displayed similar antibacterial spectrum. This study was supported by the “973 Program” (2005CB121000), the “863 Program” (2006AA10A119) and the NNSF of Guangdong Province of China (032256, 04020553).

POSTER PRESENTATION

Selection of mutants for resistance to leaf miner (*Liriomyza cicerina* Rond.) and iron deficiency chlorosis in chickpea (*Cicer arietinum* L.)

Cengiz Toker[1], Huseyin Canci[1], Nisa Ertoy Inci[1], Fatma Ceylan[1], Dilek Uras[2], Fedai Erler[3]

[1]Department of Field Crops, Akdeniz University, Antalya, Turkey, [2]Department of Soil Science, Akdeniz University, Antalya, Turkey, [3]Department of Plant Protection, Akdeniz University, Antalya, Turkey

Introduction: Yield loss due to leaf miner in chickpea may reach up to 40% in the Mediterranean region. Also, considerable yield losses due to iron (Fe) deficiency chlorosis in chickpea may occur when susceptible genotypes are grown in calcareous soils with high pH. The only practical and economical solution to overcome leaf miner damage and Fe deficiency chlorosis is through the utilization of genetic resistance.

Methods: The chickpea accessions ICC 6119 was irradiated with 200, 300 and 400 Gy gamma rays. Mutated populations were screened for resistance to leaf miner using a 1–9 scale, where 1 = free from any damage and 9 = maximum damage, and evaluated for Fe-deficiency chlorosis using a scale 1-2, where 1 corresponds to plants free of any Fe-deficiency symptoms and 2 corresponds to the youngest leaflets of plant show in chlorosis.

Results: In the M_3 generation, five mutants were selected for resistance to leaf miner and Fe-deficiency chlorosis from a single seed descent set. Maximum viable mutations were obtained from 200 Gy treatments.

Conclusions: According to literature available, this is the first report on selection of mutants for resistance to leaf miner and Fe-deficiency chlorosis in chickpea. Resistance to leaf miner and Fe-deficiency chlorosis was induced by gamma rays in a short time by altering previously unknown genes. The identified Fe-efficient and leaf miner-resistant mutants may be useful in chickpea breeding programs to develop cultivars suitable for a niche environment.

POSTER PRESENTATION

Phytophagous insects associated with *Chromolaena odorata* in continental and island habitats within its native range

Lorraine Strathie, Costas Zachariades

Agricultural Research Council - Plant Protection Research Institute, Hilton, KwaZulu-Natal, South Africa

Introduction: *Chromolaena odorata* (Asteraceae) is native to most of the Neotropics, and has invaded the Old World tropics and subtropics. Surveys of natural enemies associated with chromolaena in its native range were first conducted in Trinidad in the 1960's, for potential utilization in biological control. Since 1988, the South African chromolaena biocontrol research programme has undertaken survey and collecting expeditions in many neotropical countries.

Methods: Field surveys of phytophagous insects on chromolaena were conducted during the wet season from 1996 until 2006 in Venezuela and Jamaica, at localities up to 1500m in altitude. Insects were collected, identified, and their distribution, damage, and host range investigated. Literature records were consulted for parts of the neotropical distribution of chromolaena.

Results: The phytophagous insect community associated with chromolaena in the island habitat (Jamaica) was poor compared to that on the mainland (Venezuela). Candidate agents such as *Melanagromyza eupatoriella, Calycomyza eupatorivora* (Agromyzidae), and *Phestinia costella* (Pyralidae) were widespread throughout the entire distribution of chromolaena, but relative abundance varied: *C. eupatorivora* was common in Jamaica but rare in Venezuela. Several species, including *Carmenta* sp. nov. (Sesiidae), *Longitarsus* sp. (Chrysomelidae), *Lixus aemulus*, *Conotrachelus reticulatus* and *C. curabilis* (Curculionidae) were found only on the mainland (including Trinidad). Conversely, *Polymorphomyia basilica* (Tephritidae) and *Dichrorampha odorata* (Tortricidae) were restricted to Jamaica and neighbouring islands.

Conclusions: The geographic distributions of phytophagous insect communities on chromolaena are discussed; some species were ubiquitous while several others were restricted to either only parts of the mainland or islands in the neotropics.

POSTER PRESENTATION

Biology of the clothes moth, *Tinea translucens* Meyrick (Lepidoptera: Tineidae) and the preference analysis of their case-making materials

Po-Yen Chen, Shiuh-Feng Shiao

National Taiwan University, Taipei, Taiwan

Introduction: *Tinea translucens* is the most common household clothes moth species in Taiwan. After the general survey around Taiwan, we found there are at least two other species which also lived in our surroundings; they have similar behavior of building the portable cases, but could be differentiated by their different case shapes. Due to the fact that the different instar larvae have different size of mouthpart, the older larvae could also enlarge their outer cases. In order to further understand their case-making behavior, we focus on their casings which have the phenomenon of concentric circles, and also the different materials the larvae could choose to see their preference of case-making materials.

Methods: To understand the biology and case-making behavior of clothes moths, a field collection in Taiwan was conducted, the related environmental parameters, such as humidity, illumination, wind velocity and elevation in the collecting sites were recorded. In addition, their case shapes, male genitalia, case-building behavior and the nature enemies were also described for further references. We offered some different materials and design experiments to understand their larval case-building behavior in lab; the preference of case-making materials were then recorded and analyzed.

Results: In this study, at least there different species of clothes moths were found in Taiwan. Experiments showed there is no particular preference in their case-making materials. Although sand is the most common material the clothes moth adopted for their casing, yet if different material offered in their living environment, such as feather or hair, they could randomly use those materials around them for their case-making material.

Conclusions: Clothes moth has high tolerance to the environmental changes; they can use many different kinds of material to build their nest. On the other hand, previous studies have recorded some Tineidae larvae could be found on mammal corpses of the late dry decay stages. Thus, connecting their high tolerance to the environment and their case-making behavior to forensic entomology may be a possible way to provide some other evidences in further describing the environment of crime scene.

POSTER PRESENTATION

Behavioral syndrome, antipredator-behavior and immune defence in field crickets

Raine Kortet[1], Markus Rantala[2], Ann Hedrick[3]

[1]Department of Biology, University of Oulu, Oulu, Finland, [2]Section of Ecology, Department of Biology, University of Turku, Turku, Finland, [3]Section of Neurobiology, Physiology & Behavior, University of California, Davis, Davis, CA, United States

Introduction: Behavioral syndromes have recently drawn attention from evolutionary biologists. In the field cricket *Gryllus integer*, males are aggressive with one another and fight vigorously over females and territories. This aggressiveness is likely associated with other behavioral traits that are potentially costly in terms of resistance against parasites and pathogens.

Methods: We examined whether aggressiveness was correlated with activity in a potentially dangerous context (a novel environment,) and if anti-predator-associated behavioral traits were related to immune defence.

Results: More aggressive males, who won more fights, had shorter latencies to become active and shorter latencies to emerge from a safe refuge. Encapsulation response was positively correlated with the latency to become active and latency to emerge from a safe refuge in the high-predation-risk population, but not in the low- predation-risk population.

Conclusions: These results suggest that a behavioral syndrome exists in G. integer, in which more aggressive males are also more active in general, and possibly less cautious towards predation risk. Moreover, predation and parasitoids may increase the cricket's investment in parasite resistance, despite the potential costs of anti-predator behavior.

POSTER PRESENTATION

Subgenus Meloehelea (Diptera: Ceratopogonidae) in the Neotropical Region?

Andrea Tóthová

Masaryk University, Brno, Czech Republic

Introduction: The diverse biting midge genus, *Atrichopogon* Kieffer, contains 476 species worldwide. The subgenus *Meloehelea* Wirth includes ectoparasitic species that feed on the haemolymph of blister beetles (Meloidae) and other related coleopteran families. There are 16 species of this subgenus, 10 of which occur in the Palaearctic, 3 in the Nearctic, 2 in the Holarctic and 1 in the Afrotropical Region. Hitherto the subgenus *Meloehelea* has not previously been reported from the Neotropical Region.

Material and Methods: A slide-mounted adult males and females of *Meloehelea* (CNCI) from the Neotropical and Nearctic Regions have been examined, described and photographed with a Leica DM5500 compound microscope with Leica DFC320 digital camera. The specimens have been also compared to other Palaearctic and Nearctic *Meloehelea* species.

Results: The genus *Atrichopogon* is diverse but most species usually cannot be accurately identified and the subgeneric classification of *Atrichopogon* is poorly understood, particularly in the Neotropical region. The record of the subgenus *Meloehelea* from the Neotropical region is therefore noteworthy. The record of *A.* (*M.*) *oedemerarum* and two additional new species of the sg. *Meloehelea* from the Neotropical Region deposited at the CNCI increases our knowledge of the diverse Neotropical biting midge fauna.

Conclusions: A more thorough focus on generic and subgeneric characters of *Atrichopogon* as well as the construction of workable keys for the Holarctic and Neotropical Regions are badly needed.

The study has been supported by the Ministry of Education grant MSM No. 0021622416 and by the 6th Framework Program – The Mobility Program of Masaryk University.

POSTER PRESENTATION

Effects of Soil Fertilization on Surface Active Arachnids at Toolik Lake, Alaska

Karl Wyant[1], Paula Cushing[4], Boris Kondratieff[3], John Moore[2]

[1]Graduate Degree Program in Ecology, Colorado State University., Fort Collins, CO, United States, [2]Natural Resource Ecology Laboratory, Colorado State University, Fort Collins, CO, United States, [3]Bioagricultural Science and Pest Management, Colorado State University, Fort Collins, CO, United States, [4]Denver Museum of Nature and Science, Denver, CO, United States

Introduction: Arctic soils are nutrient limited because organic matter contained in permafrost is not available to the soil food web. Climate change models suggest that as the Arctic becomes warmer the permafrost will melt, making labile nutrients (N & P) available to microbes. This may prompt higher rates of net primary productivity, changes in plant community structure, and alteration of soil food web structure and dynamics. We initiated a study to assess changes of a major soil predator group as a result of simulated climate change.

Methods:1,758 spiders were collected from pitfall traps in moist acidic (MAT) and dry heath (DH) tundra from the Toolik Lake LTER, AK during the 2004 growing season. The field site is arranged into four (MAT) and three (DH) blocks, each with factorially-arranged nitrogen-phosphorus addition and grazing treatments.

Results: Fertilization treatments show significant increase of spider populations ($p=.003$). Diversity and richness measurements yielded contrasting results for the two study sites ($p=0.274$), and ($p=0.003$), respectively.

Discussion: We attribute these results to differences in plant cover on the fertilized plots and unique response characteristics for distinct tundra habitat types.

POSTER PRESENTATION

EMEND Entomology: Arthropod conservation and sustainable forest management

John Spence[1], Jason Edwards[1], Colin Bergeron[1], Esther Kamunya[1], Jaime Pinzon[1], Jan Volney[2], David Langor[2], Joshua Jacobs[3], Timothy Work[3]

[1]University of Alberta, Edmonton, Alberta, Canada, [2]Canadian Forest Service, Edmonton, Alberta, Canada, [3]Université du Québec à Montréal, Montréal, Québec, Canada

Introduction: EMEND is a large-scale (c. 1000 ha) forest experiment in northern Alberta, Canada initiated in 1998 to compare ecosystem effects of several approaches to retention harvest with the effects of wildfire. The objective is to illuminate harvest and regeneration methods that contribute most significantly to forest sustainability in the Canadian boreal region.

Methods: Replicated 10-ha blocks of forest, representing each of four successionally arranged cover-types were harvested (1999) to several green-tree retention (2%, 10%, 20%, 50% and 75%) prescriptions, burned in two ways or held as un-manipulated checks, after a pre-treatment year (1998). Arthropods populations representing many taxa (moths, epigaeics and saproxylics are featured here) have been monitored since.

Results: Distributed retention provided no significant 'life-boating' for any arthropod taxon, but even very small (0.2-0.4 ha) patches provided a significant degree of habitat reserve for arthropods, especially species characteristic of mature forest. Early effects, which were largely explained by cover-type, are misleading with respect to emerging long-term patterns which are driven mainly by type and degree of disturbance. Faunal recovery after harvest travels on a different trajectory of that after wildfire and certain pyrophillous faunal elements go missing on harvest-origin blocks.

Conclusions: Retention harvesting leaves important legacy elements and has conservation advantages over clear-cutting, but it is not a full substitute for fire in these boreal forest systems. Biodiversity will be best conserved by a combination of green-tree retention harvest, silvicultural methods that encourage regeneration of habitats and the use of fire as a regeneration tool.

POSTER PRESENTATION

Electroantennography for development of food-based attractants for pest Tephritidae

Paul E. Kendra, Wayne S. Montgomery, Nancy D. Epsky, Robert R. Heath

USDA-ARS, Subtropical Horticulture Research Station, Miami, Florida, United States

Introduction: *Anastrepha* fruit flies (Diptera: Tephritidae) are serious pests of vegetable and fruit crops throughout the American tropics and subtropics. Current trapping systems utilize synthetic lures which emit ammonia and other attractant chemicals that function as protein feeding cues. However, field captures are variable with synthetic lures, and this variability does not appear to be related solely to ammonia release rate. The need for improved attractants prompted research using electroantennography (EAG), a technique which measures response of antennal olfactory receptors to volatile chemical stimuli.

Methods: *Anastrepha suspensa* of known age and physiological state were used for EAG analyses. Antennae were presented with quantified chemical samples in vapor form. Upon binding with specific olfactory receptors, test chemicals evoked a measurable electrical response (an EAG spike) which represents summation of multiple receptor potentials. Analysis of the amplitude of EAG spikes provided information on appropriate doses and combinations of chemicals needed to elicit optimal antennal response.

Results: EAG response of *A. suspensa* was quantified for ammonia, carbon dioxide, putrescine, and a series of diamines homologous to putrescine. Quantitative EAG identified factors which contribute to the variability in fly response to food-based attractants, including sex, age, nutritional requirements, and reproductive status. EAG also identified potential new fruit fly attractants.

Conclusions: Information from EAG analysis will be used to determine the relationship between antennal sensitivity to fruit fly attractants and efficacy of those compounds when deployed in traps for pest *Anastrepha* species.

POSTER PRESENTATION

Comparative morphological study of three Brazilian Physodactylinae species (Coleoptera: Elateridae)

Simone Policena Rosa

Museu de Zoologia da Universidade de São Paulo, São Paulo, SP, Brazil

Introduction: Physodactylinae comprises 7 genera and 28 species distributed in South America, Africa and Southeast Asia. Eighteen species occur in Brazil. Their supposed synapomorphies are: fossorial legs, large mandibles and chin peace absent. The objective of this study was compare the morphology of the type-species of the three Brazilian genera *Physodactylus, Dactylophysus* and *Teslasena* and two *Heterocrepidius* species (Dicrepidiini, Elaterinae), in which the *Dactylophysus* species were described.

Material and methods: Since females of the majority of species are unknown only males were examined. One specimen of each species were whole disarticulated, they were dissected through traditional techniques using NaOH.

Results: *Physodactylus henningi*, *Dactylophysus mendax*, *Heterocrepidius gilvellus* and *H. depressus* share several characters as the carina on mandibular dorsal face, two long setae on mentum, basiestipe elongated with several long setae, transversal carina on mesepisternun, general shapes of mesosternum and mesoscutum, lamellate tarsomeres, sternite VIII partially sclerotized and basal piece longer than paremeres. *Teslasena femoralis* is the most conspicuous species, among its unique characters are: hind wing without wedge cell and CuA_1, mentum without setae, basiestipe short with one strong long seta and simple tarsomeres.

Conclusion: The similarities among *Physodactylus*, *Dactylophysus* and *Heterocrepidius* species suggest that should be a phylogenetic relationship between Physodactylinae and Dicrepidiini. The unique characters of *Teslasena* could be either autapomorphies or synapomorphies shared with other group does not studied here. A phylogenetic study should be carry out, including all Physodactylinae and traditionally related species, to test the monophyly of this subfamily and elucidate its position in Elateridae.

POSTER PRESENTATION

Insect importance on exhume cases and human remains in forensic investigation in Brazil

Lucila Maria Lopes de Carvalho[1], Patricia Jacqueline Thyssen[2], Fortunato Badan Palhares[3]

[1]UNESP, Rio Claro, SP, Brazil, [2]UNESP, Botucatu, SP, Brazil, [3]Instituto de patologia, Campinas, SP, Brazil

Introduction: In recent years, arthropod evidence has made its way into routine use in forensic and medico-legal investigation specially to contribute on estimating PMI. The advantage in using insects is they can be collected in any stage of investigation such as at the death scene, necropsy as well during the exhumation, besides it is possible to use them death or alive. Necropsy usually offers information regarding the manner and cause of death, stage of decomposition and location. Besides these factors, the presence of insects can be helpful to estimate the PMI, however, it is important an expert in entomology to collect all necessary samples and information. Two exhume cases of forensic interest are presented.

Methods: After exhumation, immature and adult insects were collect from bodies and taken to the laboratory to complete their development in an artificial diet or be identified.

Results: It was found only remains in both cases. It was collected dead and alive insects. There were empty puparium and adults of *Megaselia scalaris* (Phoridae) in the case 1 and maggots of *Piophila casei* (Piophilidae) in the case 2. These insects played an important role in the decomposition process.

Conclusions: In forensic investigation to obtain an accurate result it is important the participation of a diverse group of professionals such as pathologists, chemists, police officers and entomologists. Insects can contribute as evidence in an investigation especially when dead is up 72 hours. Then, a professional trained is indicated to avoid any lost of sample and minimize the error.

POSTER PRESENTATION

Pest species of Orthoptera of the central part of the Volga-Kama region (Russia)

Nikolay Shulaev, Inessa Karmazina

Kazan State University, Kazan, Russian Federation

Introduction: Orthoptera are an integral part of the fauna of natural and agrarian biocenoses- of Volga-Kama region. The central position of the Volga-Kama province took Tatarstan Republic (Popov, 1960).

Methods: The research was carried from 2005 to 2007 year in various parts of Tatarstan Republic. Research covered various biotopes and habitats. Charges were standard method.

Results: In Tatarstan at the moment orthoptera recorded 64 species belonging to 34 genera and 6 families. The family Tettigoniidae - 19 species, Gryllotalpidae - 1 species, Gryllidae - 3 species, Acrididae - 43 species, Tetrigidae - 3 species Tridactylidae - 1 species (Karmazina, Shulaev, 2008). We exhibited 4 pest species of family Acrididae (Locusta migratoria L., Calliptamus italicus L., Pararcyptera microptera F.-W., Oedaleus decorus Germ.). Two species of pests Aelopus sibiricus L. and Dociostaurus brevicollis Ev. were marked by literary date (Aleinikova, 1950).

Conclusion: We have found pest species are rare or small populations. These species do not formed large swarms. Hereby, they do not cause significant damage to agriculture of the republic.

POSTER PRESENTATION

Historical development of the suborder Heteroptera (Hemiptera)

Yuri Popov

Paleontological Institute, Russian Academy of Sciences, Moscow, Russian Federation

Heteroptera include ca. 1000 fossil (mostly Cainozoic) species in about 500 genera and 50 families. The earliest Heteroptera are known from the Late Triassic of Australia, North America, China, France, and Ukraine. They are mainly represented by aquatic Naucoridae, Triassocoridae, Belostomatidae, and Notonectidae. The oldest extinct terrestrial lygaeoid Pachymeridiidae is recorded from the Late British Triassic. A rapid radiation of Heteroptera started in the Early Jurassic in Western Europe (aquatic Belostomatidae and Corixidae, amphibious gerromorphan Mesoveliidae, littoral Ochteridae, saldoid Archegocimicidae, terrestrial Cimicomorpha and Pentatomomorpha) and in Central Asia and China (Corixidae and Shurabellidae). It is significant that diverse nepomorphan bugs widespread in Early Jurassic Laurasian deposits are represented by extant families. The extinct corixoid Shurabellidae were very common during the first half of the Jurassic in Central Asia, Eastern Siberia and Mongolia, but practically absent from the Upper Jurassic. During the Middle and Late Jurassic, Heteroptera diverged into many families, some of them being extinct, e.g. water pleoid Scaphocoridae, terrestrial pentatomoid Mesopentacoridae from the Upper Jurassic of Kazakhstan. At that time first extant Miridae, Coreidae, and Alydidae appeared among terrestrial bugs. Being quite numerous in the Upper Jurassic, cimicomorphan Miridae are not recorded in the Lower Cretaceous, but found in the Upper Cretaceous of North Siberia. The Early Cretaceous Heteroptera (mainly known from Eurasia and South America) are quite similar to the Late Jurassic assemblages. The transition from the Jurassic to Cretaceous was accompanied by the appearance of still very rare Hydrometridae, Tingidae, Reduviidae, and Aradidae. Some terrestrial groups became abundant, e.g. Archegocimicidae, Pachymeridiidae or Cydnidae. Aquatic bugs are also abundant during the Upper Jurassic and Lower Cretaceous. They are mainly represented by Corixidae (mostly Velocorixinae and Diaprepocorinae), Naucoridae, Notonectidae, and Belostomatidae. By mid-Cretaceous, the remaining Mesozoic families like water pleoid Mesotrephidae, Pachymeridiidae and Mesopentacoridae became extinct. Extant Gerroidea (Gerridae) and Coreoidea (Lygaeidae) became more numerous. The first Vianaididae and Thaumastocoridae (both Tingoidea) are found in the Turonian New Jersey amber. During the Cainozoic, the number of the still living (sub)families further increased, representing almost all main taxonomic groups.

POSTER PRESENTATION

The role of active host defensive reactions on host-instar selection by *Cotesia plutellae* (Hymenoptera: Braconidae), a larval parasitoid of *Plutella xylostella* (Lepidoptera: Plutellidae)

Robert S. Nofemela, Rami Kfir

ARC-Plant Protection Research Institute, Private Bag X134,, Pretoria 0001, South Africa

Introduction: Parasitoid fitness depends on resources provided by their hosts, and as a consequence host selection behaviour of female parasitoids is assumed to be influenced by host quality only. However, parasitoid host selection behaviour may also be influenced by differences in ability to subdue different host instars. This aspect was investigated with *Cotesia plutellae* on *Plutella xylostella* larvae.

Methods: The host-instar selection behaviour of newly emerged, mated and naïve female *C. plutellae* was investigated in no-choice, choice and preference test by observation experiments. Fitness traits such as developmental rate and survival of immature stages as well as female proportion in the offspring were also investigated.

Results: In a no-choice test, a significant preference for 3^{rd} instars followed by 2^{nd} then 4^{th} instar hosts was observed. The developmental rate of the progeny was shorter for parasitoids that started their development in 4^{th} instars than in either 2^{nd} or 3^{rd} instars. However, significantly more parasitoids completed their development in 3^{rd} instars than either 2^{nd} or 4^{th} instars. The younger the host was at the time of oviposition, the higher was female parasitoid proportion in progeny. In a choice test, a significant preference for 2^{nd} instars followed by 3^{rd} then 4^{th} instar hosts was observed. These results were validated with direct observations. The females were unable to subdue the aggressive 4^{th} instars, but preference for 2^{nd} than 3^{rd} instars in choice tests was not clear as both were subdued easily.

Conclusion: The defensive host reactions influenced the host selection behaviour in *C. plutellae.*

POSTER PRESENTATION

The infection process of *Beauveria bassiana* to *Apriona germari* larvae and defense response of the host to the pathogen

Huang Dazhuang, Li Huiping, Wang zhigang

Forestry College of Hebei Agricultural University, Baoding, China

The infection process of *Beauveria bassiana* to *Apriona germari* larvae and defense response of the host to the pathogen were studied. The results showed that the penetration process of *B.bassiana* include adherence, germination, appressoria and penetration. The conidia on the cuticle of *A.germari* larvae germinated in 16h after inoculation. The hyphae penetrated the cuticle and propagated in the coelom. Then it infected and destroyed the cutex, hemloymph lipoid and muscles, alimentary tract and malpighian tubule, etc. The phenoloxidase activity in hemolymph of *A.germari* larvae infected by *B.bassiana* increased within the early days of infection, but followed by decreasing because of the adaptability of *B.bassiana*. The phenoloxidase activity in hemolymph of *A.germari* larvae infected by successive reisolates obtained by repeatedly passing through the Czapek medium was higher than that by repeatedly passing through the *A.germari* larvae. There was some correlation between the maximal time producing phenoloxidase activity and LT_{50} of different reisolates. At the same time, a high relationship between the maximal activity and the LC_{50} was also found. All this indicated that the phenoloxidase activity can not only weigh the immunity ability of the host, but also act as an important reference index of pathogen. The hemocytes of *A.germari* larvae can resist the invasion of *B.bassiana*. The immune response mainly include adhesion, phagocytosis, aggregation, encapsulation and nodule formation. The peak response times were 2~2.5d after invasion of *B.bassiana*. The defense responses were just temporarily inhibition for the pathogen but could not clear them completely.

POSTER PRESENTATION

Life History of *Aleochara nigra* and *Aleochara formosanorum* (Coleoptera: Staphylinidae)

Shou-Wang Lin

National Taiwan University, Taipei, Taiwan

Introduction:, Researches of forensic entomology were so far mostly focused on the flies (Diptera) which appearing at the earlier stages of carrion decomposition, especially the blow flies (Diptera, Calliphoridae). Other insects also come to the carrions, like hymenopterans and coleopterans, but their biology and behavior are otherwise not well studied. Two common species of necrophagous *Aleochara* in Taiwan, *A. nigra* and *A. formosanorum*, were collected and reared in lab to study their life history and the time they arrive at the rat carrion in the field. It helps us to determine the ecological roles which they play in the carrion insect succession.

Methods: Adult beetles and their arriving time on carcasses were collected and recorded by using the pitfall traps once a day. Life history data was recorded from the lab colony which the larvae were reared in a plastic box and the pupae of their possible host species of *Hemipyrellia pulchra* and *Chrysomya megacephala* were provided.

Results: Larvae of *A. nigra* and *A. formosanorum* occurred on the carrions were observed almost at every succession stages, but mostly during the bloated to the advanced decay stage. At 28 ℃, eggs take about 3.5 and 4.3 days to hatch in *A. nigra* and *A. formosanorum,* respectively. Larvae of both species of *A. nigra* and *A. formosanorum* could use pupae of *Hemipyrellia pulchra* as hosts, and the 3rd instar larva comes out of the host's puparium, makes cocoon and then pupates inside the cocoon in the soil. Adults emerge after the pupal stages of 13.5 and 12 days in *A. nigra* and *A. formosanorum*, respectively.

Conclusions: *A. nigra* and *A. formosanorum* are necrophagous and their larvae are ectoparasitoids of *Hemipyrellia pulchra*, adult predation on maggots and larva being a parasitoid of pupae may affect the fly population and further change the composition of carrion insect fauna.

POSTER PRESENTATION

Genetic differentiation of *Rhyzopertha dominica* among geographical populations with different resistance level to PH_3

Hongyu Zhang, Xuhong Song, Yongshun Zhao, Xiaoxue Li

Institute of Urban Pests, College of Plant Science and Technology, Huazhong Agricultural University, Wuhan, China

The LC_{50} values to phosphine (PH_3) of *Rhyzopertha dominica* (Fabricius) different geographical populations were detected by a method recommended by FAO. Results showed that the LC_{50} values of populations from Banan, Chengdu, Shayang, Zhucheng, Yangchun, Xuchang was 0.04948mg/L, 0.04981mg/L, 0.58510mg/L, 3.18523mg/L, 3.2933mg/L and 3.25482mg/L respectively, their *Rf* values were 1, 1.01, 11.82, 64.37, 65.78, 66.55 times, respectively, and the resistance in order was Banan, Chengdu, Shayang, Zhucheng, Yangchun, Xuchang. Genetic differentiation among those populations was investigated using amplified fragment length polymorphism. Results showed that a genetic differentiation was found among geographical populations with different resistant level to PH_3, and the six geographical populations were clustered as 4 branches at 4.6904, the low-resistance populations such as Chengdu and Banan were clustered into one group firstly. Then they were clustered with Shayang and Yangchun which were medial-resistance populations at 4.6904. Finally, all of four were clustered with higher-resistance populations of Xuchang and Zhucheng at 3.3166. The result showed the higher resistance was, the bigger variation was. Additionally, 8 characteristic DNA bands, which may be helpful for surveying the *R. dominica* resistance to PH_3 as a molecular marker, were found using EcoRI +ATA/HpaII +TAC and EcoRI +AAC/ MspI +TAC primers. Moreover, Genetic differentiation among geographical populations of *R. dominica* was also investigated using COI, COII genes of mitochondrial DNA as molecular markers.

POSTER PRESENTATION

Genetic differentiation of *Rhyzopertha dominica* among geographical populations with different resistance level to PH_3

Hongyu Zhang, Xuhong Song, Yongshun Zhao, Xiaoxue Li

Institute of Urban Pests, College of Plant Science and Technology, Huazhong Agricultural University, Wuhan, China

The LC_{50} values to phosphine (PH_3) of *Rhyzopertha dominica* (Fabricius) different geographical populations were detected by a method recommended by FAO. Results showed that the LC_{50} values of populations from Banan, Chengdu, Shayang, Zhucheng, Yangchun, Xuchang was 0.04948mg/L, 0.04981mg/L, 0.58510mg/L, 3.18523mg/L, 3.2933mg/L and 3.25482mg/L respectively, their *Rf* values were 1, 1.01, 11.82, 64.37, 65.78, 66.55 times, respectively, and the resistance in order was Banan, Chengdu, Shayang, Zhucheng, Yangchun, Xuchang. Genetic differentiation among those populations was investigated using amplified fragment length polymorphism. Results showed that a genetic differentiation was found among geographical populations with different resistant level to PH_3, and the six geographical populations were clustered as 4 branches at 4.6904, the low-resistance populations such as Chengdu and Banan were clustered into one group firstly. Then they were clustered with Shayang and Yangchun which were medial-resistance populations at 4.6904. Finally, all of four were clustered with higher-resistance populations of Xuchang and Zhucheng at 3.3166. The result showed the higher resistance was, the bigger variation was. Additionally, 8 characteristic DNA bands, which may be helpful for surveying the *R. dominica* resistance to PH_3 as a molecular marker, were found using EcoRI +ATA/HpaII +TAC and EcoRI +AAC/ MspI +TAC primers. Moreover, Genetic differentiation among geographical populations of *R. dominica* was also investigated using COI, COII genes of mitochondrial DNA as molecular markers.

POSTER PRESENTATION

Synergistic effect of *Bacillus thuringiensis* on *Habrobracon hebetor* during combine biological control of *Plodia interpunctella*

Rotimi Akinkurolere, Hongyu Zhang

Institute of Urban Pests, College of Plant Science and Technology, Huazhong Agricultural University, Wuhan, China

The potential of combining microbial pesticides and natural enemies for integrated pest management of stored cereal was carried out using the interactions between *Bacillus thuringiensis* (Bt), Bt-intoxicated host larvae and *Habrobracon hebetor* (Hymenoptera: Braconidae) during the control of *Plodia interpunctella* (Lepidoptera: Pyralidae). Application of Bt or *H. hebetor* alone caused 41.67% and 35.35% *P. interpunctella* larval mortality respectively. However, Bt-*H. hebetor* combination treatment significantly evoked more *P. interpunctella* mortality (86%) than other treatments. Host mortality in controls was negligible. Progeny development of parasitoid wasp was dependent upon its susceptibility to Bt contaminated host. *H. hebetor* was able to successfully complete its development on the hosts though, fewer wasps emerged from Bt-parasitoid combined treatment than in none Bt treatments. The present study suggest that since Bt did not prevent parasitoid development, a combine treatment with Bt and parasitoid release, would produce better protection against *P. interpunctella* than either treatments when used singly.

POSTER PRESENTATION

Studies on the susceptibility of Colorado potato beetle eggs (Coleoptera: Chrysomelidae) to Calypso and Diflubenzuron

Ghazaleh Mohitazar, Mohammad.H Safaralizadeh, Ali.A Pourmirza, Nouaddin Shayesteh

[1]Urmia university, Urmia, Iran, Islamic Republic of, [2]Islamic Azad University, Branch of Mahabad, Mahabad, Islamic Republic of Iran

Introduction: The Colorado potato beetle *Leptinotarsa decemlineata* (Say) is one of the important pest of potato throughout the world. Control of CPB is a challenge for crop-producers because of its overlapping generations. The pest has developed resistance almost to all conventional insecticides. Therefore to delay resistance manifestation to chemical agents control of this pest warranted application of new class of control methods. At peresnt time the majority of control measure are forced on larval stage. At this research the susceptibility of eggs of CPB to Calypso and Diflubenzuron was determined.

Methods: Experimental design was CRD with 6 treatments and 3 replications. Bioassays were conducted with dipping and leaf disk methods. Percentage mortality was recorded 5 days initiation of trials and result were analyzed using probit procedur of SPSS software.

Results: The percentage of unhatched eggs showed significant difference between the chemicals. The maximum mortality rate was observed for Calypso and Diflubenzuron with 1.2 and 5600 ppm respectively. Based on the collected data LC_{50} values and confidence limits were 0.59(0.8021 – 0.4728) and 1491.05(1722.756 – 1269.191) ppm respectively.

Conclusions: The results revealed that Calypso have formidable effects on suppression of CPB eggs hatch.

POSTER PRESENTATION

Evaluation the level of resistance to diflubenzuron in house flies (*Musca domestica* L.) from different areas in Antalya, Turkey

Huseyin Cetin[1], Fedai Erler[2], Atila Yanikoglu[1]

[1]Akdeniz University, Department of Biology, Antalya, Turkey, [2]Akdeniz University, Department of Plant Protection, Antalya, Turkey

Introduction: The house fly, *Musca domestica* L. is a well-known cosmopolitan pest of both farm and home. This species is always found in association with humans or activities of humans and it is an important vector in transmitting various bacterial, viral and protozoal infections. Because of its importance as a public health pest, many insecticides have been used by man directly or indirectly in the control of *M. domestica*.

Methods: Field strains of *M. domestica* were collected between June 2006 and June 2007 from Antalya province, southwest of Turkey (Serik, Kumluca, Manavgat and Center). In the feeding tests, diflubenzuron was applied to larval breeding jars. Twenty grams of medium were put in a jar, and then 2.5 ml of water containing diflubenzuron or water alone was added and mixed into the medium. First instar larvae of the test species, 0–6 h old, were used in the assays. Four replicates of twenty-five larvae were used for each concentration level. The number of emerging flies was recorded during the 3 week-test period. The resistance ratios determined by comparing LC_{50} values of of the test populations and sensitive strain of SRS/WHO were compared.

Results: The resistance ratios ranged from 0,1 to 11.8 in test period (June 2006-June 2007). The highest ratios were determined in the Kumluca populations (4.7-11.8).

Conclusions: As the levels of insecticide resistance continue to increase, it is more important monitoring of resistance for effectively control of housefly populations.

POSTER PRESENTATION

Taxonomy, phylogeny and distribution of *Necrophila* sensu lato (Coleoptera: Silphidae) from south-eastern Asia

Jan Ruzicka

Czech University of Life Sciences, Prague, Czech Republic

Introduction: Eastern Palaearctic and Oriental carrion beetles of the subfamily Silphinae are only poorly known. Their taxonomy was strongly influences by the work of G. Portevin (papers published 1903-1943), and is in a need of recent revision. Taxonomy and species diversity of *Necrophila* Kirby et Spence sensu lato in south-eastern Asia is revised here.

Methods: External morphology characters of the adults are used for cladistic analysis. Distribution was tracked from museum specimens and recently collected material.

Results: The preliminary results present phylogenetic analysis of the following taxa (treated as separate genera or as subgenera of *Necrophila* by different recent authors): *Calosilpha* Portevin, *Chrysosilpha* Portevin, *Deutosilpha* Portevin and *Eusilpha* Semenov-Tian-Shanskiy. In total, 14 valid species/subspecies from this region are reported, and their distributional pattern is summarized.

POSTER PRESENTATION

Impact of herbivory by the mite, *Orthogalumna terebrantis* (Acarina: Galumnidae) on water hyacinth (*Eichhornia crassipes*) growth parameters and leaf chlorophyll content

Danica Lukac[1], Marcus Byrne[2], Martin Hill[1]

[1]*Department of Zoology and Entomology, Rhodes University, Grahamstown, South Africa,* [2]*School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, Johannesburg, South Africa*

Introduction: *Orthogalumna terebrantis* is a biological control agent of water hyacinth. Very little is known about its impact on the growth of the plant. Here we determined what numbers of mites per plant are needed to cause significant damage to the plants and how mite herbivory on the plants was affected by the nutrient status of the water in which plants were grown.

Methods: 1) Density trial – mites were placed onto plants at four different densities (120, 80, 40 and 0 mites per plant). 2) Nutrient trial – plants were grown at three different nutrient concentrations (high, medium and low) and 100 mites were placed onto each plant. Plant growth parameters (*i.e.* wet weight, number of leaves, number of ramets, petiole lengths, root length and plant turn-over rate) were measured weekly on each plant for both trials. Leaf surface area damaged by mite galleries was recorded. Additionally, the chlorophyll content of leaves was measured in the nutrient trial.

Results: The density trial showed that the plant growth rate of certain parameters (*e.g.* wet weight) was slower at high mite densities, but not significantly. High mite densities did, however, cause significantly more damage to the leaf surface area than lower densities. It appears that mite herbivory reduces the photosynthetic ability of leaves.

Conclusion: Water hyacinth growth is not impacted negatively at the mite densities used in this experiment, however, damage to the leaf surface area caused by mite herbivory increases as mite numbers increase. Mite herbivory, at the populations tested here, does not have significant impacts on plant growth. Under high nutrient conditions, the mites are less effective against the plant.

POSTER PRESENTATION

Field Efficacy of *Melia azedarach* L. Fruit Extracts on the Survival of *Ommatissus lybicus* DeBerg.(Homoptera : Tropiduchidae).

Hussain F. M.Ali[2], Ahmed .Al-Dhamin[1], Mohammed Al-Rawy[1]

[1]Univ. of Baghdad, College of Science, Dept. of Biology, Jadhrya, Baghdad, Baghdad, Iraq,
[2]Ministry of Sci. & Tech., IPC Res.Ctr., P.O.Box 765, Baghdad, Iraq

Introduction: Dubas bug *Ommatissus lybicus* DeBerg. is consider the most serious insect pest of date palms in North Africa and the Near East.). In Iraq and since the thirties, the only control method used is spraying synthetic chemical insecticides . Presently, botanical insecticides offer a promising alternative to synthetic insecticides . In this article, we investigate the effects of *M. azedarach* fruit crude extracts on the survival of the dubas bug, *Ommatissus lybicus* infesting date palm offsets under field conditions.

Methods: Ripe fruits of *M. azedarach*, of Baghdad origin were used for preparing water and organic (hexane followed by methanol)crud extracts using Soxhelt extracts. Bioefficacy of different concentrations of extracts as well as two commercial insecticides were tested on naturally infested offsets with eggs and nymph instars (1^{st}, 3^{rd} and 5^{th}).

Results: A negative correlation between egg hatchability and increase in any extract type concentrations were depicted. The results also showed the death of first nymphal instar hatched from eggs treated with alcoholic extract. Treated first nymphal instar, fed on the leaflet was found to be more susceptible than older instars at both generations. Mortalities were directly correlated with concentrations, regardless the type of crude extract used. In general it was found that methanol extract was more effective, followed by hexane. Meanwhile, synthetic insecticides used showed the highest efficacies.

Conclusions: the results obtained clearly indicated the feasibility of integrating crude extracts of *M. azedarach* fruit in the control programme of dubas bug, *Ommatissus lybicus*.

POSTER PRESENTATION

The sign stimulus for virgin queen execution in the stingless bee *Melipona beecheii*

Stefan Jarau[1], Johan W. van Veen[2], Ingrid Aguilar[2], Manfred Ayasse[1]

[1]Institute for Experimental Ecology, University of Ulm, Ulm, Germany, [2]Centre for Tropical Bee Research, National University, Heredia, Costa Rica

Introduction: Stingless bee colonies generally contain one physogastric- and several virgin queens, which are produced all year round and subsequently killed by the workers unless the old queen has to be replaced or a filial colony is founded. Nothing is known how workers recognize virgin queens in the nest, or which stimulus induces the execution behaviour. We studied this question in *Melipona beecheii*.

Methods: We observed the interactions between virgin queens and workers in small orphan observation boxes containing one brood comb and about 30 adult bees. To investigate the potential role of chemical- and behavioural stimuli emitted by virgin queens we conducted (i) experiments with small cages containing living individuals of either caste, and (ii) bioassays with attacked virgin queens, which we killed (2min at –82°C) and subsequently put back on the comb.

Results: Virgins were only attacked when they quickly moved inside the observation boxes. The workers' aggression significantly decreased (Wilcoxon signed-ranks test, P=0.008, N=9) from 15.0 (median) to 0.0 attacks per 10min before and after a virgin queen was killed by freezing, respectively. The workers' behaviour towards an empty cage or a cage with another worker or a virgin queen inside was the same. Neither the number nor the duration of contacts with these cages differed significantly (one-way ANOVA, P>0.05, N=12).

Conclusions: Our results show that workers only attack virgin queens when they are alive and actively moving. We conclude that the sign stimulus for queen execution is the queens' behaviour rather than a specific chemical cue.

POSTER PRESENTATION

Bio-ecological comparative studies of greenhouse whitefly, *Trialeurodes vaporariorum* (Westwood) (Homoptera: Aleyrodidae) on cucumber and tomato

Shadi Movasaghi, Mehdi Zarabi, Neda Asemany, Bahare Salehi

University of Tehran, Tehran, Islamic Republic of Iran

Introduction: Greenhouse whitefly, *Trialeurodes vaporariorum* (Westwood), is a major pest of greenhouse crops. This study was conducted to investigate some bio-ecological aspects of pest on two glasshouse crops, cucumber and tomato.

Methods: In this study, a 24-h old pair released in plant cages with 4-leaves tomato and 2-leaves cucumber separately (in 15 replicates) in controlled conditions (25±2^{o}C, 60±5% RH and L-D: 16-8) and then related data about all developmental stages and population densities collected daily.

Results: Results showed no significant difference between longevity of immature forms (egg, 1-3rd larval stages, pre pupa and pupa) on hosts. Its life cycle duration was 25.6± 0.7 and 25.5± 0.5 on cucumber and tomato respectively which did not show significant differences. Population density results showed: 2.8± 0.5 and 4± 0.6 for eggs/female/day and 2.7± 0.5, 3.7±0.7; 2.3±0.7, 2±0.5; 2.2±0.5, 1.8±0.4; 2.2±0.6, 1.6±0.2 for (1-4th) larval stages, pre pupa, pupa and adults densities/day on cucumber and tomato respectively. All densities did not show significant differences but death rate of adults was 50% and 28% for population on tomato and cucumber respectively. There found no pupal death in the population of cucumber but it showed the average of 11% in tomato. The new generation sex ratio was 85.5% and 80% in the population of cucumber and tomato respectively. There was no significant difference between males and females densities on hosts but, the female's density was 59.6% on cucumber and 40.4% on tomato.

Conclusions: Lower death rate of adults and higher female's density in the colony of pest on cucumber indicate that this crop is a better host for continuing pest generations. Thus the pest's population will increase highly on cucumber in compare with tomato.

POSTER PRESENTATION

The novel function of apolipophorin-III in *Hyphantria cunea*

Hong Ja Kim[1], Young Jin Kang[2], Yong Min Kwon[1], Yong Il Kim[1], In Hee Lee[3], Byung Rae Jin[4], Yeon Soo Han[5], Hyang Mi Cheon[6], Sook Jae Seo[1]

[1]Gyeongsang National University, Jinju, Gyeongnam, [2]Yeungnam University, Daegu, [3]Hoseo University, Asan, Chungnam, [4]Dong-A University, Busan, [5]Chonnam National University, Gwangju, [6]Korea Forest Research Institute, Jinju, Gyeongnam, Republic of Korea

Introduction: Apolipophorin-III (apoLp-III) is a hemolymph protein whose function is to facilitate lipid transport in an aqueous medium in insects. Recently, apolipophorin-III in *Galleria mellonella* and *Hyphantria cunea* was shown to play an unexpected role in insect immune activation. We show here a novel possible function/role of the apoLp-III in insects.

Methods: To investigate the genes which have a relationship with apoLp-III in fall webworm larvae, we reduced endogenous *Hc* apoLp-III mRNA levels in larvae via RNA interference (RNAi). We performed DD-PCR to identify down-regulated genes during the knock-down of *Hc* apoLp-III cDNA. DNA fragmentation from the fat body cells, with or without RNAi, was assayed using an Apoptotic DNA-Ladder Kit. Visualization and localization of apoLp-III, antioxidants and ROS (or apoptosis) in the three tissues were performed using a confocal microscope.

Results: We cloned and sequenced a total of 179 cDNAs which disappeared or decreased by *Hc* apoLp-III knockdown. The RNAi-mediated *Hc* apoLp-III reduction resulted in the reduction of antioxidants, like MnSOD, catalase, and glutathione S transferase as well as immune proteins. In particular, expression of MnSOD commonly decreased in fat body, midgut, and hemocytes following the knockdown of *Hc* apoLp-III, which induced an elevated level of superoxide anion in *Hyphantria cunea* larvae.

Conclusions: The observed effect of *Hc* apoLp- RNAi suggests that *Hc* apoLp- is related to the action/expression of antioxidants.

POSTER PRESENTATION

The novel function of apolipophorin-III in *Hyphantria cunea*

Hong Ja Kim[1], Young Jin Kang[2], Yong Min Kwon[1], Yong Il Kim[1], In Hee Lee[3], Byung Rae Jin[4], Yeon Soo Han[5], Hyang Mi Cheon[6], Sook Jae Seo[1]

[1]Gyeongsang National University, Jinju, Gyeongnam, [2]Yeungnam University, Daegu, [3]Hoseo University, Asan, Chungnam, [4]Dong-A University, Busan, [5]Chonnam National University, Gwangju, [6]Korea Forest Research Institute, Jinju, Gyeongnam, Republic of Korea

Introduction: Apolipophorin-III (apoLp-III) is a hemolymph protein whose function is to facilitate lipid transport in an aqueous medium in insects. Recently, apolipophorin-III in *Galleria mellonella* and *Hyphantria cunea* was shown to play an unexpected role in insect immune activation. We show here a novel possible function/role of the apoLp-III in insects.

Methods: To investigate the genes which have a relationship with apoLp-III in fall webworm larvae, we reduced endogenous *Hc* apoLp-III mRNA levels in larvae via RNA interference (RNAi). We performed DD-PCR to identify down-regulated genes during the knock-down of *Hc* apoLp-III cDNA. DNA fragmentation from the fat body cells, with or without RNAi, was assayed using an Apoptotic DNA-Ladder Kit. Visualization and localization of apoLp-III, antioxidants and ROS (or apoptosis) in the three tissues were performed using a confocal microscope.

Results: We cloned and sequenced a total of 179 cDNAs which disappeared or decreased by *Hc* apoLp-III knockdown. The RNAi-mediated *Hc* apoLp-III reduction resulted in the reduction of antioxidants, like MnSOD, catalase, and glutathione S transferase as well as immune proteins. In particular, expression of MnSOD commonly decreased in fat body, midgut, and hemocytes following the knockdown of *Hc* apoLp-III, which induced an elevated level of superoxide anion in *Hyphantria cunea* larvae.

Conclusions: The observed effect of *Hc* apoLp- RNAi suggests that *Hc* apoLp- is related to the action/expression of antioxidants.

POSTER PRESENTATION

Characterization of hemocyte STAT gene in *Hyphantria cunea*

Hong Ja Kim[1], Young Jin Kang[2], Yong Min Kwon[1], Yong Il Kim[1], In Hee Lee[3], Byung Rae Jin[4], Yeon Soo Han[5], Hyang Mi Cheon[6], Sook Jae Seo[1]

[1]Gyeongsang National University, Jinju, Gyeongnam, [2]Yeungnam University, Daegu, [3]Hoseo University, Asan, [4]Dong-A University, Busan, [5]Chonnam National University, Gwangju, [6]Korea Forest Research Institute, Jinju, Gyeongnam, Republic of Korea

Introduction: Innate immunity responses are triggered by the immune challenge and therefore involve signaling processes. The cellular response is initiated by hemocytes and mainly involves phagocytosis and encapsulation of intruders by these cells. First report about the lepidopteran hemocytic STAT is discussed in regard to its induction and translocation into nucleus in hemocyte upon bacterial and fungal challenge.

Methods: The mRNA expression level of Hc-STAT at the embryonic, larval, pupal, and adult stages was analyzed by RT-PCR. Last instar larvae were injected with *E. coli, E. faecalis, C, albican* and total RNA was extracted from various organs at 12 h post-injection of bacteria and fungi for RT-PCR. We next investigated whether Hc-STAT can bind STAT binding motif using EMSA. To address whether Hc-STAT is activated upon bacterial challenge, we examined the subcellular location of STAT protein in hemocyte by immunostaining.

Results: A new insect member of the STAT family of transcription factors (Hc-STAT) has been cloned from the lepidopteran, *Hyphantria cunea*. The domain involved in DNA interaction and the SH2 domain are well conserved. The gene is transcribed at a low level during all stages of development, and the protein is present in hemocytes, fat body, midgut, epidermis, and Malphigian tuble. Especially, the organs showed transcriptional activation of Hc-STAT upon Gram (-) bacteria and fungal challenge. Gram (-) bacteria and fungal challenge specifically results in nuclear translocation of Hc-STAT protein and induction of DNA-binding activity that recognizes a STAT target site in *H. cunea* hemocyte. *In vitro* treatment with pervanadate translocates Hc-STAT to the nucleus in hemocyte cells.

Conclusions: Here we report the first evidence for the involvement hemocyte JAK/STAT pathway upon microbial infection in lepidopteran insect.

POSTER PRESENTATION

Comparative analysis of two attacin genes from *Hyphantria cunea*

Yong Min Kwon[1], Young Jin Kang[2], Hong Ja Kim[1], Yong Il Kim[1], In Hee Lee[3], Byung Rae Jin[4], Yeon Soo Han[5], Hyang Mi Cheon[6], Nam Gyu Ha[7], Sook Jae Seo[1]

[1]Gyeongsang National University, Jinju, Gyeongnam, [2]Yeungnam University, Daegu, [3]Hoseo University, Asan, Chungnam, [4]Dong-A University, Busan, [5]Chonnam National University, Gwagju, [6]Korea Forest Research Institute, Jinju, Gyeongnam, [7]Gyeongnam Agricultural Research and Extension Services, Jinju, Gyeongnam, Republic of Korea

Introduction: In lepidopteran insects, attacin is one of the major antibacterial proteins secreted into the hemolymph upon infection with bacteria. We describe the characterization of cDNA clones for two types of attacin A and B from *H. cunea*.

Methods: To investigate the biological activity of *H. cunea* attacin, two attacin cDNAs were introduced into a baculovirus expression system and purified using HisTrap and HiTrap desalting columns. Antimicrobial activity of two attacins was determined by a radial diffusion assay. The induction of two attacins against various kinds of microorganism was investigated by Northern blot.

Results: The two attacin cDNAs encode precursor proteins of 233 and 248 amino acid residues, respectively, and 45.9% identity at the amino acid level. Attacin B is a typical glycine-rich protein (13.8%), while attacin A is leucin-rich (13.4%). Attacin B is expressed from last instar larvae to adult, while attacin A showed stage-specific expression during the prepupal and pupal stages. Attacin A and B showed similar hydrophilicity patterns while both proteins showed different secondary structures. Attacin A shows no induction in infected larvae, while attacin B is strongly induced against Gram-positive and -negative bacteria, fungi, and viruse. Recombinant attacin A showed no antibacterial activity, while recombinant attacin B showed strong antibacterial activity in proportion to the amount of the protein applied.

Conclusions: Hyphantria attacin A and B showed low identity (49.9%) each other, different amino acid composition, and different secondary structures. Our work focused the characterization of attacin A and B in which they showed stage-specific expression and different induction activity against various microorganisms.

POSTER PRESENTATION

Life table and age-dependant reproduction of *Chrysoperla carnea* on eggs of *Ephestia kuehniella* and *Helicoverpa armigera* under laboratory conditions

Mehdi Hassanpour, Gadir Nouri-Ganbalani, Jafar Mohaghegh, Shahzad Iranipour

[1]University of Tabriz, Tabriz, [2]University of Mohaghegh Ardabili, Ardabil, [3]Irainan Research Institute of Plant Protection, Tehran, Islamic Republic of Iran

Introduction: *Chrysoperla carnea* is a widely distributed predator of soft-bodied arthropods throughout the world. Due to the importance of this predator in biocontrol programs, life table studies of this predator on different preys give the most comprehensive description of the survivorship, development, and reproduction of the predator.

Methods: Life table of *C. carnea* were studied on eggs of *Ephestia kuehniella* and *Helicoverpa armigera* at 26±1℃, a photoperiod of 16:8 (L:D) h and 70±5% RH. Newly emerged larvae of predator were reared singly with an ample supply of eggs of both prey separately (n=100). When adults emerged, the females and males were paired in a plastic cup (400 ml) with screen top and were fed on artificial diet and distilled water. The fecundity and survival were recorded daily until all of females were dead.

Results: The intrinsic rates of increase (r_m) on two prey were 0.1816 and 0.2238 female/female/day respectively. Net reproduction rates (R_0), finite rate of increase (λ), intrinsic birth (b) and death (d) rates, doubling time (DT) and mean generation time (T) of the predator feeding on two prey were 352.6777 and 579.78424 (female /female), 1.1991 and 1.2508 (day^{-1}), 0.1823 and 0.2271 (day^{-1}), 0.0007 and 0.0033 (day^{-1}), 3.8176 and 3.0974 (days), and 32.2728 and 28.4185 (days), respectively.

Conclusion: The higher values of r_m, R_0, and λ and shorter T and DT were achieved with rearing predator on eggs of *H. armigera.* This result revealed that the egg of *H. armigera* is a suitable prey for *C. carnea* than that of *E. kuehniella*.

POSTER PRESENTATION

Toxicity appraisement of Methaldehyde, Biopesticide, repellent bands and repellent colors against the land snails, X*eropicta derbentina*, *Xeropicta krynickii* (Stylommatophora: Hygromiidae)

Behnam Amiri-Besheli, Fatemeh Asgharnejad

Faculty of Agric. Univ. of Mazandaran, Sari, Islamic Republic of Iran

Different methods have been applied to control the land snail (*Xeropicta derbentina*) and (*Xeropicta krynickii*) but the chemical are realized to be the best and effective methods to control this pest. The main goal of this work was to determine the efficacy of Methaldehyde، Biological toxin, repellent band and repellent color on this pest. Methaldehyde, Biological toxin were used as bait around citrus trees and repellent band and repellent color rolled up around main stem of the citrus trees. The live snails on citrus trees were monitored at 2, 15, 29, 36, 68 and 98 days after treatments. Analysis of variance showed that there were significant differences between treatments and control, and also significant differences were found among treatments ($p<0.01$). LSD & Tukay-Test among above treatments has shown that repellent band and Methaldehyde with 5± 1.3 and 10.6± 0.9 percentage of the alive snail on trees were more effective than repellent color and Biological toxin with 14.2 ± 2.6 and 31.3±3.9 percentage alive snail on citrus trees and significant differences with control respectively. The control efficacies of the Methaldehyde and Biologic toxin were 91.87%, 82.63% respectively, also the control efficacies of the repellent band and the repellent color were 95.22% and 82.26 % respectively after 2, 15, 29, 36, 68 and 98 days of post treatment. Therefore the repellent band and methaldehyde were better than the other treatments for the management of land snail population.

POSTER PRESENTATION

Ixodid tick species infesting sheep and cattle in Kelardasht (Chloos), Iran

Mohamad Yossef Asnaashari, Mohamad Reza Yoeefi, Zohreh Saltanatpour, Afsaneh Amoei, Fatemeh Asgarian, Saeid Salehi

Mazandaran University, Sari, Islamic Republic of Iran

Introduction: Ticks are features which are of metastigmata order. All of these features are parasite of animals which only feed on them. Ticks and disease related, causes economical damages which in some case these damages reaches to million dollars each year. Because of the importance of recognition ticks, particularly Ixodidae,this research has been done on Ixodidae ticks on domestic animals at Kelardasht in Mazandaran Northern Iran.

Methods: The used method in this research it was cross-section and ticks were studied on, were collected samples,798numbers of them departed in genus and species and the rest were eliminated.

Conclusion: In this study 6 groups species. In *Ixodes* the only observed species was *ricinus*, in *Boophilus* only *anulatus* species, in *Dermacentor* only *marginatus* was identified. But in *Haemaphisalis* two different species were observed *punktata* and *inermis*. In *Hyalloma* and *Ripicephalus bursa* was observed. in these study samples the most percentages was seen in *Ixodes* (26.8%) and the minimum was in *Haemaphisalis* (0.2%).

POSTER PRESENTATION

Natural occurrence and characteristics of entomopathogenic fungi isolated from red palm weevil in Sicily (Italy)

Barbara Manachini[1], Stefano Colazza[2], Franco Palla[3]

[1]Department of Animal Biology, University of Palermo, Palermo, Italy, [2]Department of S.En.Fi.Mi.Zo., section of Entomology, Acarology and Zoology,University of Palermo, Palermo, Italy, [3]Molecular Biology Laboratory, Department of Botanical Sciences,University of Palermo, Palermo, Italy

Introduction: Originally from tropical Asia, the red palm weevil (*Rhynchophorus ferrugineus* (Olivier)) is the most dangerous and deadly pest of date, coconut, oil, sago and other palms. It has spread to Africa and Europe, reaching the Mediterranean in the 1980s, and was first recorded in Sicily (Italy) in 2005. Due to its recent introduction and the difficulty of its control, to known the natural pathogens of RPW in the introduced areas is very important.

Methods: Pupae from infested palms *Phoenix canariensis* Hort. were collected. The entomopathogenic fungi were isolated and growth. Because of it is possible to growth only the 1% of the known fungi, the identification of entomopathogens is done also using specific molecular markers (e.g. microsatellites and ITS) and microscopical analysis (SEM, CLSM).

Results and conclusion: This is the first report of a native fungal pathogen affecting the pupa of *R. ferrugineus* in Italy. About 30% of pupae collected in Palermo (Sicily) were infected with the entomopathogens. Symptoms of fungal infection included rapid pupal tissue atrophy and failure of adults to emerge, death. Dissections of infected pupae revealed dense hyphal growth inside pupae, thus suggesting fungal penetration and pathogenicity.

A GIS method for assessing different Malagasy migratory locust risks

Aurelia Decherf[1], Alex Franc[1], Tsito Andriamaroahina[2], Jean-François Duranton[1]

[1]CIRAD, Montpellier, France, [2]National Locust Centre (CNA), Tuléar, Madagascar

Introduction: The Malagasy migratory locust, *Locusta migratoria capito* (Saussure, 1884) is the most important agricultural pest in Madagascar. When solitary individuals group together, they become gregarious then causes swarm outbreaks. As rainfall discriminates annual locust population dynamics, by monitoring the eco-meteorological conditions, it is possible to locate and assess locust risk. A forecasting system is the main goal of the Malagasy National Locust Centre in running national preventive controls and establishing three levels of risk: local upsurge, major outbreak with phase transformation, and invasion.

Method: A Geographical Information System (GIS) had been created to delimit locust risks in a pilot study area (the Ejeda zone) 15% of the outbreak area (100 000 km²). This system combines first locust habitats, mapped using remote sensing data, along with rainfall data to evaluate ecological potential. Second, this ecological potential is compiled spatially in a database which includes locust data (density and phase) collected in the field. From this point, several levels of locust risk can be evaluated: 1) local upsurge risk; 2) phase transformation risk; and 3) invasion risk. These locust risks are evaluated and mapped monthly. Risk localisation can guide survey and control operations in the field to be quick and more efficient.

Results: The risk maps were validated for the pilot zone using archived data. A generalisation to the entire outbreak area is now in progress.

POSTER PRESENTATION

Citrus whitefly, *Dialeurodes citri* (Ashmead) (Homoptera: Aleyrodidae), life cycle and population fluctuation studies in Iran

Maede Kordrostami, Mehdi Zarabi, Mohamad Fazel Halaji Sani

University of Tehran, Tehran, Ministry of Jihad-Agril., Research and Teaching Organization, Citrus research Centre, Ramsar, Islamic Republic of Iran

Introduction: The citrus whitefly, *Dialeurodes citri* (Ashmead) is one of the most important pests of citrus plants in north regions of Iran. It has a high population density on citrus plants in greenhouses and gardens. In this study its life cycle and population fluctuation was studied on young Tompson Navel variety.

Methods: For this purpose five trees were selected randomly and ten leaves of each plant sampled every 3 days during early April until late December. The population of adults, nymphs and eggs evaluated on 4 ^{cm2} of these leaves area. Biological studies carried out with the field and incubation experiments by releasing one pair in leaf cages on young trees.

Results: Results showed that this pest has three generations which the early generation start at mid of May and complete its life cycle until late June. The second one observed from early August and the third one at mid of Sep. According to its population fluctuation, the nymphal density increase in early Sep. and the adult's density at June, July and October. The biological data showed that the longevity of egg, nymphs(three stages), pupa and adults was 10-13, 21-32, 10-12 and 12-15 days respectively in controlled condition (25±2^{ºC}, 75±5% RH and L-D:14-10). This data was near to fields experiments too.

Conclusions: It seems that the 2nd generation has the highest density and cause serious damage. Thus duration of its life cycle was near 65 days. Each female can oviposit up to 120 eggs in his life. The 3rd nymphal stage is the over wintering form of pest which remain on diapauses.

POSTER PRESENTATION

Changes in development of male germinal cells of Egyptian cotton leaf worm *Spodoptera littoralis* (Boisd) caused by selected compound with activity of insect hormones.

Ivan Gelbic

Biological Centre AS CR, Institute of Entomologz, Ceske Budejovice, Czech Republic

Introduction: The role of insects hormones in the process of reproduction is studied by many authors. Present paper deals with the effects of selected compounds with activity of insect hormones on the development and maturation of male germinal cells in *Spodoptera littoralis* (Boisd.).

Methods: Morphological and histological changes of testis caused by methoprene, 20-hydroxyecdysone, RH-2485 and RH-5992 were studied.

Results: Spermatogenesis begins early in the postembryonic development. Formation of spermatogonia occurs in larval instars 1-3. Meiotic division starts in instar4 and in the last larval instar all developmental stages of spermatozoa can be found. The first bundles of mature spermatozoa occurs in prepupae. In 5 day-old-pupa more than 90 % of the spermatozoa are mature. Application of juvenoids or ecdysterone caused some disorders in the development of spermatozoa. After application of different concentration of methoprene on the different developmental stages reduction of the reproductive ability of males was observed. This reduction is caused by numerous disorders in development of spermatozoa. Numerous pycnosis appear in spermatogonia, inhibition of spermatocytes and their gradual disintegration and disorders of spermateliosis take place. On the other hand, pathological changes were not found after application of 20-hydroxyecdysone or RH compounds and the spermateliosis started earlier in comparison with controls.

Conclusions: All compounds tested caused dose dependent changes in development and growth – prolongation of larval intermoult periods, formation of different larval pupal intermediates. Sterility of males was induced only by application of methoprene.

This work was supported by the grant GA CR 522/08/1407 of the Grant Agency of the Czech Republic and AV0Z50070508.

POSTER PRESENTATION

A phylogenetic study of the subtribe Dicrepidiina (Coleoptera: Elateridae: Elaterinae: Ampedini)

Sônia Casari

Museu de Zoologia da Universidade de São Paulo, São Paulo- SP, Brazil

Introduction: The subtribe Dicrepidiina is composed by 36 genera and about 1,520 species. The purpose of the present cladistic analysis is to test the monophyletism of the subtribe and to verify the relationships among the genera. All genera, except Asebis, Lamononia, Neopsephus, Semiotopsis and Spilomorphus were studied. For each genus at least the type-species was analysed**.**

Methods: Seventy eight characters of fifty two taxa were selected; multistate characters were used, always being treated as unordered. The analyses were conducted using the TNT program, based on 20000 random addition sequences with 2 trees save per replication. The swapping algorithm used was tree bisection reconnection (TBR). The characters were initially treated as unweighted. In a second analysis, they were weighted using successive weighting, and fits 5, 10, 15, 20, 25, 30, 40 and 50 were tested.

Results: The first analysis, using equally weighted characters produced 11 equally most-parsimonious trees. The second analysis was conducted after aplication of the sucessive weighting option according to the maximum value of the fitness. Using fit 5 resulted in four trees and fits from 10-50 produced one tree.

Conclusions: It was concluded that Ovipalpus Solier, 1851, does not belong to Dicrepidiina and even to Ampedini. It appears to be closely related to Prosternini (Prosterninae). The subtribe Dicrepidiina (excluding Ovipalpus) is monophyletic, defined especially by tarsomeres 2 and 3 lamellate. It is the sister group of Physorhinina. Besides, it is demonstrated that the genera Achrestus, Anoplischius, Dipropus and Propsephus are not monophyletic.

POSTER PRESENTATION

Biology of saprophagous hoverflies (Diptera, Syrphidae) and its role in degrading of pig slurry

Pilar Hurtado, Celeste Pérez-Bañón, Thomas Gladis, Berta Pastor, Santos Rojo

Instituto Universitario CIBIO. Universidad de Alicante, Alicante, Spain

Introduction: One of the most important trophic habits of syrphid larvae is the saprophagy. In fact, some species are very common in the huge volume of pig manure derived from intensive production model in Spain. We will analyze several aspects of larvae and adult biology including mass-rearing production.

Methods: Adults and larvae were collected in pig farms. Larval stages were reared in the laboratory with different media as pig slurry, oat with water and barley with water, in order to know the best media for their development. Mass-rearing included also, permanent adult colonies under controlled conditions. Different types of pollen, sugar and water were used to mature adults. Biotic interactions with parasitoids were also studied.

Results: The most common syrphid species in pig farms was *Eristalis tenax*. This species can develop its larval cycle on pig slurry. Artificial media based on oat or wheat can be used satisfactory. Four species of eristalines can be artificially reared with this technology. These results have been applied in the frame of ECODIPTERA project (LIFE-environment EU project).

Conclusions: Mass rearing of saprophagous hoverflies is possible. This fact let us use these insects as biodegrading agents or pollinators.

POSTER PRESENTATION

Is the diversity of jumping-spider mimicry in micromoths driven by jumping spider's diversity?

Mu-Yung Wang, Shen-Horn Yen

Department of Biological Sciences, National Sun Yat-Sen University, Kaohsiung, Taiwan

Biological mimicry comprises a wide range of relationships among predators and preys. If the predator is mimicked by the prey and perceptionally confused by the signals exhibited by the prey, the mimicry scenario is called "predator mimicry". It has been proved that several phylogenetically distant clades of microlepidoptera, that demonstrate distinct wing patterns and wing display behaviours, participate in this peculiar mimicry system with jumping spiders (Salticidae), and several types of visual signal, e.g. UV and fluorescence, may play important roles in promoting the mimicry. In the present study, we aim to answer the following questions using multiple approaches: (1) Do different types (and combinations) of wing patterns and display behaviours micromoths create discrete effects on this putative mimicry? (2) Is there any key feature in moths' colour pattern that promotes mimicry, which can be referred to the so-called "imperfect mimicry"? (3) If there is discrete effectiveness between different wing pattern and display behaviours, is the diversity of moths' mimetic pattern correlated with spider's diversity in responding moth's behaviour? and (4) if any moth clade that exhibits specific type of jumping spider-mimicking wing pattern has greater species richness due to the relative success in defending jumping spiders in respect to its sistergroup that does not own the colour patterns and photonic features? The results of the present study are expected to explore the unresolved mystery of this peculiar mimicry system and contribute to both behavioural and evolutionary ecology of this phenomenon which is commonly seen but being ignored for long.

POSTER PRESENTATION

Did the model obtain mimetic colouration earlier than the mimics? A preliminary analysis using the mimicry complex displaying the "*Euploea mulciber*" syndrome as a case study

Chia-Hsuan Wei[1], Li-Wei Wu[2], Yu-Feng Hsu[2], Shen-Horn Yen[1]

[1]National Sun Yat-Sen University, Kaohsiung, Taiwan, [2]National Taiwan Normal University, Taipei, Taiwan

Defensive mimicry among organisms has attracted attention from biologists for centuries and has been investigated in various areas such as psychology, ethology, visual ecology, genetics and development. In the general prediction, the model, which displays stronger secondary defence and aposematism, is expected to have evolved earlier than the co-mimic species. The less protected species, which are usually called mimics, may have participated in the mimicry sequentially. Previous studies have shown the evolutionary trend of formation of a particular mimetic syndrome within a single evolutionary lineage, but the evolutionary dynamics among multiple independent lineages that involve in one co-mimicry system has never been investigated. In the present study we focus on a mimicry complex, of which the species involved all demonstrate the sexually dimorphic "*Euploea mulciber*" syndrome. At least seven lepidopteran genera belonging to the Nymphalidae, Papilionidae and Zygaenidae and predominantly distributed in Sundaland and Indochina have been found to involve in the mimicry complex. We first inferred the individual phylogenies of the *Euploea mulciber* complex and the *Papilio* subgenus *Chilasa* based on multiple gene sequence information, and then estimated the divergence time of the lineages that are sympatric in distribution and participate in the mimicry complex. We wish to use this preliminary study case to address two questions: (1) if the putative model, which is always considered more unpalatable and abundant, has evolved earlier than the palatable mimics? and (2) if diversification of the model and mimic lineage has been driven by one of each or each other.

POSTER PRESENTATION

Use of infochemicals to attract burying beetles (Coleoptera: Silphidae) into pitfall traps

Hana Podskalska[1], Jan Ruzicka[1], Michal Hoskovec[2]

[1]Czech University of Life Sciences, Prague, Czech Republic, [2]Institute of Organic Chemistry and Biochemistry, Prague, Czech Republic

Introduction: Our team is focused on ethological and chemo-ecological research of burying beetles (Silphidae: Nicrophorinae), which are attracted by small vertebrate carrion, and are well-known for their biparental care.

Methods: In previous study, we identified the following volatile substances (infochemicals) from small vertebrate carcass using 2D-GC/MS-TOF method: methanethiol (MSH), dimethylsulfide (DMS), dimethyldisulfide (DMDS), dimethyltrisulfide (DMTS) and methylthiolacetate (MTA). Three of these infochemicals were tested in a field (220 baited pitfall traps with DMTS or blank, combined with DMS or DMDS).

Results: In a field experiment in southern Bohemia (Czech Republic) we collected a total of 362 adults of *Nicrophorus vespillo* (Linnaeus). We conclude that DMTS attracts burying beetles form a long distance, and for short distance DMDS has proven to be significantly more effective than the more volatile DMS molecules. DMTS volatility is low, compared to DMDS and DMS.

POSTER PRESENTATION

Pesticide-induced metabolism in *Caenorhabditis elegans*

Samantha Broad[2], Anthony Flemming[1], Peter Urwin[2]

[1]Syngenta, Berkshire, United Kingdom, [2]University of Leeds, Leeds, United Kingdom

We are interested in the inducible metabolic defences of organisms to applied chemicals. We used the nematode *C. elegans* to uncover genes up-regulated in response to pesticides and other toxic compounds. We identified using microarrays a number of such genes including members of classes known to be involved in xenobiotic chemical metabolism (Cytochrome P450s, Glutathione S transferases etc). Many of these genes were specific to chemical stress, though some were also induced by other forms of stress (osmotic and thermal). Strikingly we found that different compounds often induced different metabolic genes. In some cases the genes induced by one compound were almost entirely mutually exclusive to those induced by another. This implies a complex regulatory process, allowing specific metabolic responses to specific chemicals. Thus far only one regulator of metabolic gene expression has been demonstrated in *C. elegans*, the conserved nuclear hormone receptor NHR-8. Our data suggest that inducible metabolism is more complex than an all-or-nothing-response mediated by a single 'switch' and so additional regulators, acting in parallel or downstream of NHR-8 are likely to exist. Understanding how metabolism is regulated in *C. elegans* will allow us to ask framed questions about how it is regulated in pests. This, in turn, can be used for a variety of applications: to better understand metabolic field resistance to pesticides, to design small molecule pesticides that 'avoid' pest metabolism, or to discover chemical synergists that target metabolism directly.

POSTER PRESENTATION

Understanding and improving the residual efficacy of the *Cryptophlebia leucotreta* granulovirus

Wayne Kirkman, Sean Moore

Citrus Research International, Port Elizabeth, South Africa

Introduction: False codling moth (FCM), *Thaumatotibia* (=*Cryptophlebia*) *leucotreta* (Meyr) (Lepidoptera: Tortricidae), is one of the most important pests on citrus. The *Cryptophlebia leucotreta* granulovirus (CrleGV) has been developed into a successful biological control agent, registered as Cryptogran for the control of FCM on citrus in South Africa. A study was conducted to investigate biotic and abiotic factors affecting field persistence of the virus, and how to improve it.

Methods: Laboratory bioassays were conducted to determine the effect of UV-irradiation on the virus. Various products were tested as UV protectants for the virus, both in laboratory bioassays and in orchard trials. Laboratory trials were conducted to determine rainfastness of Cryptogran. The effect of the timing of applications was determined in orchard trials. The effect of the navel end of a navel orange on the efficacy of the virus was also investigated.

Results: The addition of lignin improved FCM control by up to 93%, although results were variable. Cryptogran was shown to be rainfast. Cryptogran applied early in the season was effective for up to 16 weeks compared to 6 weeks for sprays applied closer to harvest. Daytime applications were less effective than evening sprays. Sprays applied coinciding with peaks in pheromone moth trap catches were more effective than those applied between peaks. Control lasted for 17 weeks where treatments were applied to blocks as opposed to 8 weeks for single tree treatments.

Conclusion: Lignin enhanced the activity of the virus, but results were variable and the lignin product is expensive. Timing of applications and the use of effective application equipment are more important than the addition of UV-protectants.

POSTER PRESENTATION

Analysis and functional annotation of 15,000 expressed sequence tags from the gut of European corn borer (*Ostrinia nubilalis* Hübner) larvae.

Chitvan Khajuria[1], Yu Cheng Zhu[2], Ming Shun Chen[1], Lawrent L. Buschman[1], Muthukrishnan Subbaratnam[1], Kun Yan Zhu[1]

[1]Kansas State University, Manhattan, KS, United States, [2]USDA-ARS-JWDSRC, Stoneville, MS, United States

Introduction: The European corn borer (ECB) is an important lepidopteran pest of corn in the United States. Large sets of expressed sequence tags (ESTs) were sequenced from the gut of the ECB larvae. The identification of these genes will allow a better understanding of the mechanisms of Bt toxicity/ Bt resistance in insects.

Methods: A cDNA library was constructed using ZAP-cDNA synthesis kit and ZAP-cDNA Gigapack III gold cloning kit (Stratagene). Recombinant plasmid DNA was isolated with Qiagen Bio Robot- 3000 and sequenced using an ABI 3700 DNA analyzer. ESTs were analyzed using online softwares EG assembler and Blast2go.

Results: A total of 15,000 random clones were sequenced from the cDNA library constructed from the gut of ECB larvae. These sequences were assembled into 4,451 unique sequences, including 2,787 singletons and 1,664 contigs. Among these sequences, 78% encoded for putative proteins which shared significant sequence similarity with known sequences in GenBank with E-values ≤ 10^{-5}. These sequences include genes encoding various digestive enzymes such as chymotrypsin-like proteases, trypsin like-proteases, elastases, cysteine proteases, carboxypeptidases, and aminopeptidases. These putative proteins were further analyzed and sorted into different categories of molecular functions, biological processes and cellular components.

Conclusions: Our EST analysis has putatively identified many different genes expressed in the digestive system of ECB. These results provide foundation to use microarray technology for analyzing the global changes of gene expression in response to Bt protoxins/toxins between Bt-resistant and -susceptible strains of ECB.

POSTER PRESENTATION

Molecular mechanisms of proximodistal patterning during leg regeneration in the cricket, *Gryllus bimaculatus*

Taro Nakamura[1], Taro Mito[1], Tetsuya Bando[2], Ohuchi Hideyo[1], Sumihare Noji[1]

[1]Department of life system, Institute of Technology and Science, The Univ. of Tokushima, Tokushima City, Japan, [2]Tokushima Intellectual Cluster, The Univ. of Tokushima, Tokushima City, Japan

Introduction: Nymphs of hemimetabolous insects such as cockroaches and crickets possess functional legs with a remarkable capacity for regenerating epimorphically. To elucidate the mechanism of leg regeneration, we have focused on the role of *Distal-less* (*Dll*), *Epidermal growth factor receptor* (*Egfr*), and *dachshund* (*dac*), which are involved in subdivision of the leg disc along the proximal-distal (PD) axis in *Drosophila* leg development.

Methods: For loss-of-function analyses of these genes, we injected double-stranded RNA of *Gb'Egfr*, *Gb'Dll*, and *Gb'dac* in the third instar nymph and then amputated a leg at the distal or proximal tibia.

Results: We found the followings: (1) EGFR signaling are involved in re-patterning of the most distal region, the third tarsal segment and pretarsus, through the regulation of *Gb'aristaless* (*al*) and *Gb'dac* with a gradient of activity; (2) *Gb'dac* controls the tibial length and re-patterning of proximal tarsus, through the functional relationship between *Gb'Dll* and *Gb'dac*, and also act as a leg gap gene; and (3) *Gb'Dll* activity is not required for regeneration of the tibia, while in the distal blastema, high activity of *Gb'Dll* is required for re-patterning of tarsal and pretarsal segments through repression of *Gb'dac* expression and regulation of *Gb'al* and *Gb'BarH*.

Conclusions: These results suggest that EGFR signaling and Dll activity are used for providing positional information along the PD axis in the distal leg patterning in insects regardless of the mode of leg formation (leg development and regeneration).

POSTER PRESENTATION

Investigation on developmental stages and host range of *Clitostethus arcuatus* (Coleoptera: Coccinellidae)

Mehdi Zarabi[1], Maryam Yazdani[1], Abas Yazdani[2]

[1]Unive of Tehran, Tehran, Islamic Republic of Iran, [2]Plant Protection offices, Organization of Jihad- Agril., Kerman, Islamic Republic of Iran

Introduction: *Clitostethus arcuatus*, has recorded as whitefly predator in Mediterranean, Russia, North African, Asia minor, Europe and Iran. This research was carried out to study its life cycle and host range in Iran.

Methods: Newly emerged ladybirds collected from ash whiteflies colonies in early spring then reared in controlled conditions (25±2ºC, 65±5% RH and L-D: 16-8). They fed daily with different life stages of Ash whitefly and related data collected daily. In the other hand, its host rang was evaluated by random sampling of ladybirds from whiteflies host plants throughout of central parts of country (Kerman province).

Results: Results showed that, mean of longevity of egg, 1-4th larvae, pupa, female and male were 3/5±0/93, 3/5±0/53, 4/63±0/92, 5/38±1/41, 10/75±1/16, 4/5±0/53, 77/3±6/9 and 67/5±7/2 days respectively. Consequently, it has 4 generations annually that the entire life cycle from egg to adult takes an average of 32/9±3/11days. Adults remain in diapauses for 5 months in the last generation. 2nd and 3rd generations fall on aestivation in hot summer. Females laid an average of 3/89±1/76 eggs/day. Host range studies showed that the matured adults appeared in late May on Ash Whitefly, *Siphoninus phillyreae* but its larval stages were found on another whitefly colony, *Bulgariodes cotessii*. Also in late June they are seen on pomegranate trees too.

Conclusions: This predator can control all life stages of Ash whitefly on different hosts specially the Ash and pomegranate trees. In addition the *Bulgariodes cotessii* is a suitable host for predator in absent of main prey, Ash whitefly.

POSTER PRESENTATION

Investigation on developmental stages and host range of *Clitostethus arcuatus* (Coleoptera: Coccinellidae)

Mehdi Zarabi[1], Maryam Yazdani[1], Abas Yazdani[2]

[1]Unive of Tehran, Tehran, Islamic Republic of Iran, [2]Plant Protection offices, Organization of Jihad- Agril., Kerman, Islamic Republic of Iran

Introduction: *Clitostethus arcuatus*, has recorded as whitefly predator in Mediterranean, Russia, North African, Asia minor, Europe and Iran. This research was carried out to study its life cycle and host range in Iran.

Methods: Newly emerged ladybirds collected from ash whiteflies colonies in early spring then reared in controlled conditions (25±2ºC, 65±5% RH and L-D: 16-8). They fed daily with different life stages of Ash whitefly and related data collected daily. In the other hand, its host rang was evaluated by random sampling of ladybirds from whiteflies host plants throughout of central parts of country (Kerman province).

Results: Results showed that, mean of longevity of egg, 1-4th larvae, pupa, female and male were 3/5±0/93, 3/5±0/53, 4/63±0/92, 5/38±1/41, 10/75±1/16, 4/5±0/53, 77/3±6/9 and 67/5±7/2 days respectively. Consequently, it has 4 generations annually that the entire life cycle from egg to adult takes an average of 32/9±3/11days. Adults remain in diapauses for 5 months in the last generation. 2nd and 3rd generations fall on aestivation in hot summer. Females laid an average of 3/89±1/76 eggs/day. Host range studies showed that the matured adults appeared in late May on Ash Whitefly, *Siphoninus phillyreae* but its larval stages were found on another whitefly colony, *Bulgariodes cotessii*. Also in late June they are seen on pomegranate trees too.

Conclusions: This predator can control all life stages of Ash whitefly on different hosts specially the Ash and pomegranate trees. In addition the *Bulgariodes cotessii* is a suitable host for predator in absent of main prey, Ash whitefly.

POSTER PRESENTATION

The effects of herbivore induced plant volatiles on tritrophic interactions among host plants, spider mites, peach aphids and a predatory mirid bug

Hamisd R. S. Moayeri, Annie Enkegaard, Ahmad Ashouri

University of Tehran, Karaj, Tehran, Islamic Republic of Iran

Herbivore induced plant volatiles (HIPVs) are produced by herbivores attack that affects on ecology and behavioural responses of heterospecefics/conspecific herbivores and natural enemies. This study was conducted to investigate the effect of HIPVs on interaction among plants (pepper and green bean), herbivores (*Tetranychus urticae* and *Myzus persicae*) and a predatory bug (*Macrolophus caliginosus*) by using a Y-tube olfactometer and gas chromatography-mass spectrometry (GC-MS) technique. Our results show that *M. caliginosus* preferred plants infested by herbivores rather than un infested plants. The mirids did, however, not seem to exploit odours emitted directly from the prey themselves.

Furthermore, the olfactory responses of male and female *M. caliginosus* adults towards volatiles from green bean plants previously exposed to feeding by conspecifics and to direct odours from conspecifics were tested. Female *M. caliginosus* did not respond to volatiles from plants exposed to mirid feeding or to odours emitted directly by adult mirids. In contrast, male mirid bugs were attracted both to volatiles from plants previously exposed to feeding by conspecific females and to direct conspecific odours. The results suggest that female-specific HIPVs are used at least partially as mate-finding cues by the male mirids. These results suggest that female-specific herbivoreinduced plant volatiles play a role as mate-finding cues by the male mirids. The ecological implications of the findings are discussed, and the term 'sexual synomone' is introduced.

POSTER PRESENTATION

Plant host and insecticide effects on some bio-ecological parameters of Greenhouse whitefly, *Trialeurodes vaporariorum* (Westwood) (Homoptera: Aleyrodidae)

Bahare Salehi, Mehdi Zarabi, Neda Asemany, Shadi Movasaghi

University of Tehran, Tehran, Islamic Republic of Iran

Introduction: Greenhouse whitefly, *Trialeurodes vaporariorum* (Westwood), is a major pest of glass house crops. It shows resistant to different common Insecticides. In the other hand, different compounds may show special effects on host plants or vice versa. This study was conducted to evaluate effect of hosts and insecticide, Abamectin on amount of female's oviposition.

Methods: For this purpose, two leaves stand plants of cucumber and tomato dipped by dosages 50,100,150 and 200_{PPM} of Abamectin (1/8% EC). Then three 24-h old pairs released on plants under cages separately which located in controlled conditions ($25\pm2^{\circ C}$, 60±5% RH and L-D: 16-8). Number of eggs/day/female counted after 1, 3 and 5 days. Collected data were analyzed based on a Factorial design with SAS software. This experience repeated for 3 times.

Results: Results showed significant difference (level 5%) between mean of eggs/day/female in two hosts. Averages of amount of oviposition were 7.71±1.2 and 4.2 ±0.9 for cucumber and tomato respectively. There were no significant differences between times and dosages. But the mean of eggs/day/female at the dosage 200 $_{PPM}$ (average of 2.3±0.7) showed a high decreasing in comparing with the control plots (average of 8.9±1.8). In the other hand, amount of oviposition decreased in fifth day in comparing to first day after dipping.

Conclusions: Amount of oviposition on tomato showed this is not a preferred host in comparing with cucumber while it dipped with Abamectin. However, it seems that 200_{PPM} dosage of Abamectin can decrease the amount of oviposition especially after 3-5 days of pesticide usage on these hosts.

POSTER PRESENTATION

Production of queens and males in inbred and outbred population of a stingless bee species, *Melipona scutellaris* (Hymenoptera: Apidae)

Denise de Araujo Alves, Vera Lucia Imperatriz-Fonseca, Pérsio de Souza Santos-Filho

[1]São Paulo University, São Paulo, Brazil, [2]São Paulo University, São Paulo, Brazil, [3]São Paulo University, São Paulo, Brazil

Due to the high potential use of stingless bees in sustainable activities, as meliponiculture and as pollinators of crops, the production of their nests in large scale has an important role for human purposes. Our objective was to evaluate the inbreeding effects on the queens and male production in *Melipona scutellaris*, a species with high value for meliponiculture in Northeast Brazil.

We evaluated 53 brood combs (18,929 bees) from different colonies in an inbred population located at São Simão, Southeast Brazil, and 44 combs (16,812 bees) from colonies in their natural habitat (Northeast Brazil), an exogamic population. The inbred population began with two nests 12 years ago, and 30 nests were reached through successive splitting.

At the population level, the outbred population produced fewer reproductives (5.25% of queens and 10.33% of males) than the inbred population (11.52% of queens and 21.81% of males). The relative frequency of males and queens differed when we compared the populations ($p<0.001$). The colonies produce the reproductives during the whole year, but there is an asynchrony among the nests. Some of them can produce higher frequencies of males than others, due to orphanage or reproductive workers. Besides these within-nest conditions, the inbred population probably produced high number of diploid males; this hypothesis will be tested with molecular tools. The higher queen production in inbred population may be a result of the high frequency of replacement due to matched matings, which is considered a problem for insect societies, due the potential production of diploid males.

POSTER PRESENTATION

The importance of permanent monitoring of vector mosquito populations for their control in Romania

Octavian Ciolpan[1], Gabriela Nicolescu[2], Elena Claudia Coipan[2], Alexandru Filip Vladimirescu[2]

[1]University of Bucharest, Bucharest, Romania, [2]National Institute of Research-Development for Microbiology and Immunology; Cantacuzino, Bucharest, Romania

Introduction: Mosquitoes, the most important insect vectors, transmit West Nile virus infections and maintain the high risk of malaria re-emergence in Romania. The mosquito fauna (56 species) is widely distributed in the country both in urban and rural areas. The control of mosquito populations is needed to eliminate the disease transmission and the nuisance produced by them. The integrated application of control methods in appropriate areas and moments has to be in correlation with the dynamics of mosquito population in various environmental conditions.

Methods: The larvae and adult mosquitoes in Cernica forest (tourism area near Bucharest, south Romania) were investigated for five years by different collecting techniques to detect the number and succession of species, and the structure of populations in correlation with the changing environmental factors.

Results: 18 mosquito species and their qualitative and quantitative dynamics in correlation with the variation of the climatic factors were registered. The main factors favouring the development of high density mosquito populations have been detected. The results showed that the permanent monitoring of the parameters characterizing the mosquito populations under control in correlation with the environmental factors will lead to the efficient application of the adequate control measures in adequate areas and moments.

Conclusions: The mosquito control programme in a territory includes the permanent monitoring of the mosquito population as a main component of the programme which has the aim to reduce the risk of disease transmission and avoid the negative impact upon the environment and human population.

POSTER PRESENTATION

Ecdysteroids affect the expression of ftz-f1, a candidate to regulate vitellogenin in honeybee development

Tathyana Mello, Angel Barchuk, Márcia Bitondi, Michelle Soares, Zilá Simões

FFCLRP of University of São Paulo, Ribeirão Preto, Brazil

Introduction: FTZ-F1 is an orphan member of the nuclear hormone receptor superfamily. In *Drosophila melanogaster ftz-f1* encodes two protein isoforms, α and β. The latter acts as a competence factor for ecdysteroid hormones function. In *Apis mellifera*, knockdown of *vitellogenin*, a major yolk protein which also influences immune response and longevity, results in a decreased expression of *ftz-f1*. The aims of this study were to analyze the characteristics, expression profiles and functions of *ftz-f1* during honeybee development.

Results: The predicted *Amftz-f1* gene comprises 15,612bp and six exons. 1,196bp of the cDNA were sequenced. Expression profiles were determined by sqPCR and qPCR. The profiles are similar in workers and queens. As found in other insects, peaks of *Amftz-f1* expression occur during periods of low ecdysteroids titers - at the fifth larval instar (S3) and at pre-pupae (PP3) - and analyses of pupal integument samples incubated in 1µg of 20-hydroxyecdysone confirmed that this hormone inhibits *ftz-f1* transcription. The highest expression level occurs at the last pupal stage (Pbd) and is 9.4 times higher in queen fat bodies than in workers. A peak of *vitellogenin* expression is also observed at Pbd.

Conclusion: Our results suggest that also in the honeybee, FTZ-F1 has an important role as a competence factor for ecdysteroids, as its gene expression is repressed by ecdysone and occurs during periods of low hormone titer. Moreover, it is a candidate to regulate *vitellogenin* expression. Knockdown experiments are in progress in order to answer these questions about FTZ-F1 functions in honeybee development.

Financial support: FAPESP (05/03926-5)

POSTER PRESENTATION

Bumblebee importations into Ireland: growers' understanding of rewards and risks

Finbarr Horgan, Tomas Murray, Eamonn Kehoe

Teagasc Oak Park R.S., Carlow, Ireland

Introduction: Bumblebees (*Bombus terrestris*) are imported into Ireland each year for fruit pollination. The imported subspecies, *B. t. terrestris* and *B. t. dalmatinus*, are non-native. Despite risks of hybridization and competition between these and the native *B. t. audax*, importation remains unregulated. We assessed the extent of the trade in Ireland, growers' use of bees, their understanding of potential risks, and the benefits of bee importation.

Methods: Using advisory networks, a questionnaire was posted to all registered fruit growers in Ireland in 2007. Bee pollination in polytunnels was quantified and fruit/seed production monitored.

Results: We estimate that ≈ 1350 colonies entered Ireland in 2007 marking a steady increase since the late 1980s. Bee-pollination improved fruit/seed production when compared to hand-pollination. Over 50% of hives are used in strawberry pollination, mainly in glasshouses and polytunnels. Over 50% of hives are used in 'open-cultivation' systems including Spanish/French tunnels and open fields. There is a significant overlap in the occurrence of exotic and native reproductives indicating a high potential for hybridization. Growers generally do not destroy hives, but prefer to leave hives in situ or release bees to the wild. Even informed growers were unaware of how to avoid potential risks.

Conclusions: Improved fruit production is noted by growers; however, growers are generally unaware of potential importation risks and few make attempts to properly dispose of hives during periods of bee-reproductive activity. As part of this program, we are conducting a directed education campaign to improve hive management among growers.

POSTER PRESENTATION

Differential hind leg development in *Apis mellifera* castes

Ana Bomtorin, Angel Barchuk, Zilá Simões

FFCLRP of University of São Paulo, Ribeirão Preto, Brazil

The diphenism in the honeybee *Apis mellifera* results from differential feeding offered to females during larval development. Among the morphological differences between workers and queens are structures related to pollen and propolis collecting in workers hind legs, one of them is the pollen-basket. Queens hind legs have no those structures. Previous work (Barchuk *et al*., *BMC Dev Biol*, 2007) using microarray analysis showed that four out 240 differentially expressed genes in developing castes are related to leg development (*ataxin-2*, *cryptocephal*, *grunge* and *dachshund*). By using qPCR *abdominal-A*, *ataxin-2*, *cryptocephal*, *grunge* and *ultrabithorax* expression was analyzed. *cryptocephal*, *ataxin-2* and *grunge,* genes related to bristles formation and discs elongation, were not found differentially expressed. *ultrabithorax* and *abdominal-A* are expressed in the honeybee hind leg imaginal discs, and both genes are over-expressed in workers in early pupal stage. Similar pattern of *ultrabithorax* and *abdominal-A* expression can be found in hind legs of ninphal development in grasshoppers and crickets. *Drosophila* leg (with naked cuticle) also over-expresses *ultrabithorax* in this region during pupal stages. Using Scanning Electronic Microscopy we observed that leg structures and bristles are already formed in brown eyed pupa, and pollen-basket is a region deprived of bristles, containing a unique bristle in it middle that seems to be a sensorial bristle. Our results suggest *ubx* as a key player in pollen-basket formation and caste differentiation in *Apis mellifera*. Gene expression silencing using iRNA assays are underway in order to get more information on *ubx* function during leg development of honeybees.

Financial support: FAPESP (05/03926-5, 06/05437-4)

POSTER PRESENTATION

Anopheline malaria vectors in Venezuela: Two cases of morphological diagnostic characters invalidation using molecular phylogenetic analyses

Juan-Carlos Navarro[1], Monica Prado[1], Camila Hernandez[1], Gabriela Rangel-Diaz[1], Edmundo Guerrero[1], Jazzmin Arrivillaga[2]

[1]Universidad Central de Venezuela, Caracas, Venezuela, [2]Universidad Simon Bolivar, Caracas, Venezuela

Introduction: Putative diagnostic characters can be proved autapomorphic characters or instead part of the morphological intra-specific variation into a genetic pool of a mosquito population. Two different studies with females *Anopheles* in Venezuela have been addressed to prove by mean of cladistic and molecular analyses the taxonomic value of some characters used in descriptions and keys to identify similar morphological species.

Methods: At Northeastern Venezuela malaria focus, in the *An aquasalis* (main vector) studies we found several specimens identified also as *An benarrochi* (proved vector in Peru) agree with the Cova-Garcia, Rubio-Palis and Laurenço de Oliveira keys, using the scales on Medial vein, while in the *subgenus Kerteszia* studies in Venezuelan Andes, we sorted three species: *gonzalezrinconesi, rollai* and *boliviensis* by mean of scales patterns on the Anal vein *sensu* the original descriptions. We have contrast the putative morphological diagnostic characters against the PCR-COI and ND5 (mtDNA) sequences amplified and analysed by cladistic methods using PAUP4.0b10.

Results: The COI and ND5 mtDNA parsimony analyses shown a large politomy, few genetic distance and no phylogenetic structure among sequences from putative different species, suggesting the occurrence of a single species and demonstrating that the putative morphological diagnostic characters used should be considered as intra-specific variation. The *aquasalis* analysis are agree with the Faran's key and assumptions where he pointed out there are no morphological diagnostic characters in the females of *aquasalis* Vs *benarrochi* . By the other hand, the *Kerteszia* analyses suggest two possible synonymies for *An boliviensis*.

POSTER PRESENTATION

Hexamerin genes in *Apis mellifera*: sequence, developmental expression, function and evolution

Juliana Martins, Francis Nunes, Alexandre Cristino, Zilá Simões, Márcia Bitondi

[1]FMRP - University of São Paulo, Ribeirão Preto, Brazil, [2]FMRP - University of São Paulo, Ribeirão Preto, Brazil, [3]IFSC - University of São Paulo, São Carlos, Brazil, [4]FFCLRP - University of São Paulo, Ribeirão Preto, Brazil

Introduction: Hexamerins are hemocyanin-related storage proteins massively synthesized in insect larval fat body. Here we describe the structure of the four honeybee hexamerin genes, and their putative functions, as deduced from expression patterns in fat body and gonads of developing and adult workers, queens and drones. The molecular relationship among these hexamerins and related proteins from other insects was also investigated.

Methods: Hexamerin cDNAs were isolated and sequenced using conventional methods. Semiquantitative and real-time RT-PCR were used to characterize expression profiles. For a phylogenetic analysis, hexamerin sequences were aligned using ClustalW. Neighbor-joining method was used for tree construction.

Results: Except for the conserved hemocyanin domains, the honeybee hexamerin genes (*hex*) are structurally very diverse and display distinct developmental expression profiles. *hex 70a* and *hex 110* genes are expressed in the fat body of developing and adult honeybees, whereas expression of *hex 70c* and *hex 70a* is limited to different periods of larval development. Levels of *hex 70a* and *hex 110* transcripts are significantly higher in the fat body of reproductive than non-reproductive females. Ovaries and testes express *hex 70a* and *hex 110,* but not the other two hexamerin genes.

Conclusion: In the honeybee, hexamerin genes display significant differences in sequence and structure. The function of the respective proteins is not exclusively limited to metamorphosis, but is extended to other aspects of honeybee life-cycle. Phylogenetic analysis revealed that HEX 110 is ancestral to HEX 70a, b and c.

Financial support: 2005/03302-1 (FAPESP)

POSTER PRESENTATION

Life history of *Euptychia* sp. (Nymphalidae: Satyrinae) feeding on *Selaginella* (Selaginellaceae)

José Enrique Piñango Bustamante[1], Ángel Luis Viloria Petit[2]

[1]Insectario Zoológico El Pinar, Caracas, DC, Venezuela, [2]Centro de Ecología, Instituto Venezolano de Investigaciones Científicas, Altos de Pipe, Edo Miranda, Venezuela

Satyrine larvae commonly feed on monocotyledoneous plants. *Euptychia* has been traditionally used as a blanket genus for most small neotropical Satyrinae that have rounded wings with small ocelli. However, only a small, distinctive number of species within this group feeds on Selaginellaceae, a group of non-vascular plants (Lycopsida). The relationship between butterflies and spike mosses of the genus *Selaginella* is only known for three satyrine genera in the world, and it has been poorly studied in the Neotropics. Adults and immatures of *Euptychia* sp. collected at 650 m in the Guatopo National Park, Venezuela, were found feeding on two species of *Selaginella.* Eggs and larvae were observed in the field at different stages, collected, and later transferred to glass containers to be reared at El Pinar Zoo Insectarium, Caracas (905 m). Morphological observations, measurements, and development times were recorded for all life stages. Eggs are laid singly; they are green, round, smooth, and lack reticulation in the chorion surface. Larvae are also green and bear fleshy tubercles (scoli), which is an unusual feature for the Satyrinae; the head is dark. The general aspect of the larvae mimics that of their hostplants. Dry head capsules and exuviae were kept for ulterior studies. A chalcidid wasp emerged from one of the pupae collected in the wild. Further study of the morphology of the immature stages and the comparative biology of this genus and others with similar hostplant relationships might provide the basis to establish the natural affinities of the *Euptychia* butterflies, whose systematic position is still uncertain.

POSTER PRESENTATION

Studies on population dynamic of dipteran species (Calliphoridae) from Brazil: A new approach for forensic purpose

Patricia Jacqueline Thyssen, Wesley A. C. Godoy

UNESP, Botucatu, SP, Brazil

Introduction: The insects can be useful to understand the cases in which there is body displacement after the death associated to the knowledge of their geographical distribution and, in some cases, to describe the suspects' movement. None of the population censuses nor the works on entomological succession on carcass accomplished in our study area considered the hypothetical space migrations in a given place among different environments as urban, rural and forest area.

Methods: This study investigated through monthly collection, for one year, in different environments and by using mathematical models, the dynamic behavior of ten dipteran species (Calliphoridae) of forensic importance.

Results: The great majority of the collected caliphorids presented certain predominance in relation to the different types of environments, such as Hemilucilia semidiaphana, found only in forest area. Correlation calculations between species and population growth rate could demonstrate, as observed for *Cochliomyia macellaria* and *Lucilia eximia*, that some species can have more potential to explore a habitat than others, modulated by the competition or by the search for a specific resource. Thus, the discrepancy between the insect composition on a body and the insect composition from the local where the body was discovered could provide evidences that the victim was displaced.

Conclusions: The non observation of the possibility of population oscillation of certain species associated to an environment may lead to mistakes in the determination of the death place.

POSTER PRESENTATION

DNA barcodes for invasive species identification

Shelley Ball, Karen Armstrong

Lincoln University, Canterbury, New Zealand

The movement of species around the world has increased exponentially in recent years due to increased global trade and travel. The economic cost of species establishment in non-native ranges can be enormous. Consequently, the ability to accurately identify exotic and potentially invasive species is crucial towards minimising the risk. We have developed DNA barcodes for identification of exotic and pest insects. DNA barcoding involves using a small fragment (~ 650bp) of the COI mitochondrial gene as a species-specific genetic identification tag. Here we present data demonstrating that DNA barcodes have enormous potential as standardized tool for biosecurity and phytosanitary application. For example, COI barcodes were 100% successful in discriminating over 30 species of lymantriid moths and exactly the same approach was effective at distinguishing over 60 tephritid fruit fly species outside of known species complexes. As with other barcode studies, we found that mean interspecific genetic distances were an order of magnitude greater than mean intraspecific divergences, indicating that many species are easily distinguishable with COI barcodes. Furthermore, DNA barcodes are playing an important role in species discovery. For example, *Lymantria mathura* populations that had distinct COI barcode sequences also displayed inconsistencies in pheromone lure attraction; the species has subsequently been revised as two species, *L. mathura* and *L. flavida*. International collaborations are now beginning to assemble open access COI sequence libraries for a diversity of invasive and pest species, with the goal of developing an internationally standardized species identification tool for biosecurity and phytosanitary application.

POSTER PRESENTATION

larvicidal activity of magnolia officinalis root cortex compounds toward two mosquito species

Nam-Jin Kim, Tae-Kyun Hong, Young-Joon Ahn

Seoul National University, Seoul, Republic of Korea

Introduction: The toxicity of materials derived from the root cortex of *Magnolia officinalis* Rehd. Et Wils (Magnoliaceae; Houpo in Chinese), toward third instar larvae from laboratory-reared *Aedes aegypti* and *Culex pipiens pallens* were examined.

Methods: Insecticidal toxicity of materials was evaluated by paper cup direct contact bioassay. The active principle was identified as the lignin magnolol by spectroscopic analysis.

Results: Based on 24 h LC_{50} values, *Cx. pipiens pallens* larvae were slightly more susceptible than *Ae. aegypti* larvae to the magnolol tested. The LC_{50} value of *Cx. pipiens pallens* was 25.7ppm (21.03 – 30.93) and the LC_{50} value of *Ae. aegypti* was 33.4ppm (27.82 – 38.72).

Conclusions: *M. officinalis* root cortex-derived materials, particularly manolol, merit further study as potential mosquito larvicidal agents or as a lead for the control of mosquitoes for protection from humans and domestic animals form vector-borne diseases and nuisance caused by mosquitoes because of their good activity as a larvicide.

POSTER PRESENTATION

Genetic analysis of Romanian autochtonous and allochtonous silkworm (*Bombyx mori*) strains by means of RAPD technique

Alexandru Filip Vladimirescu[1], Elena Claudia Coipan[1], Daniela Usurelu[2], Alexandra Matei[3], Dan Dezmirean[4], Cristina Bojan[4], Lucian Gavrila[2], Ioan Pasca[4]

[1]National Institute of Research-Development for Microbiology and Immunology Cantacuzino, Bucharest, Romania, [2]Institute of Genetics, University of Bucharest, Bucharest, Romania, [3]SERICAROM S.A., Bucharest, Romania, [4]Apiculture Department, University of Agricultural Sciences and Veterinary Medicine, Cluj-Napoca, Romania

Introduction: Romania has 65 strains of silkworms, of which 6 are commercial hybrids, with very high productivity. Of the total number of genetic resources maintained in Romania, 12 are autochtonous. A recently started national project (COSERISTECH) aims to develop an experimental model for the conservation of the genetic potential and of the autochtonous sericultural resources, in which genetic techniques play an important role.

Methods: In this study the random amplified polymorphic DNA (RAPD) technique was used to analyze the DNA profile of 10 silkworm strains. The strains used were five autochtonous and five allochtonous. The starting material was represented by whole silkworms that were grinded after immersion in liquid nitrogen. DNA was isolated using a Qiagen kit. For the amplification we used one primer pair. The annealing temperature was lowered to 35.5 ℃ to favor the primers unspecific binding to the template DNA.

Results: Following electrophoresis homologous and specific bands were observed for the analyzed strains.

Conclusions: The resulting profiles indicate that RAPD technique can be used to discriminate between some of the important silkworm strains maintained in Romania.

POSTER PRESENTATION

Coupled spatio-temporal dynamics of the bruchid beetle *Acanthoscelides schrankiae* and its parasitoids

Ligia M.S. Rodrigues[1], Marcelo N. Rossi[2]

[1]*Universidade Estadual Paulista (Unesp), Instituto de Biociências, Botucatu, SP, Brazil,* [2]*Universidade Federal de São Paulo (Unifesp), Campus de Diadema, São Paulo, SP, Brazil*

Introduction: Using a spatially explicit approach, we investigated the spatio-temporal dynamics of the bruchid *Acanthoscelides schrankiae* and its parasitoids occurring on a *Mimosa bimucronata* population. We firstly used the Spatial Analysis by Distance Indices (SADIE) approach to investigate patterns of spatial distribution of bruchids and parasitoids. Secondly, we used an extension of the SADIE method (overall spatial association) to compare coincidences of patch and gap clusters of host and parasitoids.

Methods: Coupled dynamics between parasitoids and bruchids were evaluated within (unlagged) and between (lagged) all different sampling occasions in order to understand temporal patterns of spatial associations. Fifty branches were selected on plants and fruits were collected at 2-weekly intervals. Six and three collections were carried out on years 2006 and 2007, respectively. Each branch was mapped and positioned in a Cartesian plane with coordinates. After collection, fruits were individualized and the number of emerging adult bruchids and parasitoids was recorded for each branch.

Results: Most significant results were found for unlagged spatial associations. However, for the year 2007, significant lagged spatial associations were found. The most important significant lagged associations were found between the following sampling occasions: sampling two for parasitoids with sampling one for bruchids, sampling three for parasitoids with sampling one for bruchids, and sampling three for parasitoids with sampling two for bruchids. Therefore, the parasitoid-bruchid populations were dynamically coupled because lagged and unlagged spatial associations were observed.

Conclusions: We provided evidences that the parasitoids responded positively to the spatial distribution of bruchids shown in earlier occasions.

POSTER PRESENTATION

Evaluation of white khomein and some other Iranian onion cultivars for resistance to thrips (*Thrips tabaci* Lindeman)

Mazaher Yousefi, Ahmadreza Abasifar

Agricultural and Natural Resources Research Center, Markazi Province , Arak, Islamic Republic of Iran

Thrips tabaci L. is one of the most important pests on onion in Iran, and can make a serioues damage on onion. In this research, Khomein breeded cultivar compared with seven cultivars of onoin (Azarshahr Red, Kashan White, Native White Khomain, Qom White, Kordestan White, Shahrood Red) in a RCB design in four replications in the Agricultural & Natural Resources Research Center of Markazi Province, during 2001-2003. The numbers of thrips on five plants were recorded each two weeks. The symptom of pest feeding including chlorosis, necrosis, and curling of leaves was evaluated and recorded based on a ten scale for damaging and a six scale for leaves curling. The field of control also planted around and sprayed with current insecticide on the eight time due to decreasing thrips damage. The data was analyzed using a SAS system, and the means compared with Duncan's test. In this study, the highest number of thrips observed on Azarshar Red, breeded Khomein and Shahroud White (27.7, 25.7 and 25.3 respectively) and the lowest number recorded on Shahroud Red, Kordestan (16.01 and 15.8 respectively).Amount of damage on Azarshahr Red was the highest and Kordestan and Qom white was the lowest. In nonsprayed plots, the highest yield recorded for Kashan and Qom White cultivars (79.2 and 75.2 T/h respectively) and the lowest yield for Kordestan cultivar (61.1 T/ha). The results of the study over the three years showed that breeded onion of Khomein compare with other cultivars in Iran due to high density of thrips (an avarage of 25.7 thrips per plant) on medium of curling and damage, and intermediate yield in both spraying and nonspraying plots known as tolerant genotype. No different variation yield observed across of spraying (Average: 67.6 Tha^{-1}) and nospraying (Averag; 68.6 Tha^{-1}) blocks.

POSTER PRESENTATION

Dispersal of the broad mite, *Polyphagotarsonem*us *latus* (Banks) (Acari: Tarsonemidae), by greenhouse pests

Huseyin Gocmen, Utku Yukselbaba

Department of Plant Protection, Faculty of Agriculture, University of Akdeniz, Antalya, Turkey

Introduction: Broad mite*, Polyphagotarsonemus latus* (Banks), is an economically important pests of greenhouse grown plants and its presence in Turkey first discovered in 1992. In this study, the interaction between broad mite and other important greenhouse pests was studied to understand the dispersal process of broad mite in greenhouse vicinity.

Methods: The study was undertaken on 2 cm diameter leaf disks exposing 2400 lux light intensity at 26 ^{o}C under 16:8 L:D regime. Groups of live and dead greenhouse pests, *Bemisia tabaci* (Genn.), *Frankliniella occidentalis* (Pergande) and *Liriomyza trifolii* (Burgess) were co-located at varying times of 1, 2, 4 and 8 hours and broad mite carrying capability of each pest were evaluated.

Results: The results shown that broad mite attachment to any pest tested was minimum at 1 hour treatment whereas maximum numbers obtained in 8- hour treatment. At 20 broad mite/leaf disk density, 7.2 broad mites attached to individual *B. tabaci* adult whereas none observed on *F. occidentalis* at the end of 8 hour treatment. With dead pests at 20 broad mite/leaf disk density, the num*bers* on individual *B. tabaci* were 15.4 whereas only 3.12 were attached to *F. occidentalis.* The results further showed that *L. trifolii* was not capable of carrying broad mite.

Conclusions: Overall results indicate that *B. tabaci* has a central role in dispersal of broad mite, hence should be given consideration in management of the pests in greenhouses.

POSTER PRESENTATION

Dispersal of the broad mite, *Polyphagotarsonem*us *latus* (Banks) (Acari: Tarsonemidae), by greenhouse pests

Huseyin Gocmen, Utku Yukselbaba

Department of Plant Protection, Faculty of Agriculture, University of Akdeniz, Antalya, Turkey

Introduction: *Broad mite, Polyphagotarsonemus latus* (Banks), is an economically important pests of greenhouse grown plants and its presence in Turkey first discovered in 1992. In this study, the interaction between broad mite and other important greenhouse pests was studied to understand the dispersal process of broad mite in greenhouse vicinity.

Methods: The study was undertaken on 2 cm diameter leaf disks exposing 2400 lux light intensity at 26 ^{o}C under 16:8 L:D regime. Groups of live and dead greenhouse pests, *Bemisia tabaci* (Genn.), *Frankliniella occidentalis* (Pergande) and *Liriomyza trifolii* (Burgess) were co-located at varying times of 1, 2, 4 and 8 hours and broad mite carrying capability of each pest were evaluated.

Results: The results shown that broad mite attachment to any pest tested was minimum at 1 hour treatment whereas maximum numbers obtained in 8- hour treatment. At 20 broad mite/leaf disk density, 7.2 broad mites attached to individual *B. tabaci* adult whereas none observed on *F. occidentalis* at the end of 8 hour treatment. With dead pests at 20 broad mite/leaf disk density, the num*bers* on individual *B. tabaci* were 15.4 whereas only 3.12 were attached to *F. occidentalis.* The results further showed that *L. trifolii* was not capable of carrying broad mite.

Conclusions: Overall results indicate that *B. tabaci* has a central role in dispersal of broad mite, hence should be given consideration in management of the pests in greenhouses.

POSTER PRESENTATION

New management tools against the European pine sawfly *Neodiprion sertifer*

Paal Krokene[1], Svein Solberg[1], Andreas Bostad Thause[2]

[1]Norwegian Forest and Landscape Institute, Ås, Norway, [2]Norwegian University of Life Sciences, Ås, Norway

The European pine sawfly *Neodiprion sertifer* is a widely distributed defoliator of pines that can cause substantial growth losses over extensive areas. It attacks most species of two-needle pines in its distribution area, and have occasional short-lived outbreaks that may cover up to 200.000 ha. In Norway we have had outbreak populations in the eastern part of the country since 2004, and in an ongoing research project we are evaluating aerial application of the *Neodiprion sertifer* nuclear polyhedrosis virus (NsNPV) to control *Neodiprion sertifer*. Defoliation levels at the landscape level were measured using airborne laser scanning. Laser scanning was performed twice during the growth season; once in May, before the sawfly larvae had started feeding, and once in August, after pupation. Defoliation level was calculated as the difference in estimated leaf area index (LAI) between the two scans. Virus application significantly reduced defoliation levels in sprayed areas relative to unsprayed control areas, but since defoliation levels remained low throughout the study area the differences were small. At the end of the summer virus levels were significantly higher in sprayed areas than in unsprayed control areas, as demonstrated by a newly developed PCR-based detection method. This method is much more reliable, sensitive and flexible than the presently available microscopy-based method for virus visualization. Defoliation levels after *Neodiprion sertifer* attack was also compared with stand characteristics, such as stand age, productivity and exposure, to identify stands that were highly susceptible to attack.

POSTER PRESENTATION

Genetic mapping of CpGV resistance loci in the codling moth *Cydia pomonella*

Nadine A. Gund[1], Annette Reineke[1], Claus P. W. Zebitz[2], David G. Heckel[3], Sabine Asser-Kaiser[4], Johannes A. Jehle[1]

[1]Research Center Geisenheim, Section Phytomedicine, 65366 Geisenheim, Germany, [2]University of Hohenheim, Institute of Phytomedicine, Department Entomology, 70599 Stuttgart, Germany, [3]Max Plank Institute for Chemical Ecology, Department Entomology, 07745 Jena, Germany, [4]Agricultural Service Center Palatinate (DLR Rheinpfalz), Department of Phytopathology, 67435 Neustadt an der Weinstrasse, Germany

The codling moth, *Cydia pomonella* (L.) (Lep., Tortricidae), is a major pest in apple growing regions worldwide. Without control, infestations can result in severe damage and complete loss of marketable fruits. One of the cornerstones of codling moth control in organic and integrated apple production is the use of biocontrol agents based on the *Cydia pomonella* granulovirus (CpGV). In many countries CpGV products are among the very few codling moth control measures allowed in organic apple production. Neonates ingest the virus through feeding and die after 4-7 days. In 2004, field observations in organic apple orchards in Germany and France suggested a failure of CpGV products in controlling codling moth populations. Rearing and resistance testing of these populations revealed an up to 1,000-fold decrease in CpGV susceptibility.

For future management of CpGV resistance it is pivotal to know the resistance mechanism(s) and to identify the respective gene(s). Mass crossing experiments as well as single-pair crosses have revealed that resistance loci are located on the sex-chromosome, i.e. the Z-chromosome. To further identify and isolate the respective gene(s), linkage mapping on *C. pomonella* backcross populations is being performed. Markers located on the sex-chromosome are identified through SNP (single nucleotide polymorphism) analysis. Furthermore AFLP (amplified fragment length polymorphism) markers were generated that are located on the Z-chromosome and are putatively linked to the CpGV-resistance loci. These markers are the fundament for further linkage mapping and thus for the identification of resistance genes.

POSTER PRESENTATION

The haemocytes of *Eldana saccharina* Walker (Lepidoptera: Pyralidae): structural characteristics and proportions of subtypes

Irene Ketseoglou, Gustav Bouwer

University of the Witwatersrand, Johannesburg, South Africa

Introduction: Lepidoptera are capable of mounting a variety of immune responses to foreign bodies. The importance of haemocytes in insect immunity prompted the characterisation of the haemograms of the African sugarcane stalkborer, *Eldana saccharina* Walker (Lepidoptera: Pyralidae).

Methods: Differential and total haemocyte counts were performed on fifth instar *E. saccharina* larvae. Haemolymph was extracted from anaesthetized larvae. Differential haemocyte counts were performed by light microscopy and total haemocyte counts were obtained by haemocytometer counts. Haemolymph volume was estimated by injecting red amaranth into anaesthetized larvae and the absorbance of the cell-free haemolymph was compared against a red amaranth standard curve. Transmission electron microscopy was used to characterize haemocytes.

Results: Five haemocyte subtypes were identified and characterised in *E. saccharina* larvae by light and transmission electron microscopy. Plasmatocytes and granular haemocytes comprised the largest percentage of haemocytes in *E. saccharina*. The spherule cells, oenocytoids and the prohaemocytes made up less than 2% of the total haemocyte population. Two distinct plasmatocyte populations, spherical and spindle-shaped, were present in *E. saccharina* larvae. The granular haemocytes had lipid droplets in their cytoplasm, an uncommon occurrence in most lepidopteran species. The total haemocyte count of *E. saccharina* was generally lower than other lepidopteran species. Fifth instar *E. saccharina* larvae had slightly higher haemolymph volumes than other lepidopteran species.

Conclusions: This study provides valuable information on the haemocytes, the effectors of the cellular immune response, of *E. saccharina* and should aid in the understanding of the immune system of *E. saccharina*.

POSTER PRESENTATION

Blow fly (Diptera: Calliphoridae) early larval colonization of pig carcasses, in semi-arid Mediterranean areas (SE. Spain)

Yelitza Velasquez, Anabel Martinez, Berta Pastor, Santos Rojo

CIBIO, Alicante, Spain

Introduction: The southeast coast of the Iberian Peninsula is characterized by an important human activity. Some habitat shows adverse environmental conditions imposed by low-quality soils. Annual average temperatures range from 13-19 ºC, and the minimum average temperature of the coldest month ranges from 1-10 ºC. Annual rainfall ranges are very low.

Methods: In this study, we compare Diptera colonization in early stage of decomposition in two seasons of the year: fall (November 2007) and winter (February 2008). For each season, a domestic pig (*Sus scrofa*) was exposed in the antrophic area at University of Alicante, Spain, during ten days. On the 10th day, the pig was covered with a net in order to avoid colonization, but allowed the development of species which had already been breeding. A sample of immature stages were collected daily and reared under controlled conditions (23ºC, 70% and 14:10 photoperiod).

Results and Conclusions: The results showed there were different species breeding in two seasons. In fall season, we found *Lucilia sericata*, *Chrysomya albiceps*, *Chrysomya megacephala*, *Calliphora vicina* and *Calliphora vomitoria*. However, in winter, only *Calliphora vicina* and *Calliphora vomitoria* emerged. We also discussed the abundance of species in each season and their presence in different parts of the body.

POSTER PRESENTATION

Evaluating the phylogenetic relationships of tribe Toxomerini and *Ocyptamus* (Diptera, Syrphidae)

Ximo Mengual, Gunilla Stahls, Santos Rojo, Berta Pastor

[1]CIBIO, Alicante, Spain, [2]Finnish Museum of Natural History, Helsinki, Finland

Introduction: *Toxomerus* and *Ocyptamus* (Diptera, Syrphidae) are the New World members of the subfamily Syrphinae more diverse and abundant. *Toxomerus* constitutes the monogeneric tribe Toxomerini with more than 150 described species, while *Ocyptamus* is a very diverse genus with some subgenera and species groups.

Methods: The phylogenetic relationships between both genera were analyzed based on sequence data from three gene regions, i.e. the mitochondrial protein-coding gene cytochrome c oxidase subunit I (COI) and the nuclear 28S and 18S ribosomal RNA genes. We analyzed the data under direct optimization using parsimony as optimality criterion, under six different parameter cost schemes in a sensitivity analysis. An implied aligment resulting from the direct optimization analysis was subsequently utilized to perform a Bayesian analysis.

Results: The monophyly of Toxomerini was recovered in all the analyses, and some species groups were consistently found. Results obtained indicated paraphyly of the genus *Ocyptamus* with respect to *Toxomerus*. Several species groups were found consistently in *Ocyptamus*, indicating probably the necessity of subdivisions. Paraphyly of the genus *Salpingogaster* was proposed because subgenus *Eosalpingogaster* was always recovered embedded in *Ocyptamus*, whereas *Salpingogaster* s. str. was never placed inside this genus. Most of Syrphinae are predatory species. Comments about predation habits in the frame of the phylogenetic results are also indicated.

POSTER PRESENTATION

Molecular phylogeny of *Lasius* ants in Korea

Byung-Jin Kim, Ki-Gyoung Kim

Wonkwang University, Iksan, Jeonbuk, Republic of Korea

Introduction: Systematic study of *Lasius* ants in Korea was made using both morphological analysis and RAPD-PCR for 9 species and 2 ssp. in *Lasius*.

Methods: The molecular phylogeny of 11 species of *L.* ants in Korea was examined using random amplified polymorphic DNA markers as inputs for an analysis of molecular variance and cluster analysis to describe the relationships between species. For comparison, morphometric data were also gathered for phylogenetic analysis. Assessments of similarity between species were made, and the results of these assessments are compared for the molecular and morphological data sets.

Result: In the morphometric analysis, the following groups were identified: (i) *L. alienus*, *L.* sp.2*, L.* sp.1, *L. niger* and *L. hayashi* (87% similarity); (ii) *L. flavus* and *L. talpa* (97%); (iii) *L. crispus* and *L. spatepus* (97%); (iv) *L. meridionalis* and *L. teranishii* (90%). *Paratrechina sakurae* was 38% similar to the 11 *Lasius* species studied here. the group comprising *L. flvus* and *L. talpa*, and comprising *L. crispus* and *L. spatepus* had the highest similarity index (97%), followed by the group comprising *L. meridionalis* and *L. teranishii* (90%), and then *L. alienus*, *L.* sp.2 and *L.* sp.1 (95%). In the molecular analysis the following groups were identified: (i) *L. meridionalis* and *L. teranishii* (70%); (ii) *L. hayashi* and *L.* sp.1 (47%); (iii) *L.* sp.2, *L. crispus* and *L. talpa* (35%); and (iv) *L. flavus* and *L. alienus* (15% similarity).

Key words: *Lasius*, Korea

POSTER PRESENTATION

Predictions of range expansion of an invasive gall wasp (*Quadrastichus erythrinae*) under the double pre-industrial CO_2 concentration scenario

Tung Gene-Sheng, Hsu Chia-Chun, Hsu Chia-Chin, Yang Man-Miao

TFRI, Taipei, Taiwan

Introduction: Events of species invasion were becoming more frequent as a consequence of intensifying intercontinental transportations. However, global climate change even worsens the situation. Global warming is likely to allow range expansion of many invasive species from tropics, such as the erythrina gall wasp (EGW), which forms galls and causes severe damages on coral trees (*Erythrina* spp.) in the past few years.

Methods: The species distribution model was used to predicted range-size change of EGW and five species of host trees (*Erythrina* spp.) under the double pre-industrial CO_2 concentration scenario. Changes on the species' range size were calculated and compared.

Results: Models indicated an overall invasion risk of EGW for tropical areas and a trend of polarward expansion under the climate change scenario. Furthermore, results suggest that there are different abilities of range expansion between EGW and their host tress.

Conclusions: Our results suggest that risks associated with invasive EGW will likely become more intense under further impacts of climate change, not only for areas where EGW were reported but also regions where it has opportunities to establish populations.

POSTER PRESENTATION

Evaluation of the re-emergence risk of mosquito-borne diseases in Romania

Gabriela Nicolescu[1], Valeria Purcarea-Ciulacu[1], Alexandru Vladimirescu[1], Liviu Prioteasa[1], Elena Falcuta[1], Claudia Coipan[1], Gabriela Dumitrescu[2], Diana Popescu[2], Aurora Alexse[1]

[1]Cantacuzino Institute, Bucharest, Romania, [2]Army Centre of Medical Research, Bucharest, Romania

Introduction: The climatic and other environmental changes in the last years induced the intensifying of the circulation and transmission of West Nile virus to humans and the increased risk of malaria re-emergence in Romania.

Methods: The multidisciplinary investigations using entomological, immunological, viral and molecular biology techniques were performed for the ecological surveillance of the re-emergence risk of mosquito-borne diseases in the country.

Results: Investigation of WNV circulation showed the significant values of the seroprevalence of the antibodies against WNV in domestic birds (mean value – 10.8 %), wild birds (16.4 %) and horses (19.9 %), and their variations in correlation with the environmental factors. The virus was detected in *Coquillettidia richiardii* and *Culex pipiens* mosquitoes and was isolated from *Culex pipiens* females. The investigation of the anophelism in the former malaria endemic areas put in evidence the high abundance of the *maculipennis* group anophelines (*Anopheles atroparvus*, *A. maculipennis*, *A. messeae* and *A. daciae*), the species dominance and the main elements of their vectorial capacity in correlation with the environmental factors.

Conclusions: The investigations demonstrate the presence of the intensive and permanent enzootic circulation of WNV on extended territories in Romania and the possibility of its transmission to humans. The risk of malaria re-emergence is given by the presence of abundant populations of the potential anopheline vectors in the former endemic areas simultaneously with the constant increase of the number of imported malaria cases. The permanent surveillance of mosquitoes and implementation of integrated control programmes are adequate decisions in the risk areas in Romania.

POSTER PRESENTATION

Effect of temperature on feeding and development rates of a potential biocontrol agent, *Cornops aquaticum* Brüner (Orthoptera: Acrididae) for water hyacinth, *Eichhornia crassipes* Mart. Solms-Laubach (Pontederiaceae) in South Africa

Angela Bownes[1], Martin Hill[2], Marcus Byrne[3]

[1]Agricultural Research Council, Pretoria, South Africa, [2]Rhodes University, Grahamstown, South Africa, [3]University of the Witwatersrand, Johannesburg, South Africa

Water hyacinth remains South Africa's most problematic invasive aquatic plant, despite more than 40 years of an active biological control programme against the weed. One of the major factors identified to be constraining success of the agents currently established in South Africa is climate. Populations of the insects which are of tropical/subtropical origin decline dramatically in regions with cold winter temperatures and are slow to pick up at the start of the growing season, whereas plants bounce back quickly. Due to the limited success, an additional agent is currently under consideration for release, the grasshopper, *Cornops aquaticum*. Its distribution in South America, which extends from central Argentina around Buenos Aires as far north as Mexico suggest that it has a wide thermal tolerance, however, it would be valuable to make predictions about its potential efficacy based on its thermal physiology. Feeding trials at temperatures from 10°C to 30°C at 5 degree intervals showed that temperature had significant effects on adult ($F_{1;37}$ = 17.44; P = 0.0002) and 3rd ($F_{4;42}$ = 64.69; P = 0.0000) and 1st nymphal instar ($F_{4;42}$ = 24.30; P = 0.0000) feeding rates. No feeding took place at 10°C and in some cases 15°C. Temperature also had significant effects on development rates. These results suggest that our current culture in quarantine has a low thermal tolerance and collection and release of a strain of the insect from its southern-most distribution may need to be considered to improve chances of establishment and success in the temperate regions of South Africa.

POSTER PRESENTATION

Nectar guide removal dramatically decreases long-tongued fly visitation in *Lapeirousia oreogena*

Timotheüs van der Niet, Dennis Hansen, Steven Johnson

University of KwaZulu-Natal, Scottsville, South Africa

Flowers pollinated by insects often have contrasting colour patterns, referred to as nectar guides. These are thought to facilitate efficient feeding by the insect and thereby enhance pollination. This suggests that the presence of nectar guides has implications for plant fitness. A group of about 30 plant species in Namaqualand of diverse phylogenetic origin, all exclusively pollinated by two species of long-tongued fly (Prosoeca), is characterized by flowers with marked nectar guides. The role of nectar guides in long-tongued fly pollinated plants is currently poorly understood. We investigated the effect of nectar guide removal on plant visitation by flies using *Lapeirousia oreogena*, an actinomorphic Iridaceae with six conspicuous nectar guides with a radially symmetrical configuration. We erased the cream-coloured nectar guides of the plant using black ink so as to resemble the black colour of the tissue surrounding the nectar guide. Choice tests reveal that a decrease in number of nectar guides decreases plant visitation. Flowers with nectar guides removed receive significantly less visits than control plants. We also recorded visitation of isolated flowers with and without nectar guides. The number of approaches to plants with nectar guides was equal to plants without nectar guides. Approached plants without nectar guides were, however, never probed for nectar whereas approached plants with nectar guides were also always probed. We suggest that nectar guides in long-tongued fly pollinated plants serve for short distance orientation and that they probably are a necessary element in the evolution towards fly pollination.

POSTER PRESENTATION

Fungal associates of the conifer-infesting bark beetle, *Hylastes brunneus*

Riikka Linnakoski[1], Z. Wilhelm de Beer[2], Pekka Niemelä[1], Ari Pappinen[1], Michael J. Wingfield[2]

[1]Faculty of Forest Sciences, University of Joensuu, P.O. Box 111, FIN-80101 Joensuu, Finland, [2]Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, 0002, South Africa

Introduction: *Hylastes* bark beetles (Coleoptera: Scolytinae) are considered to be less aggressive beetles, infesting roots of declining conifers. Several *Hylastes* spp. are known to vector Ophiostomatoid fungi. However, nothing is known regarding the fungal associates of *Hylastes brunneus*, a common species infesting spruce (*Picea abies*) and pine (*Pinus sylvestris*) in the boreal forests of Finland. The aim of this study was to isolate and identify fungal associates of *Hylastes brunneus*.

Methods: Fungi were isolated from beetles and their galleries collected at two different sites in eastern Finland. Resulting fungal cultures were grouped based on morphology. ITS, β-tubulin, LSU and elongation factor 1-α sequences were obtained for isolates representing the various groups identified based on morphology. Phylogenetic analyses were done to confirm the identity the fungal species.

Results: Both spruce and pine were infested with *Hylastes brunneus*. Based on morphology and phylogenetic analyses, at least nine fungal species were found to be associated with *H. brunneus*. These included *Ophiostoma canum*, *O. piliferum*, *Grosmannia cucullata*, *G. galeiforme*, *Leptographium lundbergii*, and at least three undescribed *Ophiostoma* and one undescribed *Leptographium* species. None of the fungi were consistently isolated from *H. brunneus*, only *O. canum* was found at both collection sites.

Conclusions: The results of this study show that *Hylastes brunneus* is a casual vector of Ophiostomatoid fungi, but apparently lacks fixed fungal associates. The ecological relationships between the fungi and the beetle need further investigation. The novel species will be characterized and described as new species.

POSTER PRESENTATION

Biological control of *Sirex noctilio* with *Beddingia siricidicola*: Current status in the *Pinus radiata* plantations of the Arauco companies

Miguel Angel Poisson, Alvaro Duran, Rodrigo Ahumada

[1]BIOFOREST S.A., Concepcion, Chile, [2]Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa

Sirex noctilio is a siricid wood wasp native to Eurasia and northern Africa and it has become a significant pest of exotic *Pinus* plantations in the Southern Hemisphere. In Chile, *S. noctilio* was detected at the beginning of 2001, after which the insect has been monitored under a quarantine control system regulated by the government plant health agency (SAG). The government sector and private companies now implemented a strategy for *Sirex* control, based on early detection, biological control and improvement of plantation management. A model was developed that categorized about 90,000 ha at different risk levels to *Sirex* attack, based in silvicultural management, site index, age, average diameter, density, and distance of declared focus,. This model, supported by GIS analysis, was used to direct the monitoring and trap tree plot placement in Arauco company plantations. A total of 674 plots of trap trees (6,740 trees) were established, during the 2006-2007 season, based on this system. Of these, 267 trap tree plots (2,598 trees) distributed in 88 different fields, were inoculated with the parasitic nematode, *Beddingia siricidicola.* The first result of the parasitism levels of *S. noctilio*, following this inoculation, showed an average of approximately 10%. Future research is aiming to optimize the period of inoculation.

POSTER PRESENTATION

Sublethal effects of crop protection on honey bee pollination: foraging behaviour and flower visits

Bruno Gobin[1], Kevin Heylen[2], Roger Huybrechts[2], Johan Billen[2], Lutgarde Arckens[2]

[1]Zoology department Pc Fruit, Sint-Truiden B-3800, Belgium, [2]Zoological Institute K.U.Leuven, Leuven B-3000, Belgium

Many fruit crops depend on availability of honey bee hives for sufficient pollination to ensure maximal fruit quality (shape and size) and quantity (yield weight). In Belgium, non-commercial beekeepers and commercial fruit growers have mutual benefits from this cooperation as both honey and fruit yield increase. Fruits can however not be grown commercially without the use of crop protection agents, either from organic or chemical origin. The use of products with toxic effects is banned during flowering, and precise pre-flowering intervals have to be respected in Good Agricultural Practice. In those European countries with a monitoring scheme, acute bee poisoning incidents have decreased considerably and hardly cause problems at present.

In recent years, some concerns arose over sublethal effects (ie behavioural changes) of chemical crop protection on bees. Even though short-term effects can indeed be induced in individually exposed bees, studies that exposed complete colonies did not reveal any long-term consequences at colony level. However, from the fruit growers' viewpoint, potential short-term effects on foraging behaviour are relevant as they can bear on pollination efficacy. We observed effects of either maximal bee exposure (feeding) or in-crop exposure (treatments at flowering) of a selection of chemicals with various degrees of bee toxicity. To characterize specific behavioural changes, we chose specifically high risk levels of exposure (greater than normal agronomic use), more practically relevant exposure remains to be tested. Both changes in quantitative (food retrieval, number of visits) and qualitative (food source location) foraging parameters were observed in greenhouse and field settings. Repellent effects were minimal in both lab and field, parameters of foraging and nestbuilding behaviour were –at maximal sublethal exposure- affected by some products but not others.

POSTER PRESENTATION

A new species of *Ceresa* Amyot & Serville, 1843 (Hemiptera: Membracidae) associated with the soy culture in Brazil

Gabriel Andrade

Universidade Estadual do Oeste do Paraná, Cascavel, Paraná, Brazil

Introduction: *Ceresa* is one of the most speciose genera within the Membracidae, and was reviewed by ANDRADE (2004). This work provides a foundation for naming undescribed taxa, and also trying new data from their host plants and distribution.

Methods: Dried specimens are being examined, from the most representative collections of the Neotropical fauna, and also recent data from the literature that refers to species of this group. The usual routines in systematics and morphological taxonomy are applied, and all new data on undescribed taxa and host plants are now being compiled.

Results: Some species were already formally associated to host plants, and in recent divulgation in events, *C. brunnicornis* (Germar, 1835) was verified causing damages in soy in south Brazil. There is another, probably new species was recently found in Brazil (ZANELLA, 2007: Cultivar Grandes Culturas 97: 24-26) causing damage to soy culture in the states of Piauí, Maranhão, Tocantins and probably Rio Grande do Sul. It has distribution along the east coast, within the main domain of the Atlantic forest. It is similar to *C. fasciatithorax* Remes-Lenicov, 1973 described from Bolivia, differing mostly in color pattern, but also in the male genitalia features.

Conclusions: Although reviewed and with 34 described species, new species of this genus remain to be described. Some have been previously associated with different hosts, but all species are potential pests invasive to soy and other culture in Brazil, due to the polyphagism detected by collection data.

POSTER PRESENTATION

A new unusual, ornate species of *Ilithucia* Stål, 1867 from Costa Rica, with some considerations on other ornate Ceresini (Hemiptera: Membracidae)

Gabriel Andrade

Universidade Estadual do Oeste do Paraná, Cascavel, Paraná, Brazil

Introduction: *Ilithucia* was reviewed by SAKAKIBARA (2002), with several taxonomic changes within it and allied genera, and was the last comprehensive work on this group. Additional efforts are now being directed to all ornate genera of the tribe Ceresini. These studies are continuations of the work started by KOPP & YONKE (1979).

Methods: The specimens examined as a part of the present study are from the most representative collections of Membracoidea of the New World fauna, and specimens of a new species are from the collection of the The Natural History Museum, London, England. The usual techniques of systematics and morphological taxonomy are applied, and a manuscript is being submitted for publication.

Results: This new species conforms with the general features of *Ilithucia*, but has lateral spines on the posterior pronotal process. The three-spined posterior pronotal process is characteristic of *Poppea* Stål, 1867, *Cyphonia* Laporte, 1832 and *Eucyphonia* Sakakibara, 1968 (all Ceresini). Outside the Ceresini we find this condition in *Smilidarnis* Andrade, 1989, which appears to be a basal group for Smiliinae and Darninae, according to DIETRICH *et al.* (2001). The male genitalia features of the new species agree with both *Ilithucia* and *Poppea*, and also of *Antonae* Stål, 1867, although very different to that of *Cyphonia* and *Eucyphonia*.

Conclusions: Several features used formerly for the characterization the ornate Ceresini genera are labile and need reappraisal, and also investigation to define the reliable limits within these genera to understand the relationship between the ornate and the inornate genera of this tribe.

POSTER PRESENTATION

Genitalia description of *Hylesia metabus* (Lepidoptera: Saturniidae: Hemileucinae)

José Enrique Piñango Bustamante[1], Beatriz Herrera-Malaver[2], Carmen V. Liendo-Barandiaran[2], Cristina Sainz-Borgo[2], José Vicente Hernández[2]

[1]Insectario, Zoológico El Pinar, Caracas, DC, Venezuela, [2]Universidad Simón Bolívar, Caracas, Estado Miranda, Venezuela

Introduction *Hylesia* is a Neotropical moth genus, widely distributed from Mexico to Argentina. In Venezuela North-eastern, *Hylesia metabus* is an insect of importance in Public Health because it causes contact dermatitis with the abdominal setae released by females of this species. In general, adults and larvae present different patterns of coloration. These observations could suggest more than one species of *H. metabus* the presence in that area.

Methods Pupae and larvae were collected in different localities of Monagas, Sucre and Delta Amacuro States- Venezuela. The genitalia of females and males were extracted and observed under a binocular microscope. The material was preserved and labelled.

Results Differences in males and females genitalia were not found among compared samples.

Conclusions These results are congruent with DNA molecular analysis of *H. metabus.* Both evidences suggest that *H. metabus* is a single species.

POSTER PRESENTATION

Effects of ace inhibitors and TMOF on growth, development and trypsin activity of larval *Spodoptera littoralis*

Els Lemeire[1], Dov Borovsky[2], John Van Camp[3], Guy Smagghe[1]

[1]Laboratory of Agrozoology, Department of Crop Protection, Faculty of Bioscience Engineering, Ghent University, Ghent, Belgium, Ghent, Belgium, [2]University of Florida, Institute of Food and Agricultural Sciences, Florida Medical Entomology Laboratory, 200 9th St SE, Vero Beach, FL 32962, Vero Beach, United States, [3]Research Group of Food Chemistry and Human Nutrition, Department of Food Safety and Food Quality, Faculty of Bioscience Engineering, Ghent University, Ghent, Belgium, Ghent, Belgium

Angiotensin converting enzyme (ACE) is a zinc metallopeptidase capable of cleaving dipeptide or dipeptideamide moieties at the C-terminal end of peptides. ACE is present in the hemolymph and reproductive tissues. The presence of ACE in the hemolymph and its broad substrate specificity suggests an important role in processing of bioactive peptides. After molecular cloning and characterization of *SlACE*, this study reports the effects of ACE inhibitors on larval growth in the cotton leafworm *Spodoptera littoralis*. Feeding ACE inhibitors *ad lib* decreased the growth rate, inhibited ACE activity in the larval hemolymph and down regulated trypsin activity in the larval gut. These results indicate that *S. littoralis* ACE may influence trypsin biosynthesis in the larval gut by interacting with a trypsin modulating oostatic factor (TMOF). Injecting third instar larvae with a combination of Aea-TMOF and the ACE inhibitor captopril, down regulated trypsin biosynthesis in the larval gut indicating that an Aea-TMOF gut receptor analogue could be present. Whereas, injecting captopril and enalapril into newly molted fifth instar larvae stopped larval feeding and decreased weight gain. Together, these results indicate that ACE inhibitors are efficacious in stunting larval growth and ACE plays an important role in larval growth and development.

This work was supported by the Fund for Scientific Research (FWO-Vlaanderen, Belgium) and the Special Research Council of Ghent University (BOF-UGent).

POSTER PRESENTATION

Expression of *Sambucus nigra* agglutinin (SNA-I') from elderberry bark in transgenic tobacco plants results in enhanced resistance to different insect species

Shahnaz Shahidi-Noghabi[1], Els JM Van Damme[2], Guy Smagghe[1]

[1]Laboratory of Agrozoology, Department of Crop Protection, Faculty of Bioscience Engineering, Ghent University, Ghent, Belgium, Ghent, Belgium, [2]Laboratory of Biochemistry and Glycobiology, Department of Department of Molecular Biotechnology, Faculty of Bioscience Engineering, Ghent University, Ghent, Belgium, Ghent, Belgium

Tobacco plants (*Nicotiana tabacum* cv Samsun NN) have been transformed with the gene encoding the type-2 ribosome-inactivating protein (RIP) SNA-I′ from elderberry (*Sambucus nigra*) under the control of the cauliflower mosaic virus 35S promoter. Previous research confirmed that these plants synthesize, correctly process and assemble a fully active RIP. Variability in protein expression was observed within the transgenic lines. The effects of the type-2 RIP SNA-I′ delivered through a leaf feeding assay were evaluated in the laboratory on two economically important pest insects belonging to the orders of Hemiptera, the tobacco aphid (*Myzus nicotianae*) and Lepidoptera, the beet armyworm (*Spodoptera exigua*). In the experiment with aphids, significant effects were observed on the life parameters, such as survival, intrinsic rate of increase, net reproductive rate, mean generation time and mean daily offspring, whereas with caterpillars significant reduction in fresh weight as well as retardation in development were observed. In addition, significant increases in mortality were noted for insects fed on the transgenic lines as compared to wild type plants. This information provides further support for RIPs having a role in plant resistance to insect pest species.

This work was supported by the Fund for Scientific Research (FWO-Vlaanderen, Belgium) and the Special Research Council of Ghent University (BOF-UGent).

POSTER PRESENTATION

Ferritin and α-amylase act as putative target sites for the insecticidal snowdrop lectin (*Galanthus nivalis* agglutinin; GNA) in the cotton leafworm *Spodoptera littoralis*

Amin Sadeghi[1], Els JM Van Damme[2], Guy Smagghe[1]

[1]Laboratory of Agrozoology, Department of Crop Protection, Faculty of Bioscience Engineering, Ghent University, Ghent, Belgium, Ghent, Belgium, [2]Laboratory of Biochemistry and Glycobiology, Department of Molecular Biotechnology, Faculty of Bioscience Engineering, Ghent University, Ghent, Belgium, Ghent, Belgium

Despite numerous efforts that have been made to evaluate the toxicity of plant lectins against insects, their mechanism of action is not clearly understood. Therefore the aim of this project was to identify putative target receptor protein(s) in the midgut of larvae of the cotton leafworm (*Spodoptera littoralis*) that are responsible for binding of the insecticidal lectin from snowdrop (*Galanthus nivalis* L.; GNA). After dissection and homogenization of 800 larval midguts, the water soluble and membrane proteins were fractionated and chromatographed on an affinity column with immobilized GNA. SDS-PAGE analysis revealed many different GNA-binding proteins among which 4 soluble proteins with polypeptides of approximately 26, 42, 50 and 72 kDa, and 6 membrane proteins composed of 26, 34, 42, 50, 74 and 78 kDa subunits. N-terminal sequencing identified the 26 kDa soluble protein band (TQXHVNPVDIQDXVTG) as secreted ferritin and the 50 kDa band (YKNPYYAANRSVNVHLF) as α–amylase. The 32 and 26 kDa polypeptides from the membrane protein fraction (ADTAYQDVSGDXXAXT and TQXHVNPVTIXXEXXM) revealed sequence homology to ferritin from the midgut of the tobacco hornworm (*Manduca sexta*) and the silkmoth (*Bombyx mori*), respectively. In conclusion, we hope that with this new information we can sustain the use and exploitation of insecticidal lectins to enhance the resistance of crops against pest insects into an IPM strategy.

This work was supported by Ministry of Science, Research and Technology of Iran and Kurdistan University to AS, and Fund for Scientific Research (FWO-Vlaanderen, Belgium) to GS and EJMVD.

POSTER PRESENTATION

Ground beetle community response to commercial and alternative silviculture in Eastern boreal forests of Canada

Kit O'Connor, Timothy Work

Université du Québec à Montréal, Montréal, Québec, Canada

Introduction: Emulating natural forest structure is seen as one of the keys to maintaining biodiversity and natural ecosystem function in managed forests. Inclusion of structural components such as standing snags and large diameter downed deadwood is being considered in forest management plans as a way to buffer managed stands against major ecosystem shifts. We used carabid communities to evaluate the efficacy of a series of experimental silvicultural treatments for maintaining beetle biodiversity over a 270-year successional gradient in the mixedwood boreal zone of western Quebec.

Methods: Beetles were collected over 2004-2007 using pitfall traps from a series of replicated whole-stand treatments including, partial cutting (both dispersed and aggregated), clearcutting, prescribed burning, whole-tree harvesting and a series of treatments that altered quantities of standing and fallen deadwood. We used naturally burned and uncut stands from three successional cohorts as controls. We used multivariate regression trees to quantify compositional differences.

Results: We collected more than 22,400 carabids representing 52 species. Aspen and mixedwood clear-cuts most closely resembled natural wildfire while conifer-dominated clear-cuts contained distinct insect assemblages. Gap-cut mosaic communities were similar to those found in clear-cuts while dispersed cuts removing equivalent basal area hosted communities similar to uncut control stands. Deciduous stands were tolerant of up to 2/3 stem removal without detectable community change. Jack pine thinning treatments emphasized the role of downed dead-wood in determining carabid communities.

Conclusion: These findings underscore the need to adapt coarse-filter management to stand-level characteristics such as successional stage and structural components to maintain biodiversity.

POSTER PRESENTATION

On the polymorphism of Membracoidea (Hemiptera), with emphasis on *Phormophora maura* (Fabricius, 1803) (Membracidae)

Gabriel Andrade

Universidade Estadual do Oeste do Paraná, Cascavel, Paraná, Brazil

Introduction: Morphology is the main base for systematics, and new features for interpretation can still be discovered. The observations found are presented to call attention to special features in studies on groups that are gregarious and on polymorphic, especially Membracoidea.

Methods: Dried specimens were borrowed from the most representative collections of the Neotropical fauna, along with field observations of species of Membracidae that aggregate in family groups. Of special note is *Phormophora maura* in Minas Gerais State, Brazil, of which we found adults and immatures attacking *Piptocarpha* sp. (Asteraceae) and associated with the ant *Cephalotes atratus* (Linné,1758).

Results: Within this species we found polymorphism and sexual dimorphism, in both adults and immatures, and a polychromism within the females. The males differ from females in their smaller size, brown groundcolor, and in pronotal and forewing sculpture. Within the females, the general color black can be thoughout or can be ornate, with a variable green spot on the sides of the pronotum. This peculiarity was used to distinguish the *P. maura* from *P. dorsata* by FABRICIUS. The immatures presents also dimorphism, in size and most by color. These observations agree with that all gregarious Membracoidea presents polymorphism, as noted here and some authors.

Conclusions: Studies within gregarious species of Membracoidea show that the polymorphism are quite common, and requires caution in the interpretations of characters. It is very important to examining specimens from the same aggregation, and the male genitalia features are generally the reliable apomorphies.

POSTER PRESENTATION

Pathogenicity of *Beauvaria bassiana* against the plum curculio

Daniel Cormier[1], Claude Guertin[2], Gérald Chouinard[1]

[1]Institut de recherche et de développement en agroenvironnement, St-Hyacinthe, Québec, Canada, [2]INRS-Institut Armand-Frappier, Laval, Québec, Canada

Introduction: The plum curculio, *Conotrachelus nenuphar* (Herbst), is one of the most destructive insects of pome and stone fruit in North America and control is achieved mainly by insecticide applications. Laboratory bioassays were conducted to evaluate the pathogenicity of two isolates of the microbial agent *Beauveria bassiana*, (Balsamo) Vuillemin against this pest and also on the predatory lady beetles, *Coleomegilla maculata lengi* Timberlake.

Methods: Suspensions of the *B. bassiana* isolates *INRS-CFL* and *INRS-IP* were prepared to a concentration of 0,10^4, 10^6, 10^7 and10^8 conidia/ml. Thirty plum curculio adults from both the hibernating and summer populations were soaked during five seconds into each solution, then placed in Petri dishes in an environmental chamber. The pest mortality was recorded every 48h for 14d, to determine the $LC_{10, 50, 90}$. Twenty lady beetles were soaked in 0 and 10^7 conidia/ml and predator mortality was recorded daily for 14d. Each bioassay was repeated 3-5 times.

Results: A significant difference was observed between the lethal concentrations of the *INRS-CFL* and *INRS-IP* isolates for both the hibernating and summer populations of the plum curculio. However, using a dose of 10^7conidia/ml, the survival time of this insect was not significantly different when treated with either isolates suggesting that both isolates had similar virulence against this insect pest. Moreover, both *B. bassiana* isolates had low toxicity on the lady beetles.

Conclusion: The two isolates of the entomopathogen *B. bassiana* are promising as microbial agent to control the plum curculio while having little negative impact on lady beetle.

POSTER PRESENTATION

Assessing lethal and sublethal effects of insecticides with different modes of action in bumblebees *Bombus terrestris*

Veerle Mommaerts[1], Xavier Cuvelier[1], Sofie Reynders[1], Guido Sterk[2], Guy Smagghe[3]

[1]Laboratory of Cellular Genetics, Department of Biology, Faculty of Sciences, Free University of Brussels, Brussels, Belgium, Brussels, Belgium, [2]Biobest NV, Westerlo, Belgium, Westerlo, Belgium, [3]Laboratory of Agrozoology, Department of Crop Protection, Faculty of Bioscience Engineering, Ghent University, Ghent, Belgium, Ghent, Belgium

Nowadays bumblebees are widely used in greenhouses for the pollination of several crops like tomatoes, sweet peppers and eggplants. Moreover due to Integrated Pest Management (IPM) programs cultivators are spraying less broad-spectrum pesticides in order to control pest insects and mites. Although it remains important to determine possible negative effects of pesticides on bumblebees as pollination must be guaranteed. This study examined the adverse effects of several classes of pesticides on the survival and on the reproduction of the beneficial organisms *Bombus terrestris*. In total nine commercial insecticides/acaricides were tested: three neonicotinoids (imidacloprid, thiacloprid, flonicamid), three acaricides (bifenthrin, milbectine, spirodiclofen) and three insect growth regulators (chitin synthesis inhibitor: flucycloxuron, juvenile hormone analogue: pyriproxyfen, ecdysone agonist: tebufenozide). The bumblebees were exposed in in-house made artificial nests (Mommaerts *et al.,* 2006) to the compounds via three different routes of exposure: topically via dermal contact, and orally via the drinking of treated sugar water and via eating treated pollen. The compounds were tested at their respective maximum field recommended concentrations (MFRC). In general, these risk hazard tests showed that only few of the tested pesticides showed acute worker toxicity. In addition, during 11 weeks the numbers of drones were scored at weekly basis as endpoint of sublethal effects against reproduction. The compatibility of each compound to be used in combination with *B. terrestris* within an IPM approach is discussed in relation to routes of uptake and effects.

Mommaerts, V., Sterk, G., Smagghe, G. (2006). Hazards and uptake of chitin synthesis inhibitors in bumblebees Bombus terrestris. Pest Management Science, 62, 752-758.

POSTER PRESENTATION

Changes in integument structure during the imaginal molt of the honeybee, *Apis mellifera*

Moysés Elias-Neto, Michelle Soares, Márcia Bitondi

São Paulo University, Ribeirão Preto/SP, Brazil

Introduction: The sequencing of the honeybee genome brought a new dimension to the study of the integument (cuticle and associated epidermis) in social insects. Information on the structural changes that the integument undergoes during molting cycles is of interest for the characterization of differential expression and regulation of cuticle protein genes in the context of metamorphosis. In the present work we combined information on the external morphology of the honeybee with a description of the changes taking place in the integument during the pupal-imaginal molt.

Methods: Thoracic and abdominal integuments were dissected and prepared for light microscopy. Cross sections were stained with methylene blue and basic fucsin. Whole mounts were also examined.

Results: The temporal sequence of integument sections and whole mounts revealed considerable changes in epidermis and cuticle structure during the pupal-imaginal molt. In the sequential morphological patterns, the periods of deposition and differentiation of the adult cuticle were clearly distinguished. Apolysis and the subsequent deposition of the adult cuticle were marked by an increase in the thickness of epidermal cells, which also changed their shapes. But epidermis becomes thin as cuticle differentiation advances. We also observed that thoracic cuticle was deposited earlier and showed to be thicker than the abdominal.

Conclusions: It is hoped that data presented here will be of help in studies on functional genomics on the context of metamorphosis and adult exoskeleton formation.

Financial support: FAPESP (05/03301-5)

POSTER PRESENTATION

Use of bumblebees and microbiological antagonists in the battle against plant pathogens

Veerle Mommaerts[1], Guido Sterk[2], Guy Smagghe[3]

[1]Laboratory of Cellular Genetics, Department of Biology, Faculty of Sciences, Free University of Brussels, Brussels, Belgium, [2]Biobest NV, Westerlo, Belgium, [3]Laboratory of Agrozoology, Department of Crop Protection, Faculty of Bioscience Engineering, Ghent University, Ghent, Belgium

A promising alternative for fungicides are microbiological control agents (MCAs). Although in the field the ability of these MCAs to control plant pathogen infections is limited. The success of MCAs is depending on several factors but the most important one is being present at the site of infection. Here bumblebees that are already used in modern greenhouses may play an important role as they can transport by use of a dispenser system the MCAs directly to the flowers which are the main entry point of many plant pathogens. In a first part of this study the effect of MCAs was evaluated on the pollinator *Bombus terrestris*. The bumblebees were exposed to a powder formulation of each antagonist via walking through a miniature dispenser. In this work we tested three commercial MCAs: Binab T-vector, Prestop Mix and Serenade, containing *Trichoderma atroviride* and *Hypocrea parapilulifera*, *Gliocladium catenulatum* J1446 and *Bacillus subtilis* QST713, respectively. These tests showed that the Binab T-vector, Prestop Mix and Serenade did not cause acute worker toxicity nor caused an adverse effect on the reproduction (production of drones). In a second part of the study, bumblebee hives were mounted with a dispenser and the efficiency of bumblebee workers to carry MCAs was evaluated. In this test we compared an existing system, the side by side passageway (SSP), and an own developed system, the Funnel-dispenser. In both systems the bumblebees workers needed to walk through a 0.5 cm layer of commercial MCA product. Then the amounts of CFU present on the head, the thorax, the abdomen and the legs were determined in order to get more insight in the transport capacity of the two systems. The results showed that the whole body of the bumblebees was treated after walking through the dispensers, and that the F-dispenser showed higher CFUs per tissue than the SSP dispenser.

Overall, the results indicated that the Binab T-vector, Prestop Mix and Serenade are safe to be used in a vectoring system of flying doctors. Here the F-dispenser is a promising system, although further optimizations are necessary.

POSTER PRESENTATION

Analysis of testes in the production of ecdysteroids in Lepidoptera (*Spodoptera littoralis*)

Masatoshi Iga, Tim Vleugels, Guy Smagghe

Laboratory of Agrozoology, Department of Crop Protection, Faculty of Bioscience Engineering, Ghent University, Ghent, Belgium

Over the last decade there have been some reports on production of ecdysteroids and a testis ecdysiotropin by testes from *Lymantria dispar* and *Rhodnius prolixus* (Loeb *et al*., 2001; Vafopoulou & Steel, 2005) In this project we tested the potency of the testes from the cotton leafworm, *Spodoptera littoralis* (Lepidoptera: Noctuidae), to produce ecdysteroids at different levels. In our approach, we measured the *in vivo* ecdysteroid titers of the hemolymph and the testes at different moments in the last larval stage to see the relationship between them by using an enzyme immunoassay (EIA). Then testes were cultured in Grace's insect medium and tested the effect of insulins and peptides as these are reported as inducers of ecdysteroid biosynthesis. The ecdysteroid amounts in the cultured testes and the culture medium were followed. In addition, the expression of the Halloween genes such as *spook*, *phantom*, *disembodied* and *shadow* were evaluated as criterion of *de novo* ecdysteroid biosynthesis. For this study we compared to the situation of the prothoracic glands. Finally the results are discussed in relation to potential different resources of ecdysteroids and developmental stages.

This work was supported by the Fund for Scientific Research (FWO-Vlaanderen, Belgium)

POSTER PRESENTATION

Ecdysteroid-resistance mechanism independent from ecdysteroid receptor function in cell lines from the polyphagous noctuid pest *Spodoptera exigua*

Luc Swevers[1], Thomas Soin[2], Hadi Mosallanejad[2], Kostas Iatrou[1], Guy Smagghe[2]

[1]Insect Molecular Genetics and Biotechnology, Institute of Biology, National Centre for Scientific Research "Demokritos", Aghia Paraskevi Attikis, Athens, Greece, [2]Laboratory of Agrozoology, Department of Crop Protection, Faculty of Bioscience Engineering, Ghent University, Ghent, Belgium

In this project we describe an analysis of the ecdysteroid receptor signaling pathway in ecdysteroid-resistant Se4 cell lines resistant towards the insect molting hormone 20-hydroxyecdysone (20E) or a non-steroidal ecdysone agonist (methoxyfenozide). In contrast to other ecdysteroid-resistant cell lines described in literature, our data support the existence of a normal functioning ecdysteroid receptor complex in the resistant Se4 cell lines: (1) using a recombinant BmNPV baculovirus as a transduction tool, activation of an ecdysone-responsive luciferase cassette was demonstrated; (2) the early gene *HR3* is constitutively expressed in the resistant cell lines that are grown in the presence of 20E or methoxyfenozide. Quantitative RT-PCR indicated that expression levels of *SeEcR* mRNA were comparable among sensitive and resistant cell lines. Sequencing revealed the presence of *SeEcR* mRNA with a wild-type ligand-binding domain in resistant cells. Finally, a possible role for the gene *FTZ-F1*, whose expression correlates with the absence of circulating ecdysteroids during insect development, in the resistance mechanism was investigated. However, it was observed that *FTZ-F1*, in contrast to what is observed during insect development, is constitutively expressed in Se4 cells and that its expression is not regulated by the addition of ecdysteroid. It is proposed that the resistance mechanism in Se4 cells resides at the coupling between the conserved hierarchical cascade of early and early-late gene expression and the differentiation program in the Se4 cell line.

This work is supported by General Secretariat for Research and Technology, Ministry of Development in Greece, a doctoral grant from the Ministry of Science, Research and Technology (SRT) and Agricultural Research Organization of Iran (Plant Pest and Disease Research Institute, the Institute for the Promotion of Innovation by science and Technology in Flanders (IWT, Belgium) and the Fund for Scientific Research (FWO, Belgium).

POSTER PRESENTATION

Response of weevil assemblages (Coleoptera: Curculionidae) to edge effects in tropical lowland forests adjacent to different matrix habitats.

Alida Mercado Cárdenas[1], Christopher Buddle[1], Héctor Barrios[3]

[1]Department of Natural Resource Sciences, McGill University, Ste-Anne-de-Bellevue, Quebec, Canada, [2]Smithsonian Tropical Research Institute, Panama, Panama, [3]Programa Centroamericano de Maestría en Entomología, Universidad de Panamá, Panama, Panama

Introduction: Deforestation and fragmentation in tropical regions is increasing the proportion of edges between forests and modified adjacent habitats. The contrast between adjoining habitats are expected to influence the effects created by edges. Few consistent patterns have been determined on the response of insects to edge effects as different species show opposite responses.

Methods: The response of insect species to edge effects is being studied in tropical lowland forests in Panama using weevils (*Coleoptera: Curculionidae*) as focal taxon. The influence of the adjacent habitat to the forest is being assessed by sampling at three transects located adjacent to coffee plantations and three to pastures (July and October 2007). Insects are collected sifting leaf-litter at five distance points from the edge into the forest (0, 10, 50, 100 and 250 m).

Results: A total of 2001 beetles were collected, of which 248 are weevils of 14 species. The highest number of species is found further away from the edges. 13 species (111 specimens) have been collected from the coffee plantation transects and 9 species (137 specimens) from the pasture transects. The number of species found at and near the edge is lower in pasture sites than in coffee plantation sites.

Conclusion: Forest edges have a negative effect on species richness of leaf-litter weevils. The results show a trend of a higher extent of edge effects between sites with a higher contrast. However, we have yet to find supporting evidence to state that weevil assemblages differ between pasture sites and coffee sites.

POSTER PRESENTATION

Evaluation of resistance mechanism to two spotted spider mite on some chiti bean genotype in greenhouse condition

Mazaher Yousefi, Hamidreza Dori

Agricultural and Natural Resources Research Center of Markazi Province, Arak, , Islamic Republic of Iran

Tetranychus urticae (Koch) is one of the most important pest on bean field in our country , according to its high economical damage in the area of our country , this investigation carried out in order to recognize new resistance resource . in this study , resistance and its mechanism evaluated to related of *Tetranychus urticae* , that including : Antixenosis (number of placed *Tetranychus urticae* after 24 and 48 hours in genotype of chiti bean) , Tolerance (evaluated amount of damage in genotypes based on 1 – 6 scale) and Antibiosis (average of nymph in every genotype) by using greenhouse standard test in 12 chiti bean genotype (screened of 300 chiti bean genotype in field condition)and 24 genotype (resulted from same genotype in greenhouse condition). The result of mean comparison by Douncans test showed that genotypes with numbers Ks-21184, Ks-21479 and local Khomein chiti have high symptom of damage for *Tetranychus urticae* and the lowest amount of toleration to pest observed in genotypes Ks-21104, Ks-21201, Ks-31163, Ks-41235 and Ks-21343. The highest amount of antibiosis counted and recorded from genotypes with numbers Ks-41144, Ks-21246, Ks-21365 and Ks-21184 and the lowest recorded from genotypes with numbers Ks-21102, Ks-21112, Ks-21429, Ks-21156, Ks-21360, Ks-31163and Ks-41235. The highest amount of antixenosis counted and recorded from genotypes with numbers Ks-21320, Ks-21343, Ks-21390, Ks-31144 and Ks-21429 and the lowest recorded from genotypes with numbers Talash, Ks-21283, Ks-41144, Ks-21143, Ks-21189, Ks-21102 and Ks-21178. The highest amount of Plant Resistance Index observed in Ks-21178 and Ks-21235 with amount (104.8 and 63.4) and the lowest amount of PRI from genotypes with numbers Ks-21320, Ks-21324 and Ks-31144. The result of this study showed that different and desired mechanism resistance or tolerance in chiti bean genotype on combination with their yield and its component could be suitable base for recognizing genetic resources of *Tetranychus urticae.* The resistance genotype of this research could be recommend to farmers after succefull experiment in to culture on extend area.

POSTER PRESENTATION

Novel mosquito traps in the fight against urban dengue – from monitoring to control

Andreas Rose[1], Martin Geier[1], Alvaro E. Eiras[2], Maria da Gloria Teixeira[3], Maria das Gracas Vale Barbosa[4], Maria Paula Gomes Mourao[4]

[1]BioGents AG / University of Regensburg, Regensburg, Germany, [2]Federal University of Minas Gerais, Belo Horizonte, Brazil, [3]Federal University of Bahia, Salvador, Brazil, [4]Tropical Medicine Foundation of the Amazon, Manaus, Brazil

Dengue vector surveillance relies on the identification and analysis of larval habitats, on ovitraps, and also on sticky traps that catch ovipositing females. A recent addition to the arsenal is the BG-Sentinel trap for host-seeking females. This trap is very efficient for *Aedes aegypti*, *Ae. albopictus* and also *Ae. polynesiensis*. Due to its efficacy, it allows for a quick and meaningful population assessment in vector control programs and also for a better evaluation of the dengue transmission risk.

Still, a sustainable *Aedes* control remains a challenging task. Even combinations of adulticidal fogging, the reduction of oviposition sites in clean-up campaigns, and treating larval habitats with insecticides have only lead to limited success, especially over longer periods of time.

Recent field and laboratory tests have shown that the BG-Sentinel is not only a highly sensitive trap for dengue vector surveillance, but also that its trapping efficacy should be large enough for the trap to be used as an actual suppression tool against dengue. The data suggest that an area-wide use would significantly shorten the average life expectancy in the vector population and reduce vector density. This would lower the vectorial capacity and reduce the risk of dengue transmission.

To evaluate the impact of this strategy in the real world and with support from the World Bank and the Gates Foundation, we are currently beginning a pilot project involving several hundred households in Manaus, Brazil. In our presentation, we will introduce this project, presenting the underlying data and further explaining the concept.

POSTER PRESENTATION

Three new Hymenoptera species obtained from important agricultural pests

Helena Onody, Ágatha Gil, Ivy Melo, Manoel Dias, Angélica Penteado-Dias

Universidade Federal de São Carlos, São Carlos, SP, Brazil

Introduction: The parasitoids are one of the most important agents in the control of agricultural pests, either by their natural occurrence in the environment or for their use in biological control programs. The Hymenoptera predominate among insects entomophagous. Despite its importance, there is major insufficiency knowledge of their biology and taxonomy especially in neotropical region. This paper records the occurrence of new Hymenoptera species occurring on important agricultural pests.

Material and Methods: The collects of the lepidopterous caterpillars were made in organic crops São Carlos, SP, Brazil region. The caterpillars were transferred to the laboratory, aiming to verify the emergence of natural enemies.

Results: It was observed the occurrence of three new Hymenoptera species parasitizing important agricultural pests. From a *Diaphania hyalinata* Linnaeus, 1758 caterpillar, a new *Eiphosoma* Cresson, 1865 (Ichneumonidae; Cremastinae) species was obtained. A specimen of *Colpotrochia* Holmgren, 1855 (Ichneumonidae, Metopiinae) emerged from the pupae of *S. eridania* (Cramer, 1782). A new species of *Hypomycrogaster* Ashmead, 1898 (Braconidae, Microgastrinae) was obtained from *Hellula phidialis* (Walker, 1859) caterpillar. There was no previous register of some *Colpotrochia* and *Hypomicrogaster* species parasitizing the hosts cited above.

Conclusion: The data gathered here point out the necessity for more studies about the Hymenoptera parasitoids in the neotropical region. The increase in taxonomic and biology knowledge of the group can offer more possibilities for its use in biological control programs.

POSTER PRESENTATION

The Campopleginae (Hymenoptera: Ichneumonidae) fauna of Brazilian savannah

Diogo Sandonato, Helena Onody, Angélica Penteado-Dias

Universidade Federal de São Carlos, São Carlos, SP, Brazil

Introduction: In Brazil, the savannah occupies about 20% of its territory. It can be found in plain regions that have dry climate with tortuous trees which grow in poor and acid soil. Considered as a "hot spots", it´s one of the most rich, endemic and threatened areas of the planet. Only 3% of its original extension is protected in parks and reserves. The Campopleginae (Hymenoptera, Ichneumonidae) are endoparasitoids cenobiontes mainly of Lepidoptera larvae. They are a cosmopolitan subfamily with 19 genera occurring in the neotropical region.

Methods: The analyzed material was collected with Malaise and Moericke traps, "sweeping" the vegetation and at light in 9 places in the Southeast and Center-west of Brazil.

Results: A total of 4002 specimens were identified in 14 different genera. *Microcharops* (38, 1 %), *Casinaria* (27, 4 %) and *Venturia* (18, 8 %) were the most common genera collected; the rarest genera were *Campoplex, Diadegma, Xanthocampoplex* and *Prochas*. The results obtained here differ from a similar study realized in another important Brazilian ecosystem, the Atlantic forest, where more than 60% of the material collected belonged to the genus *Dusona*.

Conclusions: The studied material revealed a large number of morphospecies, which points out the necessity of taxonomic studies to be conducted for the group. A higher knowledge of the biodiversity of this Brazilian biome can be useful in the management and conservation plans of the extremely threatened areas.

POSTER PRESENTATION

Integrated genomic and gene expression data for insect vectors of disease at VectorBase

Robert M. MacCallum, Seth Redmond, Fotis C. Kafatos, George K. Christophides

Imperial College London, London, United Kingdom

Introduction: VectorBase provides genomic bioinformatics resources for mosquito species and other insect vectors of disease. In addition to the annotation and visualisation of genomic data, a core role for VectorBase is to make gene expression data available to the community in an easily digested form for non-microarray experts.

Methods: It is vital to establish the relationship between each reporter (a.k.a. probe) on a microarray and its corresponding gene(s) or genomic region(s). This is usually done through alignment of reporter sequence to the genome. Since genome assemblies and gene sets go through many revision cycles, we have to have a robust method which is easy to apply to each new assembly/gene build. Since VectorBase uses the Ensembl genome annotation system, we can add the reporter alignment and gene assignment to the gene build process to ensure timely and reliable updating.

The experimental data is loaded into an open-source microarray management system called BASE. Each experiment is put through a standard processing pipeline, including normalisation. One or more statistical tests are then applied to the expression data with respect to the experimental factors being tested (e.g. developmental stage). The biologist is presented with a simple web page for their gene of interest. This page highlights the experiments that show differential expression and describes their results with a short text summary, which is searchable. More detailed plots and tables are also available to view or download, and access to the BASE analysis platform is available for experts.

Results: For *Anopheles gambiae*, experiments submitted by the community include developmental series, blood meal time-courses, tissue and organ comparisons, insecticide resistant strain comparisons. For *Aedes aegypti* we have developmental series, strain comparisons, viral infection and xenobiotic exposure. We welcome data from all VectorBase organisms.

Availability: The VectorBase website can be found at http://vectorbase.org

POSTER PRESENTATION

Genetic patterns of *Phyllonorycter platani* - an invasive leaf miner moth with Mediterranean origin

Ferenc Lakatos[1], Sylvie Augustin[2], Carlos Lopez-Vaamonde[2]

[1]University of West-Hungary, Sopron, Hungary, [2]INRA, Orleans, France

Introduction: *Phyllonorycter platani* (Staudinger) belongs to the family Gracillariidae, a large lepidopteran family having a high number of invasive species (e.g. *Cameraria ohridella*, *Phyllonorycter robiniella*). The species have invaded several parts of Europe in the last decades, however the expansion of the species range can be traced back to the 19th century. Its current distribution ranges from Denmark and South-Sweden in the north, to Great Britain and Spain in the west. Fortunately the colonization history of *P. platani* is well known (for review see Sefrova, 2001). The endemic area of the species is thought to be in the southern part of the Balkans, and to be aligned with the natural distribution of its main host *Platanus orientalis*. Due to wide cultivation of different *Platanus* species - mainly in urban areas - *P. platani* has now potential hosts throughout all of Europe. The aim of our study was to look at the pattern of genetic variation of *P. platani* to find possible colonization patterns within the present distribution of the species.

Methods: We used sequences of a 570bp long fragment of the mitochondrial COI gene to study the genetic variability of *P. platani* across its present distribution in Europe.

Results: Our results show moderate genetic variation in Europe with a reduction in genetic diversity of *P. platani* populations from east-to-west and from south-to-north across Europe.

Conclusions: Our findings confirms the hypothesis that *P. platani* have invaded the central and western part of Europe from the Balkans.

POSTER PRESENTATION

Detritivorous hairstreak butterflies (Lycaenidae: Theclinae: Eumaeini): phylogenetic analysis of the *Lamprospilus* Section

Marcelo Duarte[1], Robert Robbins[2]

[1]Museu de Zoologia, Universidade de São Paulo, São Paulo, SP, Brazil, [2]National Museum of Natural History, Smithsonian Institution, Washington, DC, United States

Introduction: Recent fieldwork indicates that facultative or obligate detritivory is more widespread in Lycaenidae than previously reported, occurring in *Lamprospilus*, *Arumecla*, *Camissecla*, *Ziegleria*, *Electrostrymon* and *Calycopis*, which were preliminary grouped in the *Lamprospilus* Section of the Eumaeini. The purpose of this contribution is to establish a phylogenetic basis for this section and its component genera. It is intended to be used to study the evolution of detritivory in Lycaenidae.

Methods: Adult morphology were used to infer phylogenetic relations. The ingroup included species (82) for which both sexes were available for study species. Equal-weight most parsimonious trees were searched in NONA 2.0. To test the assumption of equally weighed characters, implied weighting option of TNT was used. A variety of fit functions (k=3, 10, 50, 100, 1000) was tested.

Results: There were 50,000 equal-weight most parsimonious trees retained with 166 steps. There were either 594 or 1188 implied weight most parsimonious trees with k=10, 50, 100, 1000. The implied weight tree with k=3 rooted the ingroup in the middle of *Electrostrymon* and were not among the equal-weight most parsimonious trees. A new genus was erected and thirteen new combinations were established.

Conclusions: *Lamprospilus* Section was monophyletic in all analyses. Phylogenetic relations among genera were resolved and identical in the set of 594 or 1,188 trees that were most parsimonious with equal weights and with implied weights ranging from k=10 to 1,000. For this reason, we consider it to be the best estimate, albeit provisional, of relations among the *Lamprospilus* Section genera.

POSTER PRESENTATION

Orientation flights in bumblebees, *Bombus terrestris*

Andrew O. Philippides[1], Natalie Hempel de Ibarra[2], Olena Riabinina[1], Thomas S. Collett[1]

[1]University of Sussex, Brighton, United Kingdom, [2]University of Exeter, Exeter, United Kingdom

Introduction: When bees and wasps leave the nest to forage they perform learning flights. Several components of the flights seem to be adapted for the active acquisition of visual information allowing the animals to find their nests at return. Here we present an analysis of the learning flights of bumblebees when they are close to their nest in the ground.

Methods: Single, individually marked bumblebees were video-recorded when leaving their colony that was located under an artificial ground covered with a textured white carpet in a semi-open outdoor area. Two or four conspicuous landmarks, i.e. upright black cylinders, were set 15 cm from the nest hole.

Results: Flights start with a phase in which the bee flies in tight circles close to the nest hole and low on the ground. This component seems to be less prominent in the learning flights of other insects that have been recorded. It leads into the more usual semi-circular arcs backing away from the nest which resemble those of solitary wasps. These arcs appear to consist of a number of linked phases with behaviour consistent across arcs.

Conclusions: Bees tend to look at the landmarks from similar locations during learning and return flights possibly for learning and retrieving snapshots of landmarks and surrounding visual background.

POSTER PRESENTATION

Influence of clothianidin-based seed treatments on maize yield in North America.

Billy Fuller[1], Bradley McManus[1], Larry Bledsoe[2], Mark Boetel[3], Eileen Cullen[4], Chris DeFonzo[5], Bruce Eisley[6], Lance Meinke[7], James Oleson[8], Kenneth Ostlie[9], Mark Sears[10], Jon Tollefson[8], Roger Youngman[11]

[1]South Dakota State University, Brookings, SD, United States, [2]Purdue University, West Lafayette, IN, United States, [3]North Dakota State University, Fargo, ND, United States, [4]University of Wisconsin-Madison, Madison, WI, United States, [5]Michigan State University, Lansing, MI, United States, [6]The Ohio State University, Columbus, OH, United States, [7]University of Nebraska-Lincoln, Lincoln, NE, United States, [8]Iowa State University, Ames, IA, United States, [9]University of Minnesota, St. Paul, MN, United States, [10]University of Guelph, Guelph, Ontario, Canada, [11]Virginia Tech University, Blacksburg, VA, United States

Anecdotal reports suggest the possibility of increased yield in corn fields where clothianidin (Poncho) insecticide-treated seeds are planted. Higher yield would be expected in cases where this treatment might provide protection from feeding injury by corn rootworms and other soil-dwelling insect pests. However, some reports indicate higher yields from these seed treatments when rootworm densities were very low. Preliminary data from several states in did little to support or rule out clothianidin-related yield enhancements. Therefore, a 3-yr study was begun in 2004 by a multi-state/national corn rootworm committee (NCCC46) to more fully investigate this issue. Evaluations were designed to evaluate clothianidin-treated seed in comparison with conventional granular insecticides, transgenic hybrids, and untreated control plots. Combined results from this investigation indicated that occasionally higher yields were obtained in clothianidin-treated plots than would have been expected for corn fields with moderate to high corn rootworm infestations. In other instances, clothianidin-treated seed produced no yield enhancements, even where no rootworms were present. This mixed response could relate to the wide geographical range (10 U. S. states and one Canadian province) and variety of environmental conditions among research sites used for this project.

POSTER PRESENTATION

Seed treatment insecticide technology for managing soil insect pests of sugarbeet

Mark A. Boetel[1], Robert J. Dregseth[1], Allen J. Schroeder[1], Ayanava Majumdar[2]

[1]Department of Entomology, North Dakota State University, Fargo, North Dakota, United States, [2]North Dakota State University Extension Service, Finley, North Dakota, United States

Introduction: North American sugarbeet fields are often at risk of infestation by one or more soil-dwelling arthropod pests that can cause major yield losses. Granular and liquid insecticide formulations have been used to manage soil insect pests for decades. Insecticidal seed treatments, if found efficacious against these pests, would be attractive control alternatives because they are simple and relatively safe to deploy.

Methods: Four years of field trials (2004 to 2007) were carried out to compare experimental seed treatments and conventional insecticides for efficacy against the following: 1) sugarbeet root maggot (SBRM), *Tetanops myopaeformis* Röder; 2) wireworms (*Limonius* spp.); and 3) subterranean springtails (Collembola).

Results: Poncho (clothianidin) + cyfluthrin at 60:16 g active ingredient (a.i.) per unit (100,000 seeds) provided similar levels of SBRM control to the conventional insecticide (terbufos 15G applied at 2 kg a.i./ha]). Excellent wireworm control was provided by Poncho+betacyfluthrin (60:8 g a.i./unit seed), Cruiser 5FS (thiamethoxam; 60 g a.i./unit), and terbufos 15G (1.7 kg a.i./ha). Springtail trials demonstrated that seed treatments (V-10170, V-10170+danitol, and Poncho+betacyfluthrin) were comparable in performance to low and moderate rates (1 to 1.7 kg a.i./ha) of terbufos 15G.

Conclusions: Seed treatments appear to be less likely than conventional insecticides to cause phytotoxicity and associated yield losses. The experimental seed treatments we evaluated are likely to provide similar efficacy as moderate rates of currently labeled conventional soil insecticides for controlling SBRM, wireworms, and subterranean springtails; however, they should not be relied on as the sole control tactic in areas heavily infested by SBRM002E

POSTER PRESENTATION

New predator of redgum lerp psyllid in *Eucalyptus* plantations in Brazil

Carlos Wilcken[1], Thaise Dias[1], Pedro Ferreira Filho[1], Luiz Alexandre Sá[2], Hélcio Gil-Santana[3]

[1]UNESP - campus of Botucatu, Botucatu, SP, Brazil, [2]Embrapa Meio Ambiente, Jaguariuna, SP, Brazil, [3]Fiocruz, Rio de Janeiro, RJ, Brazil

Introduction: In 2003 Redgum Lerp Psyllid (RLP), *Glycaspis brimblecombei* (Hemiptera: Psyllidae) was detected in eucalyptus forests in State of São Paulo, Brazil and it spread quickly by central and south regions, reaching other countries including Uruguay and Argentina. This pest causes defoliation, sooty mold and dieback in *Eucalyptus camaldulensis* and in *E. grandis x E. urophylla* clonal plantations. In 2004 it was started a biological control program using an exotic parasitoid, *Psyllaephagus bliteus* (Hymenoptera: Encyrtidae), with partial success of control. The most common predators, like ladybirds, lacewings and hover flies are not effective in control of this pest until now.

Methods: In August, 2007 a new predator, identified as *Atopozelus opsimus* Elkins, 1954 (Hemiptera: Reduviidae) was discovered during a pest survey in *E. camaldulensis* plantation at Luiz Antonio, SP, Brazil**.**

Results: *A. opsimus* is the first Brazilian native predator that specialized in attacking RLP. The adults of this reduviid look for the pest in leaves and branches of eucalyptus, predating adults and nymphs. About the lerp protection, predators place their stylets under the lerp until released it and after rises it with the front legs to eat the nymph. Predator can capture adults of psyllid in fly. Bioecology and predatory capacity studies of *A. opsimus* are in development and this predator has demonstrated to be an important agent in biological control of RLP in Brazil, mainly in cerrado region, where the parasitoid is not effective during the outbreaks in dryer periods.

POSTER PRESENTATION

Seasonal changes in dietary preferences of the European red ant in its invasive range.

Eleanor Groden, H. Alejandro Arevalo-Rodriquez, F. A. Drummond

University of Maine, Orono, ME, United States

Introduction: *Myrmica rubra*, the European red ant, a common northern temperate ant in Europe, has been introduced and become invasive in coastal areas in the northeastern US and parts of Maritime Canada. In addition to its pestiferous stinging behavior, high density populations of *M. rubra* are also impacting native North American flora and fauna. This study on the feeding ecology of *M. rubra* was initiated to assess how this ant sustains the large populations observed in the invasive range and its impact on native species, and to provide information about potential baits for management.

Methods: We evaluated preferences of different nutrients types using a standard diet matrix to which set concentrations of the nutrients were added. Diets were presented to ants in choice experiments in the field throughout the field season. Colonies were also collected regularly and the rate at which different nutrient-based diets were transferred throughout the colony was measured using flourescent tracers.

Results: As ant activity increased post diapause, a strong initial preference for sugars was seen, with the combined sucrose and honeydew diet accounting for greater than 53% of the diets consumed in the first month. Sugar preference declined in mid season as a stronger preference for protein was exhibited. However, as populations approached pre-diapause conditions, sugar consumption increased again.

Conclusions: Diet preferences corresponded to changing needs associated phenology of the colonies. Transitions in preference from sugars to proteins and back to sugars tracked the needs of the maturing colonies.

POSTER PRESENTATION

Effect of a new insecticide of the diamides chemical class(chlorantraniliprole) for control of: whitefly, *Bemisia tabaci* Biotype B; thrips, *Frankliniella schultzei*; leafminer, *Liriomyza huidobrensis*; and tomato pinworm, *Tuta absoluta*, on tomato

Geraldo Papa, Mario Sergio Oliveira, Dhiego Duvaresch, Fernando Celoto, Shizuo Seno

Sao Paulo State University -Unesp, Ilha Solteira/SP, Brazil

Introduction: The new insecticide (chlorantraniliprole) of the diamides chemical class has activity on a broad spectrum of economically important pest species. The mode of action is activation of insect ryanodine receptors. The objective of this work was to evaluate the performance of this insecticide on the control of the early pests in tomato.

Methods: The experiment was installed in greenhouse conditions, in Ilha Solteira/SP/Brazil, in tomato. The design was randomized blocks, whit 4 replicates. The treatments consisted: chlorantraniliprole 350 WG (at 20, 40 and 80 g a.i./ha), imidacloprid 700 WG (at 210 g a.i./ha) and thiamethoxam 250 WG (at 50 g a.i./ha) at 3 applications through chemigation by drip irrigation (15 days interval between each application, being the first application accomplish just after the transplant of the seedlings). The evaluations were accomplished until 25 days after the last application, by counting the number of insects in 5 plants per plot.

Results: In the evaluations after the second and third applications, all the treatments were differences significantly of the untreated treatment. The insecticide chlorantraniliprole 350 WG, at the doses of 40 and 80 g i.a./ha showed efficiency on control of the early pests (up to 85%) in tomato crop.

Conclusions: The insecticide chlorantraniliprole after 3 application by drip irrigation, at 40 and 80 g a.i./ha, were efficient on control of the *Bemisia tabaci* Biotype B, *Frankliniella schultzei, Liriomyza huidobrensis* and *Tuta absoluta,* in tomato, being a new tool for IPM in tomato crop.

POSTER PRESENTATION

Activity of a new insecticide of the diamides chemical class (chlorantraniliprole) for control of the stem borer, *Diatraea saccharalis* (Lepidoptera: Pyralidae), in sugarcane

Dhiego Duvaresch, Mario Sergio Oliveira, Willian Takao, Mauricio Rotundo, Geraldo Papa

Sao Paulo State University, Ilha Solteira/SP, Brazil

Introduction: The sugarcane is an important crop in Brazil, your produce are linked with the ethanol and sugar production. The stem borer, *Diatraea saccharalis,* is the most important insect pest in sugarcane in Brazil. The new insecticide (chlorantraniliprole) of the diamides chemistry class has activity on a broad spectrum of economically important pest species. The mode of action is activation of insect ryanodine receptors. The objective of this work was to evaluate the performance of this insecticide on the control of stem borer in sugarcane.

Methods: The experiment was carried out at field conditions in São Paulo/Brazil. The two foliar applications (interval of 14 days) was accomplished being used pressurized backsprayer. The design was randomized blocks. The treatments were: chloroantraniliprole 350 WG (10.50; 15.75 and 21.00 g a.i/ha) and novaluron 100 EC (10.00; 15.00 and 20.00 g a.i/ha). The evaluations were accomplished to the 13, 28 and 45 days after the second application, by counted the percentage of damaged plants by stem borer.

Results: In the evaluations of 13 and 28 days after second application all the treatments were differences significantly of the untreated treatment. The insecticide chlorantraniliprole 350 WG, at the dose starting from 15.75 g i.a./ha showed efficiency on control of the stem borer, up to 83%. Novaluron at the dose of 20.00 g i.a/ha showed 75% of efficiency.

Conclusions: The insecticide chlorantraniliprole and novaluron were efficient on control of the *Diatraea saccharalis*, being a new tool for IPM in sugarcane in Brazil.

POSTER PRESENTATION

Activity of a new insecticide of the diamides chemical class (chlorantraniliprole) for control of soybean looper, *Psedoplusia includens* (Lepidoptera: Noctuidae), in soybean

Mario Sergio Oliveira, Dhiego Duvaresch, Willian Takao, Fernando Celoto, Geraldo Papa

Sao Paulo State University - Unesp, Ilha Solteira/SP, Brazil

Introduction: The caterpillars represent a constant problem to the soybean growers in Brazil. The most important species are velvetbean caterpillar, *Anticarsia gemmatalis,* and soybean looper, *Pseudoplusia includens*. The current technological progress in the chemical area has been providing the introduction of new molecules that are safer and more appropriate for use in the agriculture. Chlorantraniliprole (diamides chemical class) is a new insecticide with a novel mode of action: activation of insect ryanodine receptors. The objective of this work was to evaluate the performance of this insecticide on the control of soybean looper in soybean crop.

Methods: The experiment was carried out at field conditions in Mato Grosso do Sul/Brazil. The one foliar application was accomplished, being used pressurized backsprayer. The statistic design was randomized blocks with 4 replicates. The treatments were: chloroantraniliprole 200 SC (2.5; 5.0; 7.5 and 10.0 g a.i/ha), permethrin 384 EC (25 g a.i./ha) and methomyl 215 sac (215 g a.i./ha). The evaluations were accomplished to the 0, 2, 5 and 10 days after the application, by counted the number of caterpillars by plot.

Results: In the evaluations of 5 and 10 days after application, the insecticide chlorantraniliprole 200 SC, at the doses of 7.5 and 10.0 g i.a./ha showed efficiency on control of the soybean looper, up to 85%, overcoming the insecticides permethrin and methomyl, whose control efficiencies were inferior to 80%.

Conclusions: The insecticide chlorantraniliprole was efficient on control of the *Pseudoplusia includens*, being a new tool for IPM in soybean crop in Brazil.

POSTER PRESENTATION

Testing the monophyly of the Australian leaf beetle genus *Paropsis* (Chrysomelidae: Chrysomelinae)

Gunter Maywald[1], Lyn Cook[1], Chris Reid[2]

[1]The University of Queensland, Brisbane, Australia, [2]Australian Museum, Sydney, Australia

The leaf beetle genus *Paropsis* Olivier (Chrysomelidae) comprises 78 described species and is endemic to Australia and New Guinea, where its members feed mainly on eucalypts (Myrtaceae). The genus is part of a larger group of more than 400 species (the paropsine beetles), a group that has not been taxonomically revised for over 100 years. Affiliations within this group and relationships to the rest of the Chrysomelinae are unclear. A recent revision of the genera of Chrysomelinae of Australia (Reid, 2006, *Zootaxa* 1292) has redefined the genus *Paropsis*, assigning to it those species previously placed into *Procrisina* Aslam.

In order to test the monophyly of *Paropsis*, a 750bp segment of the D2 region of the 28S nuclear gene for a range of species in the genus has been sequenced. The same gene fragment has also been sequenced from representative species of most of the other paropsine genera. A number of outgroup species from the Chrysomelidae have also been included. The results were analysed using PAUP* and MrBayes, and seem to be consistent with a monophyletic *Paropsis* as defined in Reid (2006). Relationships within the paropsine genera are also discussed.

POSTER PRESENTATION

Perspectives of entomopathogenic fungi to control scale pests in Georgia

Ekaterine Tabatadze

L. Kanchaveli Institute of Plant Protection, Tbilisi, Georgia

Introduction: Fauna of scale insects (*Homoptera, Coccoidea*) in Georgia have been mainly formed by the adventive's species introduced together with plants. Many species of them have very important economical significance for agriculture of Georgia. 23 species of scale insets have constantly registrated on citrus : *Diaspidida*e – 10 species, *Coccidae* -9 species, *Pseudococcidae* – 3 species, *Monophlebidae* – 1 species. Biological control agents – entomopathogenic fungi play important role in number regulation of insects and successfully used as alternative for chemical control.

Material and Methods: The investigation and study of scales infectious pathology have been conducted in West Georgia (Adjara,Guria) during 1989 - 2007 according the established methods.

Results :Fungal epizootics of different scale insects in subtropical zones of Georgia (Adjara, Guria) were discovered. Among 33 species of entomopathogenic fungi detected in citrus orchards at present the most important are: *Aschersonia rubra* Tabatadze&koval (a recently identified species in Caucasus), *Lecanicillium lecanii* (Zimm.) Zare et W. Gams., *Fusarium larvorum* (Fask.) Bilai and *F.* sp.. Infestation of armored (*Diaspididae)* scales : Japanese scale –*Lopholeucaspis japonica* Ckll., by *A.. rubra* and *Fusarium* varied from 20,5 up to 94,0%; Dictiospermum scale – *Chrysomphalus dictyospermi* (Morg.) 6,0 -65,5%, Yellow scale – *Aonidiella citrine* (Craw.) – 4,1 -57,1%. Infestation of Coccids (*Coccoidae)* - *Coccus hesperidum* L., by the *L. lecanii* varied from 8 up to 72,2 %, Japanese wax scale – *Ceroplastes japonicus* Green 6,3-31,8% and citrus wax scale – *Ceroplastes sinensis* Guerchio - 9.0 -28,6%.

POSTER PRESENTATION

Natural Enemies of Scale Insects *(Homoptera, Coccoidea)* in Citrus Plantings of West Georgia

Ekaterine Tabatadze

L.Kanchaveli Institute of Plant Protection, Tbilisi, Georgia

Introduction: 23 species of scale insects registrated in citrus plantings of Georgia, but 8-10 species may achieve presently high density and would damage the plants: *Chrysomphalus dictyospermi* Morg., *Lopholeucaspis japonica* Ckll., *Aonidiella citrina* (Craw.), *Coccus hesperidum* L., *Ceroplastes sinensis* Green. The complex of natural enemies of scales includes: parasitoids, predators and entomopathogenic fungi.

Materials and Methods: The observation have been conducted in West Georgia (Adjara,Guria) during 1989-2007. The fluctuation of scales population and efficacy of fungi were determined by monitoring in citrus orchards.

Results: Twenty two species of parasitoids (*Hymenoptera,Chalcidoidea*) are recorded as entomophagous of scale insects in citrus groves. The list includes: *Aphelinidae* – 14 species, *Encyrtidae* - 5 species, *Pteromalidae* – 2 species, *Signiforidae* – 1 specie. *Encarsia citrina* (Craw.)(=*Aspidiotiphagus citrinus*) as oligophagous species is the major effective parasitoids of armored scales (*Homoptera, Diaspididae*). Parasitism's often reaches up to 40%. From 2 up to 90% of coccids (*Homoptera, Coccidae*) are destroyed by *Coccophagus lycimnia* (Walker.). In citrus orchards of Georgia on coccids recorded 10 species of predators: 8 species of *Coleoptera, Coccinellidae* and 2 - *Acari. Chilocorus bipustulatus* L. is more common and effective then *Ch. renipustulatus* Scriba and *Exochomus guadripustulatus* L. The scale mortality varied between 0, 2 -16, 6 %. At present on coccids detected 33 species of entomopathogenic fungi. More effective are: *Aschersonia rubra* Tabatadze&Koval, *Lecanicillium lecanii* (Zimm.) Zare et W.Gams, *Fusarium larvorum* (Fask) Bilai and *Fusarium* sp. Efficacy of *A. rubra* varied from 4, 1 up to 94, o and *L. lecanii* 6, 3-72, and 2%.

POSTER PRESENTATION

Maximizing student learning through active learning in entomology: service learning, case studies, and wikis

Linda Hooper-Bui, Albert Lee, Rachel Strecker, Kaitlin Baudier

Dept. Entomology, Louisiana State University, Baton Rouge, La, United States

Students maximize their learning through the constructing of their own knowledge structure rather than listening to lectures and viewing Power Point. Service learning requires students to take course concepts and identify a community need that addresses those concepts and meet that need through a service project. Entomological examples of service-learning projects include: donation of insect collections to schools, libraries and service clubs (general entomology or taxonomy class), creation of butterfly gardens in area needy schools (insect ecology), and suppression of urban pests in community centers or public swimming pool areas (urban entomology). Case studies can be used to measure student knowledge before a topic is taught and can be continued and expanded through the course. These case studies allow student "judgement of learning" in a formative manner rather than a summative manner (tests) and allows the students to find out what they know and fill in the gaps in their knowledge. Case studies are especially useful in courses where theory is extensively taught such as Insect Ecology. Lastly, wikis can be useful in helping students self-construct knowledge and can replace the classic term paper. Students often use wikis for their personal interests, and this shows them an academic way of using Web 2.0 interfaces. If the wiki information is placed on Wikipedia, then the students are creating something useful while their learning is maximized. Examples from LSU Insect Ecology wikis will be used. Students respond positively to these techniques when they see that their learning is maximized.

POSTER PRESENTATION

Pnigalio agraules-*P. mediterraneus* (Hymenoptera: Eulophidae): a true synonymy?

Gennaro Viggiani

Dipartimento di Entomologia e Zoologia Agraria; Università di Napoli, Portici, Italy

Introduction: Several species of the genus *Pnigalio* are still poorly characterized and difficult to identify due to the variations of features considered diagnostic in the known keys. In the framework of a biosystematic study of the group, we tried to evaluate the status of two described species, namely, *Pnigalio agraules* (Walker, 1839) and *P. mediterraneus* Ferrière & Delucchi (1957). They were synonymized by Askew (1984). The first species, originally described on one collected female in England, subsequently keyed (Graham, 1959) and partially redescribed (Graham, 1963), was recorded from several hosts, particularly *Tischeria ekebladella* (Bjerkander) (Lepidoptera: Tischeriidae) and congeneric species. *P. mediterraneus* was originally described as parasitoid of *Bactrocera oleae* (Rossi) (Diptera: Tephritidae) and then recorded also from other hosts. The proposed synonymy influenced some views on the biocenotic relationships in the olive agroecosystem, where the olive fly is the key pest, and the measures to increase the functional biodiversity.

Methods: To verify the validity of the synonymy of *P. mediterraneus* under *P. agraules*, we compared populations of the mentioned species obtained from their typical hosts, respectively *B. oleae* and *T. ekebladella*, but also from other ones. We used an integrative approach, combining morphological (dimension of new laid eggs), biological (mating tests) and molecular (nuclear and mitochondrial DNA sequences).

Results: 28S-D2 and COI sequences, along with the mating tests and the dimension of the eggs, clearly show that *P. agraules* and *P. mediterraneus* represent two valid species.

Conclusions: Our results allow a more rational management of the biodiversity in several agroecosystems.

POSTER PRESENTATION

Determination of midgut pH of sun pest, *Eurygaster integriceps*, using the color changing of chemical materials

Majid Kazzazi, Vahid Hoseini Naveh

Bu Ali sina University, Hamedan, Islamic Republic of Iran

Introduction: Sun pest *Eurygaster integriceps* is one of the most important pests of wheat and barley in most parts of Iran. This pest was found abundantly on wheat in all over the country, spatially western. It causes considerable damage in most wheat farms of Iran. Enzymatic study of digestive system of bugs on midgut pH is important characters in physiological studies.

Methods: In this study midgut of *Eurygaster integriceps* is divided into four sections (V1-V4) respectively. A universal buffer pH 3-8 was made by mixing equal portions of 0.02 M for each one of Succinate, Mes and Glycine and adusting the pH with NaOH 1 normal. To obtain standard color changing, various chemical materials:Thymol Blue, Bromophenol Blue, Bromothymol Blue, Methyl Orange, Bromocrosol Purple, m- Crosol purple and Nutral Red were put into buffer tubes. The effects these materials on midgut sections (V1- V4) and color variations were compared with standard color.

Results: In this study pH V1=6.5 , V2= 6.3, V3= 6 V4= 5.8 were determined respectively. The acetic slope of midgut sections were increased from V1 to V4. This study showed that midgut of sun pest has acetic property.

POSTER PRESENTATION

Relationship of body size and egg maturity in *Culex pipiens pallens* depending on population densities

Jong-Jin Lee, Yeon-Kook Kim, Eun-Mi Park

Chonbuk National University, Chonju, Chonbuk, Korea

In most mosquitoes, female require additional protein after emergence to initiate vitellogenesis. In general, seeking sugar solutions is a common behavior for most of them and for both sexes. Feeding on sugar solutions as an energy source extends their life span and improves their reserve energies, mainly in lipids. On the other hand, there has been much interest in using mathematical models or correlates of the intrinsic rate of increase to identify factors affecting population growth in the female mosquitoes. However, use of these models requires date relating morphological factors such as body size with population growth factors such as egg maturity. Recent use of correlates of the intrinsic rate of increase and models to study population dynamics in mosquitoes has emphasized the need for species specific data on the relationship of morphological factors such as body size to life history parameters such as egg maturity. *Culex pipiens pallens* is of concern because of its continued spread and population growth in Korea and the potential for Japanese encephalitis every year. This study had examined the relationships between pupal weight and adult female wing length and between female wing length and egg maturity in the first reproductive cycle of *Culex pipiens pallens.* There was a significant positive relationship between pupal weight and adult wing length. The relationship between wing length and egg maturity was also significant and positive, but with lower correlation coefficients and higher variance indicating that other factors also affect egg maturity.

POSTER PRESENTATION

Insecticidal activities of the outer seed coat of gingko against *Ochlerotatus togoi* (Diptera: Culicidae) larvae

Jong-Jin Lee, Se-Won Oh, Chung-Un Lee

Chonbuk National University, Chonju, Chonbuk, Republic of Korea

Potent insecticidal components against *Ochlerotatus togoi* larvae were isolated from the *Ginkgo biloba* (L.) leaves and outer seed coats through organic solvent extraction method, and various chromatographic techniques. Molecular weights of these compo-nents extracted from the leaves and seed coats were measured by gas chromatography mass spectrum. The insecticidal activity of the extracts from *Ginkgo biloba* outer seed coat was higher than that of leaves. LC_{50} of methanol extracts of *Ginko biloba* leaves was 272.90 ppm and that of outer seed coats was 171.74 ppm, respectively. Methanol extract of *Ginko biloba* outer seed coats was sequentially partitioned into n-hexane, chloroform, ethyl acetate, and water-soluble portions. Chloroform fraction purified was 43g, and was shown to have a strong insecticidal activity against *Ochlerotatus togoi* larvae. Chloroform fraction was further isolated by column chromatography and 8 fractions eluted were collected. Amongst 8 fractions, C_2 amounted to 3.07g, and was highly active for mortality tests, against *Ochlerotatus togoi* larvae. C_2 was further isolated repeatedly by the same method as above, yielding C_{222} fraction, which was very active against *A. togoi* larvae. C_{222} produced five fractions after being purified by HPLC. Fractions purified as C_{2223} and C_{2224} with molecular weights of 220 and 279 respectively were shown to have high insecticidal activities against *Ochlerotatus togoi* larvae.

POSTER PRESENTATION

Economic threshold for diamondback moth, *Plutella xylostella* (L.) (Lepidoptera: Plutellidae), on leaf broccoli (*Brassica oleracea* var. *botrytis italiana*)

Seon-U Choi[1], Ki-Kwon Lee[2], Ju-Rak Lim[2], Ju-Hee Kim[2], Dae-Hyang Kim[2], Jeong-Sik Choi[2], Yeong-Geun Choi[2], Chang-Yeon Hwang[3]

[1]Floriculture Resources Research Institute, Namwon sity Jeollabuk-do, Republic of Korea, [2]Jeonllabuk-do Agricultural Research and Extension Service, Iksan sity Jeollabuk-do, Republic of Korea, [3]Chonbuk National University, Jeonju city Jeollabuk-do, Republic of Korea

Introduction: This study was conducted to develop the economic threshold for the diamondback moth (*Plutella xylostella* (L.) on Leaf Broccoli(leaf vegetable) in 2007.

Methods: To investigate the relationship between initial density of diamondback moth larvae and broccoli leaf yield, experimental plots with five treatments(0, 0.5, 1.0, 2.0, 4.0 larvae per plant) as initial density were established. We inoculated larvae in chesses cloth covering to survey larvae density change.

Results: When grown to eat, leaves of broccoli were harvested by periods. 60-70% of larvae were removed whenever we picked the leaves. High levels of larvae were associated with significant reductions in leaf yield. There were 85%, 64%, 58%, and 56% yield reductions from the diamond back moth larvae density in 0, 0.5, 1,0, 1.5, 2.0 per plant, respectively 25days after larvae inoculation. The regression equation used to predict leaf yield based on the number of initial larvae density per a plant was $y=1635-393x(R^2=0.79)$.

Conclusions: The economic injury level of diamondback moth on leaf broccoli was 2-3 larvae per 10 plants for a damage level of 5%. The economic thresholds was 1-2 larvae per 10 plants. Thus, the diamond back moth management should be initiated 1-2 larvae occurrence per plant.

POSTER PRESENTATION

Intraguild predation: molecular detection of carabid-spider interactions within cereal crops

Jeffrey Davey[2], King Andrew[2], James Bell[1], Michael Bruford[2], David Bohan[1], William Symondson[2]

[1]Rothamsted Research, Harpenden, Hertfordshire, United Kingdom, [2]Cardiff School of Biosciences, Cardiff, Wales

Carabid beetles and spiders dominate the generalist predator community in arable crops in Europe and elsewhere. Both help to control crops pests, such as aphids and slugs, yet very little is known about interactions between these predators. Although positive synergistic interactions are known (for example where aphids are dislodged, fall to the ground and are eaten by the carabids) little is known about the negative interactions that may arise from direct predation on the spiders by the carabids. We report the first use of molecular analyses to quantify this trophic interaction.

Species- and group-specific primers were developed for the analysis of predation on the major species of spider found at our field sites. Feeding trials were conducted with each pair of primers to determine the mean detection period following ingestion. This information was then used to adjust recorded rates of predation in the field so that direct comparisons could be made between predation by the carabid *Pterostichus melanarius* on each spider species. Around 650 beetles were collected from the field and analysed. We demonstrated, for example, that ~20% of the beetles had been consuming the spider *Tenuiphantes tenuis* but only 0.32% had consumed *Bathyphantes gracilis*. Rates of predation were related to prey density and location in the crop in relation to ground-hunting carabids. We also report the development of multiplex PCRs that allowed simultaneous detection of predation on different spider species. The plan is to use these primers to quantify the effects of intraguild predation on aphid numbers.

POSTER PRESENTATION

Intraguild predation: molecular detection of carabid-spider interactions within cereal crops

Jeffrey Davey[2], King Andrew[2], James Bell[1], Michael Bruford[2], David Bohan[1], William Symondson[2]

[1]Rothamsted Research, Harpenden, Hertfordshire, United Kingdom, [2]Cardiff School of Biosciences, Cardiff, Wales

Carabid beetles and spiders dominate the generalist predator community in arable crops in Europe and elsewhere. Both help to control crops pests, such as aphids and slugs, yet very little is known about interactions between these predators. Although positive synergistic interactions are known (for example where aphids are dislodged, fall to the ground and are eaten by the carabids) little is known about the negative interactions that may arise from direct predation on the spiders by the carabids. We report the first use of molecular analyses to quantify this trophic interaction.

Species- and group-specific primers were developed for the analysis of predation on the major species of spider found at our field sites. Feeding trials were conducted with each pair of primers to determine the mean detection period following ingestion. This information was then used to adjust recorded rates of predation in the field so that direct comparisons could be made between predation by the carabid *Pterostichus melanarius* on each spider species. Around 650 beetles were collected from the field and analysed. We demonstrated, for example, that ~20% of the beetles had been consuming the spider *Tenuiphantes tenuis* but only 0.32% had consumed *Bathyphantes gracilis*. Rates of predation were related to prey density and location in the crop in relation to ground-hunting carabids. We also report the development of multiplex PCRs that allowed simultaneous detection of predation on different spider species. The plan is to use these primers to quantify the effects of intraguild predation on aphid numbers.

POSTER PRESENTATION

Varying glucosinolate profiles in *Arabidopsis* influence plant defense against generalist and specialist caterpillars differently

I. Mewis[1], J.G. Tokuhisa[2], J. Gershenzon[3], H.E. Hummel[4], Ch. Ulrichs[1]

[1]Humboldt University Berlin, Institute for Horticultural Science, Urban Horticulture, Berlin, Germany, [2]Virginia Tech University, Horticulture Department, Blacksburg, VA, United States, [3]Max Planck Institute for Chemical Ecology, 07745 Jena, Germany, [4]Justus-Liebig-University Giessen, Organic Agriculture, Giessen, Germany

Glucosinolates (GS) are characteristic secondary defense compounds in Brassicaceae and other families in the order Brassicales. To date more than 120 different GS are described sharing a common chemical core structure with varying side chain. Depending on the chemical nature of the side chain they are classified as aliphatic, aromatic or indolyl GS. All GS containing plants store in different compartments and cells GS hydrolyzing enzymes, so called myrosinases. After tissue damage such as herbivory the actual biologically active compounds are released. The GS-myrosinase system is an effective defense system especially against generalist insects, pathogen and other herbivores. But many specialists are using these compounds in host-recognition.

The aliphatic GS profiles of the model plant *Arabidopsis thaliana* L. and other members of *Brassicaceae* are highly variable, but indolyl GS are widely distributed in this plant family. Indeed studies are missing to discover the function of GS classes and the effect of different GS side chains on insect resistance. To study the effect of GS classes on different insects, the host plant suitability of two *A. thaliana* mutants with altered GS profile compared to Columbia wild type (WT) for three lepidopteran species was tested. The performance of the generalist caterpillar *Spodoptera exigua* (Hübner) was better on *mam3*$^{+}$, lower aliphatic GS content, followed by *cyp79B2*$^{-}$*cyp79B3*$^{-}$, absence of indolyl GS, when compared to WT. No significant differences within weight gain and herbivory on genotypes was found for the specialist lepidopteran *Pieris rapae* L. and *P. brassicae* L. The impact of different GS within plant defense response is discussed.

POSTER PRESENTATION

Possible factors affecting bark beetle outbreaks after forest fires

Maria Lombardero

University of Santiago, Lugo, Spain

Fires are one of most important threats to forest, not just because of the direct effects but also because of the later consequences, including increased risks of insect outbreaks, especially bark beetles. How forest fires may facilitate insect outbreaks is not well known. We tested three general hypotheses that included the three main factors that regulate insect populations: (1) Fire may compromise tree defenses; (2) Burned trees may be more nutritionally suitable for bark beetle; (3) Natural enemies may be less abundant in burned forest. In support of hypothesis 1, the flow of defensive oleoresin from pines was reduced by fire. However, the recovery depended on crown damage. Resin defenses never recovered in trees with scorched crowns and most of those trees were attacked and killed by bark beetles. But burned trees with undamaged crowns recovered their resin defenses and actually produced twice as much resin after 24 days compared to control trees; none of these trees were attacked by beetles. Therefore, bark beetle outbreaks probably depend on time of year when the fire occurs relative to the abundance of adult bark beetles in the area during the period of low resin immediately after the fire. Contrary to hypothesis 2, burned trees were no more nutritionally suitable for bark beetles; in fact, beetles in burned trees survived less well, had to excavate longer galleries, and laid fewer eggs compared to control trees. Hypothesis 3 was supported in that natural enemies were less abundant and with lower specific richness in burned forests. Therefore, forest fires facilitate tree colonization by bark beetles by decreasing tree defences and providing vulnerable host trees for the beetles. In addition the pressure of natural enemies is lower in burned forest which may affect positively bark beetle population even if burned trees have lower nutrient contents.

POSTER PRESENTATION

Stable isotope analyses to determine plant host origins of mating *Helicoverpa armigera* (Lepidoptera: Noctuidae) within Bt cotton crops in Australia

Colin Tann, Geoff Baker

[1]CSIRO Entomology, Narrabri, NSW, Australia [2]CSIRO Entomology, Canberra, ACT, Australia

In Australia, as in many other parts of the world, the noctuid moth *Helicoverpa armigera* represents a serious pest problem to a large number of agricultural crops including cotton. The introduction of genetically modified (Bt) cotton in Australia has been very successful in reducing the pest status of *H. armigera*, but the potential for this moth to develop resistance to the two insecticidal Bt proteins (Cry1Ac and Cry2Ab) contained within the BOLLGARD 11® cotton product is a serious threat, particularly given that the Australian cotton industry is so reliant on the technology (approximately 90% of cotton grown is Bt-based).

Refuge crops (selected for high attractiveness to *Helicoverpa spp*.) and which have the capacity to produce large numbers of Bt susceptible *H.armigera* moths, are grown in conjunction with the Bt cotton, with the aim of reducing the chances of resistance developing.

One of the key assumptions within this strategy is the notion of random mating occurring between moths emerging from different crop origins. However, little research has thus far tested this assumption. The work described in this paper involved a series of studies aimed at understanding *H. armigera*'s movements and breeding within landscapes containing Bt cotton and refuge crops. It utilised stable isotope analyses of moths, captured whilst mating within Bt cotton crops, to provide signatures of plant host origins. Carbon isotope analyses suggested that moths from both C3 and C4 plant origins mated at random within the Bt cotton crops. We had anticipated that additional analyses of nitrogen isotope signatures would further separate the C3 plant host origins (e.g. separate cotton from legumes such as pigeon pea) but this has not yet proven possible, probably due to poor N fixation by pigeon pea.

POSTER PRESENTATION

Regulation of protocatechuic acid synthesis in female *Periplaneta americana*.

David Whitehead

Oxford University, Oxford, United Kingdom

Introduction: The sclerotin oothecal walls are formed by combining the secretion of both colleterial glands. The left gland secretes 3,4-dihydroxybenzoicacid glucoside, proteins (oothecins) and a phenoloxidase enzyme (1) The resulting quinone formed from the 3,4-diphenol cross-links the oothecins to form the oothecal walls (2a, 2b). JH (juvenile hormone) regulates the synthesis of oothecins in the left colleterial gland of cockroaches. (3,4,5)

Methods: Plasmatocytes washed with saline from colleterial glands were isolated and incubated with [14C] L-p-Tyrosine or [14C]-tyramine. Resulting metabolites were separated by paper chromatography (BAW 4:1:1) and HV electrophoresis (pH 1.9 or 4.2). 1 cm strips were counted in a scintillation counter.

Results: Plasmatocytes show an enhanced ability to decarboxylate and deaminate tyrosine if treated with JH whereas α-ecdysone has no effect. By contrast, injecting α-ecdysone into newly emerged adult females significantly ($p \leq 0.001$) inhibited synthesis of the phenolic 4-o-β-D-glucoside in the developing left gland but not of the β-glucosidase produced by the right gland (7). p-Hydroxyphenylacetic acid is derived from tyrosine via tyramine (6) when incubated with the gland plasmatocytes but is not synthesized in the gland itself (6) .

Conclusion: It is proposed that in adult female cockroaches, tyramine is oxidized in plasmatocytes and then hydroxylated in the gland to give 3,4-dihydroxyphenylacetate (8). Regulation of the synthesis of the oothecal sclerotizing agent is possibly controlled by JH acting directly on plasmatocytes adhering to the left colleterial gland. Scanning and thin section EM show their presence on the gland but significantly they are absent on the right colleterial gland.

POSTER PRESENTATION

Organic insecticides and nematicides for small-scale cotton farmers

Lawrence Malinga, Eugen Eulitz

ARC-IIC, Rustenburg, South Africa

A study was conducted at Vaalharts and Rustenburg in South Africa to test different plant extracts with insecticide and nematicide possibilities for the use by small-scale cotton farmers. Five organic nematicides, khaki weed (*Tagetes minuta*), Marigold (*Tagetes erecta*), tobacco (*Nicotinia tabacum*), thorn-apple (*Datura sp.)* and caster oil (*Ricinus communis*) were compared with Temik®. Four organic insecticides, tobacco (*Nicotiana tabacum*), khaki weed (*Tagetes minuta*), thorn-apple (*Datura sp.)* and garlic (*Allium sativum*) were compared with Mospilan® (*Acetamiprid*) and Decis® (*Deltamethrin*). Khaki weed, castor oil plant and the control had more *Meloidogyne* species nematodes. Castor oil and thorn apple had more *Pratylenchus* nematodes. Ring nematodes (*Criconematidae*) were higher in khaki weed, tobacco and marigold treatments. Temik® gave the highest yield. Castor oil and marigold gave the lowest yield. Tobacco, khaki weed and thorn apple shown promise in seed yield. The four organic insecticides did not give a good control of bollworms (*Helicoverpa armigera, Diparopsis castanea, and Earias insulana*). Mospilan®, Decis® and the tobacco treatments exhibited significantly less leafhopper (*Amrasca terraereginae*) damage on the cotton leaves. There was no significant difference on aphid (*Aphis gossypii*) population in all the treatments with the exception of the Decis® which exhibited a significantly higher aphid population. There were no significant differences in the whitefly (*Bemisia argentifolii*) numbers in all the treatments. Garlic, Mospilan® and Decis® exhibited significantly higher spider mite numbers. The seed yields of Mospilan® and Decis® were significantly higher than the yields of the control and the four organic treatments.

POSTER PRESENTATION

The distribution of Trichoptera and Ephemeroptera in the tributary rivers of the Doring and mainstream Olifants Rivers, South West Cape, South Africa and implications for conservation planning

Ferdinand C. de Moor, Helen M. Barber-James

[1]Albany Museum, Grahamstown, South Africa, [2]Rhodes University, Grahamstown, South Africa,

Introduction: Research on freshwater invertebrates in the southern and south Western Cape has revealed a diverse fauna, largely endemic to the Cape Floral Kingdom. Phylogenetic relationships suggest that some lineages are relict survivors of a once widespread temperate southern fauna dating back about 140 million years prior to the breakup of Gondwana. The aquatic pre-imaginal stages of invertebrates representing this Gondwana fauna in rivers flowing off the Cedarberg need further study. Firstly the relationship between this Cedarberg group and the rest of the southern and south-western Cape must be confirmed. Secondly, can a broader-based approach incorporating more aquatic faunal groups for conservation of aquatic ecosystems be developed? The first aspect needs the collection of adult insects to confirm species identification. For the second, the use of diverse assemblages of species to identify distinct river signatures, will help evaluate uniqueness. This provides a broader approach to biodiversity conservation of rivers than the use of only rare or endangered species.

Methods: Based on distribution patterns of rare endemic fish, a selection of eleven rivers, tributaries of the Olifants River in the Cederberg, Western Cape were surveyed for aquatic macroinvertebrates. The study focused on Trichoptera, Ephemeroptera and Diptera (Simuliidae). Diverse collecting techniques ensured maximum species representation.

Results: Analysis of fauna from 52 biotopes surveyed, recorded Ephemeroptera (32 species), Trichoptera (45 species) and Simuliidae (8 species). The species distribution pattern between the tributaries of the Doring and Olifants Rivers was significantly different. The survey of these rivers revealed 14 undescribed species. More survey work covering more rivers and sampling selected rivers over several seasons is recommended.

POSTER PRESENTATION

Action threshold for controling pistachio psylla nymphs (Hemiptera: Psyllidae) on *Pistacia vera* cv. Ohadi

Mohammad Reza hassani, Gadir Nouri-Ganbalani, Hamzeh Izadi, Mahmoud Shojai

Islamic Azad University, Rafsanjan, Islamic republic of Iran

Introduction: The pistachio psylla, *Agonoscena pistaciae* Burckhardt & Lauterer is a major pest of pistachio trees in Iran. The economic injury level is an important practical tool for decision-making in IPM programs. Our objective was to determine economic injury level for *A. pistaciae* on pistachio cultivar Ohadi.

Methods: Different density levels of *A. pistaciae* nymphs were maintained on pistachio trees by application different dosages of insecticides. Nymph densities were monitored weekly by counting nymphs per terminal leaflet. At harvesting time, yield of every tree was individually harvested and samples of weight of 1000 nuts measured. Regression analysis was used to determine the relationship between nymph densities and weight of 1000 nuts. The economic injury level was estimated by using pedigo *et al*., (1986) equation.

Results: The infestation levels of psylla nymphs were different between treatments at different control levels. The weight of 1000 nuts was significantly affected by number of nymph. Regression equation obtained to describe the relationship between nymph densities and yield loss is: $Y= -2.89X+841.21$, $R^2=0.96$. The economic injury level estimated for various combinations of management cost and market value. The economic injury level is a function of market value, management costs and efficiency of insecticide. The economic injury level for pistachio psylla nymph on cultivar Ohadi ranged from 7.7 to 30.7 nymphal-days per terminal leaflet.

Conclusion: This information may be considered by pistachio plantation for decision-making and help to reduce costs and insecticides application based on economic injury level.

POSTER PRESENTATION

Development of organic certification for honeybee products in Mwingi District, Kenya

Esther Kioko, Suresh Raina, Elliud Muli, Ken Fening Okwae

[1]ICIPE, Nairobi, Kenya, [2]National Museums of Kenya, Nairobi, Kenya

Introduction: Mwingi, a district situated in a semi-arid region of Kenya, has limited distribution of modern agricultural systems. Bee keeping is a traditional activity in the district. This project undertook steps to develop organic certification for honeybee products in the district.

Methods: A Survey was undertaken in the district to identify the key divisions. suitable for organic certification. This was followed by training at different levels, nomination of internal group inspectors, writing of the internal control system (ICS) manual, registration of farmers and certification of the honey-processing center.

Results: Seven divisions, Kyuso, Mumoni, Nguni, Nuu, Ngomeni, Central and Mui were identified for the organic certification process. Training was done for forty-five group secretaries and seven field officers to lead as community trainers in producer group preparation for certification and to participate in the making of the internal control system (ICS) manual. A total of 1013 beekeepers owning 27,331 traditional beehives were registered in the seven divisions. The processing center has set up the required procedures and opened an ICS office at the Mwingi honey marketplace.

Conclusion: The process has advanced and the first external inspection was undertaken by the Institute for marketecology (IMO) in November 2007.

POSTER PRESENTATION

Variation of the local populations of the Asian corn borer, *Ostrinia furnacalis* (Guenee), in the Philippines: some preliminary results

Merdelyn Lit, Adelina Barrion, Gelyn Sapin, Roberta Garcia, Ayn Kristina Beltran, May Flor Cuaresma, Cleotilde Caldo

UP Los Baños, College, Laguna, Philippines

Variation exists among the Asian corn borer populations in the Philippines. This was first reported by Barrion in 1988 using morphometric differences and cytological studies. Later, Mendoza *et al* (1994) using isozyme analysis had found variation in the local populations. Recent study by Caasi Lit et al (2006) also showed variation in larval duration. This paper presents some preliminary results on the variation of the local populations of the ACB.

Samples were collected from six regional sites and the life history (F2 generations) were studied using IPB modified diet. For cytogenetic study, ACB populations were mass-reared and ten adult male were fixed in Carnoy's solution and stained with lacto-aceto orcein. For isozyme analysis, midgut of the fifth instar larvae was removed and homogenized in cold distilled water, the resulting slurry was centrifuged and the supernatant was collected.

Results revealed that populations from Laguna and Leyte, respectively, underwent six and five larval instars which suggest that there could be mixed populations of ACB. The meiotic indices were highest on Leyte and lowest on Bukidnon. Being a bisexual species, such meiotic indices suggest variation in the reproductive potentials of the local populations. Based on the behavior of the meiotic chromosomes, ACB possesses small and holokinetic chromosomes. Differences in esterase banding patterns were observed by the presence of both slow and fast moving bands in the first zone of activity. For acid phosphatase, the two samples from Camarines Sur and Bukidnon also showed a fast moving band and a slow moving band.

POSTER PRESENTATION

LC-MS/MS analysis of the *Diachasmimorpha longicaudata* entomopoxvirus (DlEPV) proteins and their expression in host haemocytes

Pauline Lawrence

University of Florida, Gainesville, Florida, United States

Introduction: The *Diachasmimorpha longicaudata entomopoxvirus* (DlEPV) is injected into *Anastrepha suspensa* (Diptera: Tephritidae) larval hosts during oviposition by the female wasp (Hymenoptera: Braconidae). DlEPV replicates in the host's haemocytes and inhibits encapsulation. The objectives were to identify major DlEPV proteins, haemocyte classes of host larvae, and their differential/temporal expression of DlEPV proteins.

Methods: DlEPV proteins, fractionated by 1-D SDS-PAGE, were excised from the gel and component proteins reduced, alkylated, and trypsinized and separated by HPLC on a PepMap C18 column. Inline MS/MS analysis was carried out on a hybrid quadrupole- time-of-flight (TOF) mass spectrometer and the peptides identified against the available database (http://www.ncbi.nlm.nih.gov/; NCBInr_20061201) using the Mascot 2.0.01 search engine and the Scaffold (version -01_06_03) software. Hemocytes from 3rd instar unparasitized (control) *A. suspensa* and larvae 24-124 h post parasitism (hpp), were analyzed by flow cytometry then measured under a confocal microscope and sorted by size. Mouse polyclonal and monoclonal DlEPV antibodies were used in immunoconfocal microscopy to identify temporal and/or differential expression in haemocytes. TEM of haemocytes was also performed to identify onset of virus infection.

Results: Over 10 DlEPV proteins were identified including homologues of the poxvirus major virion core proteins P4a and P4b, early transcription factor, nucleoside triphosphate phosphohydrolase I (NPH I) and II (NPH II), and DNA-directed RNA polymerase. Virions invaded haemocytes via elongated protein spikes within 6-12 hpp. DlEPV proteins were expressed in three (5-8, 11-18, and 20-28 μm) haemocyte classes but not in the fourth (30-35 μm), a highly vacuolated type. Proteins of ~46 kD and ~ 70 kD were seen by 24 hpp and ~127 kD and 208 kD by 48-72 hpp. These were homologues of NPHI, early transcription factor, and DNA polymerase and an unknown protein respectively. By 124 hpp, the P4 major core proteins (~70-75 kD and 127 kD) were expressed.

Conclusion: The DlEPV proteins and their temporal (but non-sequential) expression are consistent with known poxvirus replication and morphogenesis. Infection induces granularity and blebbing in all three cell types that are involved in encapsulation inhibition.

POSTER PRESENTATION

Molecular phylogeny of the banana weevil, *Cosmopolites sordidus* (Germar) (Coleoptera: Curculionidae), based on AFLP analysis

J De Graaf[1], P Govender[2], A.S. Schoeman[2], A. Viljoen[3]

[1]Westfalia Technological Services, Tzaneen, South Africa, [2]Department of Zoology and Entomology, University of Pretoria, Pretoria, South Africa, [3]Department of Plant Pathology, University of Stellenbosch, Matieland, South Africa

Introduction: The banana weevil, *Cosmopolites sordidus*, is a serious pest of banana and plantain (*Musa*) and has been distributed to most areas where the crops are grown. Pest status is variable around the world, and may be influenced by genetically distinct populations of weevil. The aim of the study was to quantify the genetic relatedness within and among geographically separated populations of *C. sordidus*.

Methods: Six populations from four countries were sampled: Australia, Costa Rica, South Africa (South Coast, North Coast and Tzaneen) and Uganda. DNA was isolated and subjected to amplified fragment length polymorphism (AFLP) analysis using five selective primer sets.

Results: Empirical analysis of the AFLP fingerprints showed that, within populations, genetic diversity varied from 16-53%, with the South Coast and Tzaneen/Australian populations the least and most variable, respectively. The coefficient of gene differentiation showed that the Tzaneen population were the most differentiated from the South Coast population, while the South and North Coast populations were the most similar. All the populations showed statistically distinct marker frequencies, except for the Costa Rican and South and North Coast populations, which were similar. A neighbour-joining tree showed the Australian, Ugandan and South African coastal populations produced monophyletic groups, while the South African Tzaneen population were removed from the other populations and presented an ancestral state.

Conclusion: The data suggested that the South African coastal, Australian, Ugandan, and Tzaneen populations could be classified as separate taxonomic units.

POSTER PRESENTATION

Phylogenetic analysis of recent giant water scavenger beetles allows the character-based study of fossil record of the group (Coleoptera: Hydrophilidae: Hydrophilina)

M. Fikacek[1], A. E. Z. Short[3], S. Wedmann[4], J Prokop[2]

[1]National Museum, Department of Entomology, Praha, Czech Republic, [2]Charles University in Prague, Faculty of Science, Department of Zoology, Praha, Czech Republic, [3]University of Kansas, Natural History Museum & Biodiversity Research Center, Division of Entomology, Kansas, United States, [4]Senckenberg Research Institute, Research Station Grube Messel, Messel, Germany

The majority of the Tertiary hydrophiloid fossils is represented by large and strongly sclerotized aquatic forms of the subtribe Hydrophilina. Five recent genera are recognized (*Hydrophilus*, *Hydrobiomorpha*, *Hydrochara*, *Tropisternus* and *Sternolophus*) and two additional are to be described or up-graded to generic level based on the phylogenetic revision using 80 morphological characters of adults. The analysis supports the monophyly of the subtribe Hydrophilina and all recent genera except of *Hydrochara* and defines synapomorphies of the clades allowing a character-based study of fossil record of the subtribe. Based on this phylogenetic background, fossil material of the subtribe Hydrophilina was studied on selected Tertiary localities in Germany (Grube Messel, Enspel, Seifhennersdorf) and Czech Republic (Bílina mine). Three genera were recorded: *Hydrophilus* from most localities examined, recent pan-tropical genus *Hydrobiomorpha* from all Eocene to Oligocene localities, and the genus *Hydrochara*, which is reliably recorded only from the Eocene locality of Grube Messel so far. All recorded genera belong to the monophyletic “greater hydrophilines clade” characterized by the seventh antennomere divided into lobes, disorganized field of clypeal systematic punctures, ultimate maxillary palpomere shorter than penultimate and two characters of ventral morphology not seen in fossil material.. Simultaneous occurrence of all three mentioned genera in locality of Grube Messel proves that the diversification of the clade had to pre-date middle Eocene and took place most probably during the Paleocene.

POSTER PRESENTATION

Virosoft^{CP4} field trials in an organic apple orchard

Caroline Provost[1], Harnaivo Rasamimanana[2], Charles Vincent[3], Jose Valero[1]

[1]Biotepp Inc., Mont St-Hilaire, Quebec, Canada, [2]Biotepp Inc., Cap Chat, Quebec, Canada, [3]Horticultural Research and Dvelopment Center, Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu, Quebec, Canada

Introduction: The codling moth, *Cydia pomonella* L (Tortricidae), is a major pest of several orchard crops throughout major apple-producing areas of the world. Its management requires several insecticidal treatments per year. However, several populations of codling moth recently developed resistance to insecticides, notably in Europe, so that the treatments are less effective. Some alternative methods are available to control this insect, among them Baculovirus-based insecticides.

Methods: The viral insecticide Virosoft^{CP4} was evaluated in field trials in an organic apple orchard located in souththern Quebec, where codling moth populations were historically very high. The experimental protocol varied during these years to address different questions. In 2003 and 2004, we evaluated the impact of the frequency of treatment (4 vs 7 treatments) and the presence or not of additives (Surround and Soya oil) on the product efficacy. In 2006, we used different Virosoft^{CP4} concentrations to determine an optimal dose in organic orchards.

Results : In 2003, 7 treatments of Virosoft^{CP4} reduced significantly codling moth damage. The presence of Surround did not increase efficacy of Virosoft^{CP4}. In 2004, 4 and 7 treatments significantly reduced codling moth damage. The presence of Soya oil did not increase efficacy of the CpGv-based insecticide. In 2006, no significant difference was observed between the different concentrations.

Conclusions : In an agricultural context where very high codling moth populations exerted considerable and recurrent pressures on insect management programs, Virosoft^{CP4} caused significant and important reductions of the percentage of codling moth damage at harvest. It is a valuable alternative to chemical insecticides in organic orchards.

POSTER PRESENTATION

Measuring the economic value of biological control of the maize stemborer *Busseola fusca* Fuller (Lepidoptera: Noctuidae) in the Kenyan highlands

Anderson Kipruto Kipkoech[1], Fritz Schulthess[1], Wilson K Yabann[2], Henry K Maritim[2], Dagmar Mithofer[1]

[1]International Centre of Insect Physiology and Ecology, Nairobi, Kenya, [2]Moi University, Eldoret, Kenya

The scelionid egg parasitoid *Telenomus isis* Polaszek from West Africa and a virulent strain of the braconid larval parasitoid *Cotesia sesamiae* Cameron from western Kenya were introduced to control the noctuid maize stemborer *Busseola fusca* Fuller in the Taita Hills, in coastal Kenya. While *T. isis* is absent in Kenya, the virulent strain of *C. sesamiae*, which, unlike the avirulent strain, successfully develops in *B. fusca*, is common in some parts of the Kenyan highlands but absent in the Taita Hills. This study assesses the *ex-ante* economic impact of the establishment of the two parasitoids in the Taita Hills. The results are then extrapolated to assess the economic impact of the establishment of the parasitoids in their entire potential niche in Kenya. The output loss due to stemborers before the releases of parasitoid was estimated at 28.5%. Yield losses could fall to less than 10% in ten years, if pest reduction by each of the parasitoids grows to at least 20% or if one parasitoid only established but achieved a pest reduction of 40% by year 10. This study demonstrates the economic potential of redistributing parasitoids indigenous to Africa for the control of African stemborers. Because the benefits of biological control are positively scale-dependent while the costs are generally scale irresponsive, biological control programs would accrue more benefits when parasitoids are released to a wider area.

POSTER PRESENTATION

Monitoring populations of *Scyphophorus acupunctatus* Gyllenhal (Coleoptera: Curculionidae) with sexual pheromone in *Polianthes tuberosa* L.

Georgina Torres-Jimenez[1], Victor Lopez-Martinez[1], Iran Alia-Tejacal[1], Ramon Cuellar-Valdes[2], Jorge Vargas-Barrena[2], Armando Burgos-Solorio[3]

[1]Universidad Autonoma del Estado de Morelos, Facultad de Ciencias Agropecuarias, Cuernavaca Morelos, Mexico, [2]Feromonas y Compuestos Sinteticos de Uso Agricola de Mexico, D.F, Mexico, [3]Universidad Autonoma del Estado de Morelos, Centro de Investigaciones Biologicas, Cuernavaca Morelos, Mexico

Introduction: The black weevil is an important pest in *Polianthes tuberosa* (Liliales: Agavaceae) in Morelos, Mexico. Natural baits (agave, pineapple) have been employed to monitoring adult pupulations, but captures are too low. The sexual pheromone was synthesized recently, but no exist evaluations in natural conditions.

Methods: In a *P. tuberosa* plot (18°39'4.25'' N, 99°22'6.78'', 3 ha, 991 msnm) were ubicated the following treatments: Pheromone, Pheromone and pineapple, Pheromone and agave, pineapple, agave, water, all disposed inside yellow plastic traps. Each treatment has four repetitions completely randomized. The period of collect was 2008 January 26th to March 28th; the period of revision was 8.

Results: 366 adults have been collected in the experiment. Combination of pheromone and pineapple were the best treatment with 158 black weevils (43.17 % of captures). When the natural baits are only employed, the number of insects detected is reduced (18 adults in agave, 18 in pineapple). The pheromone capture 8.11 weevils/trap/week, but the cost and time to check it, is minor in comparison with the rest of treatments, the attraction in natural conditions losses after four weeks.

Conclusions: Is possible to increase effectiveness of black weevil traps using a combination of pheromones and pineapple.

POSTER PRESENTATION

Sticky traps and sexual pheromone to collect thrips in chrysanthemum (*Dendranthema grandiflorum* Kitam.)

Victor Lopez-Martinez[1], Ramon Cuellar-Valdes[2], Jorge Vargas-Barrena[2], Iran Alia-Tejacal[1], Maria De Jesus Garcia-Ramirez[3], Armando Burgos-Solorio[4]

[1]Universidad Autonoma del Estado de Morelos, Facultad de Ciencias Agropecuarias, Cuernavaca Morelos, Mexico, [2]Feromonas y Compuestos Sinteticos de Uso Agricola de Mexico, D.F, Mexico, [3]Universidad Autonoma de Campeche, Escuela Superior de Ciencias Agropecuarias, Campeche, Mexico, [4]Universidad Autonoma del Estado de Morelos, Centro de Investigaciones Biologicas, Cuernavaca Morelos, Mexico

Introduction: Sticky blue traps are used to monitoring thrips pupulations in ornamental species in Morelos, Mexico. But until now, none thrips pheromones has been employed to increase sticky trap´s captures.

Methods: Two doses (60 and 300 mg) of the sexual pheromone Tripslure ® were ubicated in sticky blue traps (60 x 20.5 cm) suspended 10 cm above chrysanthemum (*D. grandiflorum*) in Coatlán del Río, Morelos (18° 44' 30.71'' N, 99° 26' 7.00'' W, 0.15 ha). The sampling period was from 2008 January 26th to April 8th, each 8 days the traps were sampled and transported to laboratory for thrips counting. Each treatment has five repetitions and a completely random distribution, sticky blue traps without pheromone were used to compare our results.

Results: Using pheromone as bait, increase in 40% effectiveness of sticky traps, doses of 300 mg captures 500 thrips/trap/week, in comparison with 300 thrips/trap/week when no pheromone is used. The pheromone attraction is maintained in a month as a maximum period of collect.

Conclusions: Tripslure® as a complement for sticky blue traps improvement number of thrips collected in chrysanthemum plots.

POSTER PRESENTATION

Thrips (Insecta: Thysanoptera) in Sapotaceae flowers in Morelos, Mexico

Victor Lopez-Martinez[1], Iran Alia-Tejacal[1], Roberto M. Johansen-Naime[2], Aurea Mojica-Guzman[2], Maria De Jesus Garcia-Ramirez[3], Armando Burgos-Solorio[4]

[1]Universidad Autónoma del Estado de Morelos, Facultad de Ciencias Agropecuarias, Cuernavaca Morelos, Mexico, [2]Departamento de Zoología, Instituto de Biología, Distrito Federal, Mexico, [3]Universidad Autónoma de Campeche, Escuela Superior de Ciencias Agropecuarias, Campeche, Mexico, [4]Universidad Autónoma del Estado de Morelos, Centro de Investigaciones Biológicas, Cuernavaca Morelos, Mexico

Introduction: In Morelos three Sapotaceae have commercial valor: mamey sapote (*Pouteria sapota*), caimito (*Chrysophyllum cainito*) and chicozapote (*Manilkara zapota*). Thrips are common insects associated to Sapotaceae flowers, but their identities are largely unknown.

Methods: Flowers of three Sapotaceae species were collected in 2005 (August to November) in commercial and house orchards in Morelos, México. Specimens were extracted and maintained in alcohol at 70% for conservation. The preparation and identification process follows standard procedures. The material is deposited in UNAM Insect Collection.

Results: 1200 specimens were collected. The genus determined was *Frankliniella*. *Frankliniella curiosa* is the principal species determined until now, and was collected in mamey sapote and caimito. Other species collected were *F. albacuriosa* (mamey sapote), *F. aureauriosa* (chicozapote and mamey sapote) and *F. difficilis* (chicozapote). All host records are reported for the first time for all *Frankliniella* species determined. Four new species of *Frankliniella curiosa* group are detected.

Conclusions: Eight species of Frankliniella are reported for the first time associated to Sapotaceae flowers in Mexico.

POSTER PRESENTATION

Some aspects of the preliminary biology of *Leptinotarsa lacerata* Stål (Coleoptera: Chrysomelidae)

Jose Manuel Pineda-Uriostegui[1], Armando Burgos-Solorio[2]

[1]*Laboratorio de Parasitologia Vegetal, Centro de Investigaciones Biologicas, Mexico,* [2]*Universidad Autónoma del Estado de Morelos, Mexico*

The family Chrysomelids or leaf beetles constitute one of the most abundant and diverse insects, however, there is little information about the biology of this rate with the exception of species of economic importance. It provides information on aspects of the biology of *Leptinotarsa lacerata*, the result of 10 years of research on this beetle on tropical deciduous forest distributed in the state of Morelos, Mexico. *L. Lacerata* is distinguished from the rest by presenting a crisomelids oval body height of 14 mm, black with irregular rows, flavous bands at base cross zigzagging, flavous color or white. The life cycle includes several important events among these is the emergency teneral adults which emerge from the soil; courtship takes place on the host plant, it has been observed that precopule is that the male rubbing the elytra from the female, copulation, the male mounts and inmobilize the female with his forefeet, and put in a position to carry out after the sexual act. The female selects carefully oviposition site usually located on the lower side of leaves. Eggs are yellow, oval-cylindrical with an average length of 0.30 mm and 0.18 mm wide, up positions in masses of 40 and 60 eggs per mass. Larvae are cifisomatic, yellowish in its early stages of development, with transverse black stripes on the back and whitish in later stages features four stages of development and can reach a maximum size of 15 mm in length. Legs are dark brown. The pupa exarata is white with dark shades, with a long of 18 mm in length. This state starts at the moment when the larvae stops feeding and is buried in the soil and usually makes near the host plant. Teneral adults are clumsy in their slow movements, these are uploaded to the host plant and remain still. His body is soft and the color is opaque, a little active. After five days, they are sexually mature and active. The species is bivoltine and life cycle lasts about 30 to ± 40 days on average. *L. Lacerata* usually associated with *Montanoa grandiflora* (Asteraceae) and is prey to a bird and bug *Oplomus* sp (Hemiptera: Pentatomidae).

POSTER PRESENTATION

The bark and ambrosial beetles from state Morelos, México

Armando Burgos-Solorio[1], Armando Equihua-Martinez[2]

[1]Laboratorio de Parasitología Vegetal Universidad Autónoma del estado de Morelos, C.P, Mexico, [2]Entomología Forestal Instituto de Fitosanidad Colegio de Postgraduados Montecillo, C.P, Mexico

The bark and ambrosia beetles of the family Scolytidae and Platypodidae and are commonly known as "bark and ambrosia beetle" "borers in the wood." The tunnels constructed in ways adults subcortical on their host plants and through a series of processes of specialization, have diversified their feeding habits, so that almost any plant is susceptible to insect infestation, which has resulted in the success the same, this feature makes them distinctive from the rest of the beetles. We present a checklist of species of the families Platypodidae and Scolytidae associated to seven kind of forest in the state of Morelos, México. The state is located in the south central part of the Mexican republic, has a territorial extension of 4598 km^2 and presents seven types of vegetation; the most important thing is tropical deciduous forest and pine-oak forest. Little it is known about the distribution that they present these coleopters in this type of community.

As many as eight species within two genera belonging to platypodidae and 213 species were collected within 31 genera to Scolytidae. The tribe was more diverse with Corthylini genera 8 and 86 species. It has been reported in 19 species of bark beetles for the state. Concerning the different types of vegetation in the which these insects are established 75 % of the species live in tropical deciduous forests, 25 % in the pine and oak forests. This outstanding difference remarks the richness of the species in the vegetation plant associations. In this sense, as many as 101 plants species were determined included in 33 families. The Fabaceae and Pinaceae was frequent host for these coleopterans. Considering feedings habits, we found seven feeding habits, the phloeofagy was the most habit (56.3 % of all beetles) being the Scolytidae the most represented. In terms of specificity to a host plant, monophagy was the predominating category (62.9 %) in 30 genera of both families. Biogeographic affinity of these insects group is remarkable among the species, being the neotropical the most relevant (74.5 % of all species), followed by the circumtropical distribution (3.2 %), the Mexican (1 %), the neartic (20.6 %) and the worldwide (0.7 %).

POSTER PRESENTATION

Implication of exotic volatiles as a new strategy for management of *Coleophora obducta* (Meyrick)

Shan-Chun Yan, Hui Yang, Lu-Lu Gao

Forest Entomology Division, College of Forestry, Northeast Forestry University, Harbin, China

Coleophora obducta (Meyrick) (Lepidoptera: Coleophoridae), a kind of larch defoliators that exclusively latent in leaves. We tested the EAG and behavioral responses of *C. obducta* to nine kinds of larch volatile compositions, namely *R*-α-pinene, *S*-α-pinene, β-pinene, ocimene, phellandrene, 3-carene, myrcene, camphene and phytol by EAG and Y-tube olfactometer. The results showed that, in concentration of 0.4 mol·L^{-1}, most volatile compositions had significant EAG responses compared with the blank ($P<0.05$), except females to *R*-α-pinene, males to *R*-α-pinene and phellandrene; Besides, EAG responses between males and females also existed differences. Observations of behavioral responses of *C. obducta* to nine kinds volatile compositions in a series of concentrations of 0.0004, 0.004, 0.04, 0.4, 0.8 mol·L^{-1} had been carried out with the application of Y-tube olfactometer. Females were inclined to *S*-α-pinene, *S*-ß-pinene, phellandrene, 3-carene, and phytol to some extent ($P<0.05$), and males were inclined to ocimene, myrcene, camphene and phytol to some extent ($P<0.05$). In order to explore insect-control agent using exotic host plant volatile components dueing to larva's special habit of feeding latently, we further adopted volatile compositions that activated to females, then sprayed them singly to healthy larch seedlings, most larvae that feeding on twigs sprayed with volatile compositions were dead compared to the blank ($P<0.01$) with exception of myrcene 0.004 mol·L^{-1} which had no significance ($P>0.05$), Thereinto, *S*-α-pinene 0.04 mol·L^{-1} caused most larvae dead, which accounted for 86.677% of total number. The result suggested that volatile compositions have some influences on larvae developing and feeding, and may be implicated as a new strategy for forest health and pest management.

POSTER PRESENTATION

Biology of Wolbachia and its interaction with insects

A.R. Bandani, M. Mehrabadi

Department of plant protection, university of Tehran, College of Horticultural Science and Plant Protection, Karaj, Islamic Republic of Iran

Genera of *Wolbachia* are a group of bacteria that have closely related with Rickettsia and similar to them ,are obligate intracellular and mainly be in reproductive tissue of arthropods. *Wolbachia* can transmit to next generation through egg cytoplasm. *Wolbachia* was first observed by Herting and Wolbach in the ovaries of the mosquito *Culex pipiens* and since then, have been detected in most order of insects and are believed to be the most widespread genera between endoparasitic bacteria. This distribution is due to presence of *Wolbachia* in reproductive tissue and manipulation of reproductive system in hosts. Our study was documented- analyzed research include of library, books, papers and internet sources. The most importance of this manipulation is cytoplasmic incompatibility (CI). This situation happened when an infected male coupled with an uninfected female.CI has different types including of monodirectional (infected with one strain of *Wolbachia*), bidirectional (infected with tow strain of *Wolbachia*) and even infected with different strain of *Wolbachia*. The propose models for the mechanism of CI are, Lock and Key model, Titration – Restitution and Slow motion. At last concluded that the lock and key model is the most parsimonious and realistic one.

POSTER PRESENTATION

Queenless *Apis mellifera* and *A. cerana* colonies do not reject more non-nestmate workers than queenright colonies

Nadine C. Chapman[1], Piyamas Nanork[2], M. Shankar Reddy[3], N. Shankar Bhat[4], Madeleine Beekman[1], Benjamin P. Oldroyd[1]

[1]Behaviour and Genetics of Social Insects Laboratory, School of Biological Sciences A12, University of Sydney, NSW, Australia, [2]Department of Biology, Mahasarakham University, Mahasarakham, Thailand [3]Center for Apiculture Studies, Department of Zoology, Bangalore University, Bangalore, India, [4]Department of Apiculture, University of Agricultural Sciences, Bangalore, India

When a honey bee (*Apis*) colony becomes queenless and broodless its only reproductive option is for some of its workers to produce sons before the colony perishes. However, for this to be possible the policing of worker-laid eggs must cease. This makes queenless colonies vulnerable to reproductive parasitism by workers from other nests. Such reproductive parasitism is known to occur in *A. florea* and *A. cerana* and sometimes occurs in *A. mellifera*. Genetic analysis of worker populations has demonstrated that the proportion of non-natal workers present in *A. mellifera* and *A. cerana* colonies declines after a colony is made queenless. This suggests that queenless colonies may be more vigilant in repelling potentially parasitic non-natal workers than queenright colonies. We compared rates of nestmate and non-nestmate acceptance in both queenright and queenless *A. mellifera* and *A. cerana* colonies using standard assays. We showed that colonies of *A. mellifera* and *A. cerana* reject more non-nestmate workers than nestmates and that queenless colonies are no more likely to reject non-nestmate workers than queenright colonies.

POSTER PRESENTATION

Queenless *Apis mellifera* and *A. cerana* colonies do not reject more non-nestmate workers than queenright colonies

Nadine C. Chapman[1], Piyamas Nanork[2], M. Shankar Reddy[3], N. Shankar Bhat[4], Madeleine Beekman[1], Benjamin P. Oldroyd[1]

[1]Behaviour and Genetics of Social Insects Laboratory, School of Biological Sciences A12, University of Sydney, NSW, Australia, [2]Department of Biology, Mahasarakham University, Mahasarakham, [3]Thailand, Center for Apiculture Studies, Department of Zoology, Bangalore University, Bangalore, India, [4]Department of Apiculture, University of Agricultural Sciences, Bangalore, India

When a honey bee (*Apis*) colony becomes queenless and broodless its only reproductive option is for some of its workers to produce sons before the colony perishes. However, for this to be possible the policing of worker-laid eggs must cease. This makes queenless colonies vulnerable to reproductive parasitism by workers from other nests. Such reproductive parasitism is known to occur in *A. florea* and *A. cerana* and sometimes occurs in *A. mellifera*. Genetic analysis of worker populations has demonstrated that the proportion of non-natal workers present in *A. mellifera* and *A. cerana* colonies declines after a colony is made queenless. This suggests that queenless colonies may be more vigilant in repelling potentially parasitic non-natal workers than queenright colonies. We compared rates of nestmate and non-nestmate acceptance in both queenright and queenless *A. mellifera* and *A. cerana* colonies using standard assays. We showed that colonies of *A. mellifera* and *A. cerana* reject more non-nestmate workers than nestmates and that queenless colonies are no more likely to reject non-nestmate workers than queenright colonies.

POSTER PRESENTATION

Utility of the DNA barcoding gene for phylogeographic inference in black flies (Diptera: Simuliidae)

Julio Rivera[1], Douglas C. Currie[2]

[1]Department of Ecology & Evolutionary Biology, University of Toronto, Toronto, Canada, [2]Department of Natural History, Royal Ontario Museum, Toronto, Canada

The COI barcoding gene provides accurate species-level identification in many groups of insects. As a mitochondrial marker, the barcoding gene also has potential for elucidating intraspecific processes at the population level. This latter aspect has so far received little attention in the literature. In this study we use the barcoding gene to infer phylogeographic patterns within the cordilleran black fly species *Prosimulium travisi* and *Prosimulium neomacropyga.* Whereas *P. travisi* is widely distributed in western North America (from Yukon to California), *P. neomacropyga* exhibits a markedly disjunct distribution (Alaska/Yukon and Colorado). The present-day ranges of both species include areas that were affected by glacial oscillations during the Pliocene-Pleistocene epochs. Our analyses reveal that these events had a marked impact on the distribution and population genetics of these two species, as considerable population structure was observed. Glacial refugia, post-glacial migratory routes and areas of secondary contact were all identified in our analyses. Furthermore, cryptic diversity, presumably the result of these historical events, was also revealed. The phylogeographic patterns observed in *P. travisi* and *P. neomacropyga* were largely congruent with those observed in numerous other western Cordilleran organisms. These findings suggest that the COI barcoding gene has potential to reveal both interspecific and intraspecific patterns, giving 'valued added' information for species sampled throughout their geographical range.

POSTER PRESENTATION

Ant morphological traits and assemblage structure: patterns in remnant and pasture habitats along an environmental gradient.

Michelle Yates[1], Saul Cunningham[2], Heloise Gibb[2], Nigel R. Andrew[1]

[1]Discipline of Zoology, School of Environmental and Rural Science, University of New England, Armidale, NSW, [2]Australia, CSIRO Entomology, Canberra, Australia

Assessing how insect assemblages change along environmental gradients today enables predictions to be made about how animals may respond to climate change and other environmental disturbances.

This study used three techniques to try to understand what influences ant assemblages in two differing habitat types (pastures and native remnant forest) across a regional environmental gradient encompassing 296.5 km distance gradient, a 7.3°C temperature gradient and a 285.1mm rainfall gradient. Measures to assess changes in assemblage structure along the environmental gradient included (1) species diversity and composition; (2) ant functional groups; and (3) a range of morphological traits.

Within three regions of Northern NSW (Australia), three properties containing pasture and remnant sites were selected. Three sets of five pitfall traps were left open for seven days and data were then recorded.

Ant communities were more similar in pastures than in remnants across the gradient. This may be because pastures have an inherently similar structure (more than 80% grass cover) which is most suitable to grazing. Remnants are grazed to a lesser extent due to the high density of trees (more than 80% tree cover). Ant communities differed more between regions than between habitats. as a result of high variation in climate, elevation and geography between regions.

Results examining the effects of the environmental gradient on Species diversity, showed that there is a significant difference between regions. Results also showed that there is a significant difference between habitat types, however the difference between regions is much more significant.

POSTER PRESENTATION

Biology of *Allobaccha sapphirina* (Wiedemann)(Diptera: Syrphidae) with feeding on *Diaphorina citri* in Baluchestan

Nia B. Motamedi

Natural Resources & Agricultural Research Center of Baluchestan, Iranshahr, Islamic Republic of Iran

Diaphorina citri is one of the major pest in Baluchestan. In natural enemies, *Allobaccha sapphirina* is the predator of *Diaphorina citri* . adults and nymphal were collected from Sarbaz(Baluchestan). The biology of *A.sapphirina* was studied under laboratory conditions at 22±2 ℃ , 70-75% R.H and 14:10 L.D. The oviposition mean for each female was 101.8±44.1 eggs in cage(60*60*100 cm). The mean duration of development times of *A.sapphirina* from egg to adult were 14.1 ± 0.9 days feeding on *Diaphorina citri* in petri dishes(6 * 1.5 cm). The mean longevity of adult males and females were 3 ±0.5 and 3.5±0.5 days without feeding. Nutrition had not effects on male and female. Feeding capacity was increased with age of larvae and mean total larval feeding on *Diaphorina citri* was 98.2 ±16.2 .

POSTER PRESENTATION

Study of insect growth regulators (Hexaflumuron and Pyriproxyfen) and Fipronil on vegetative and conidia germination of *Beauveria bassiana*.

Ahmad Baghdadi[1], Marzieh Rashid[1], Aziz Sheikhi[2], Mehran Ghazavi[2]

[1]*Department, College of Abouraihan, Tehran University, Tehran, Islamic Republic of Iran*
[2]*Pests and Plant Diseases Institute, Tehran, Islamic Republic of Iran*

Use of pesticides with entomopathogenic fungi can decrease the pest resistance to pesticides. Effects of Fipronil (20, 80, 1600 ppm), Pyriproxyfen (10, 500, 1500 ppm) and Hexaflumuron (15, 45, 80 ppm) with *Beauveria bassiana* was studied on vegetative growth and sporulation at SDA medium. For determining the conidia germination of *B. bassiana* malt agar (as control) and mixed with pesticides at 500, 100, 400 ppm concentrations used. Mean comparison of inhibitory vegetative growth at different concentrations of insecticides, indicated that inhibitory percent for Pyriproxyfen (1500 ppm) and Hexaflumuron (80 ppm) is %100 and for Fipronial (1600PPm) is %76.6. At lowest concentrations of all insecticides, inhibitory percents are %10-20.For all insecticides conidia production inhibitory of fungi has not significantly different among highest concentration of all insecticides and conidia production inhibitory was %80-100.At different concentrations of insecticides mean comparison of conidia germination indicated that there was no significant difference at different concentrations of Hexaflumuron and Pyriproxyfen. The results showed that,Hexaflumuron decrease significantly conidia germination of *B. bassiana*, therefore could not use with fungus for control of any pest.

POSTER PRESENTATION

Biology of *Scolothrips longicornis* Priesner (Thysanoptera: Thripidae), as a predator of two-spotted spider mite *Tetranychus turkestani* Ugarov & Nikolski (Acari: Tetranychidae)

Mehdi Gheibi[1], Ebrahim Soleymannejadian[2], Parviz Shishebor[1]

[1]Department of Plant Protection, College of Agiculture, Islamic Azad University, Shiraz, Shiraz, Islamic Republic of Iran, [2]Department of Plant Protection, College of Agriculture, shahid Chamran University, Ahvaz, Islamic Republic of Iran

Introduction: The two spider mite, *Tetranychus turkestani* U. & N. is a major agricultural pest in Iran. Many natural enemies of the pest have been known but *Scolothrips longicornis* P. has been recognized as a promising predator of tetranychid mites.

Methods: The biology, feeding activity, development, fecundity as well as some ecological aspects of *S. longicornis* P. on *T. turkestani* were investigated under laboratory conditions (27±1 ℃, 70±5% R.H. and 16L : 8D). A stockculture of *S. longicornis* and the two-spotted spider mite was provided on cowpea. In all experiments, each predator was held on leaf discs cut from cowpea leaves infested with different stages of *T. turkestani*.

Results: *S. longicornis* females required a mean of 14.26 and10.38 days at 26 and 35ºC respectively, to complete development from egg to adult. The immature stages of thrips consumed a mean of 86.9 and 12.8 spider mite eggs and females, respectively. Females thrips killed a mean of 49.1 eggs and 11.7 female mites per day and a mean of 1861 and 453 eggs and females respectively during adult stage. The rate of predation was influenced by temperature. The thrips ate an average of 0.3 *T. turkestani* females/day at 5ºC compared with 17.1 females/day at 40ºC. Eggs of *S. longicornis* were inserted into the leaf tissue. Mating was not necessary to induce oviposition. Unmated females produced only male progeny. Mated females produced a mean of 226 eggs on cowpea during oviposition period of 37.5 days. The mean age mortality of adult female thrips was 21-25 days which was nearly equal to the life expectancy (e_x) at the time of adult eclosion. The highest sex ratio for females was 0.88 on first day of egg laying and it decreased gradually and reached to less than 0.46 after day 26. It is suggested that in mass rearing of predatory thrips, the culture should be renewed after 26th days of the beginning egg-laying. Leaves of cowpea were more suitable than sugarcane for oviposition by *S. longicornis*.

Conclusions: the results of the study suggest that *S. longicornis*, in comparison with other predators of tetranychid mites especially predatory mites, shows promising qualities as a predator of spider mites.

POSTER PRESENTATION

The effect of different vineyard management systems on the epigaeic arthropod assemblages in the Cape Floristic Region, South Africa

Rene Gaigher, Michael Samways

Department of Conservation Ecology and Entomology, Faculty of AgriSciences, Stellenbosch University, Stellenbosch, South Africa

Introduction: In the Cape Floristic Region of South Africa, where wine grape production and biodiversity conservation are of major importance, innovative management of the landscape is necessary to integrate the two activities. This study assessed the potential of alternative vineyard management i.e. organic and biodynamic vineyard management, to conserve epigaeic arthropod diversity, relative to the more widespread integrated vineyard management in the CFR.

Methods: A hierarchical design was used, consisting of three localities, each including an alternative vineyard, an integrated vineyard and a natural vegetation site as reference habitat. Arthropods were sampled using pitfall traps. Nested ANOVAs were used to test for differences in abundance and species richness of total assemblages and selected predatory taxa. Canonical correspondence analyses were used to evaluate the effects of environmental variables, management practices and landscape variables on community composition.

Results: Alternative vineyards supported a higher overall arthropod abundance and species richness, and more abundant and speciose spider and staphylinid assemblages than the integrated vineyards. Results for carabid beetles were variable. The differences could be explained in part by higher non-crop vegetation complexity and reduced management intensity of the alternative vineyards. Community composition was influenced by a combination of management practices, the surrounding landscape and geographic locality.

Conclusions: Alternative vineyard management seems to be a promising option for reducing the impact of agriculture on arthropod diversity. Because of the complex nature of these agroecosystems, it is recommended that multi-scale and site-specific studies should precede efforts to integrate it into conservation strategies.

POSTER PRESENTATION

Locust Control Support Project, a tool for a sustainable management of desert locust and trans-boundaries pests

Amadou Bocar Bal

Projet d'Appui à la Lutte Anti-acridienne, Niamey, Niger

Introduction: The objective of the Locust control Support Project is to reduce the economic impact of the Desert Locust (DL) damages and to minimiser/prevent the harmful effects on the environment of the control operations. It is funded by USAID for 2 and ½ years duration and is carried out by AGRHYMET Regional Centre since April 2006.

Methods: The project invoves the members countries of the Permanent Inster states Committee for Drought control in the Sahel (CILSS). It is carried out in Burkina Faso, in Cape Verde, in Gambia, in Guinea Bissau, in Niger (national and regional levels) and in Chad.

Results: Mass rearings of DL are developed and maintained in Niamey and Agadez. Research activities are going on, on the use of Phényl-Acéto-Nitrile (PAN)and Green Muscle®, a biopesticide which active ingredient is *Metarhizium anisopliae* var. *acridum*, in the management of the DL populations. Data-processing equipment was provided to the countries. Visits of exchange were organized in Alger (Algeria), Agadir (Morocco) and Akjoujt and Nouakchott (Mauritania) for the reinforcement of the sub-regional collaboration. One thousand six hundred and sixty sixteen (1676) staff members of the national services of agriculture, phytosanitary brigades and producers were trained into 2007 on the safety use of pesticides and on transboundary pests.

Coclusion: The execution of the project proceeds as planned and will continue with the farmers trainings on the transboundary pests and research on the PAN and Green Muscle®.

POSTER PRESENTATION

Role of topoclimatic and land cover factors predicting butterfly distributions at fine scales: a case study in central Spain.

Javier Gutierrez[1], David Gutierrez[1], Robert J Wilson[2]

[1]Biodiversity & Conservation Area, ESCET, University Rey Juan Carlos, Mostoles, Spain, [2]Centre for Ecology and Conservation, University of Exeter, Cornwall Campus, Penryn, United Kingdom

Species distribution modelling is a potentially useful tool to evaluate global change effects on biodiversity, but there is debate over whether habitat or topoclimatic models offer higher prediction accuracy.

In this study, we tested the ability of land cover and topoclimatic variables to predict the abundance and distribution of 48 butterfly species in the Sierra de Guadarrama (central Spain). This mountain region of c. 100 x 80 km has a pronounced elevational gradient (500-2430 m), and widespread, clearly-defined areas of grassland, scrub and woodland habitat.

Butterflies were sampled on transects at independent locations stratified by altitude and landcover type in 2004 and 2005. Distribution and abundance models were developed for each year using generalized linear models based on topoclimatic or habitat variables sampled at 100 m resolution in GIS, or a combination of the two,. Models from each year were then used to predict occupancy and abundance at the independent sites sampled the alternate year, and the accuracy of models was evaluated using AUC (distribution models) or correlation coefficients (abundance models).

Even at this relatively fine scale, topoclimate models gave more accurate predictions of distribution and abundance for most species, across a range of species abundances, distribution sizes and elevational associations. For relatively few species land cover variables outperformed topoclimatic models, or improved model performance when combined with topoclimatic variables in the model.

The results raise concerns about the capacity of landcover variables to predict species distributions, and of habitat management to buffer species against climate change in mountainous regions.

POSTER PRESENTATION

Development of a light emitting diode (LED) system for effective attraction of stored product insects

Me-Chi Yao[1], Chi-Yang Lee[1], En-Cheng Yang[2], Kuang-Hui Lu[3]

[1]Applied Zoology Division, Agricultural Research Institute, Council of Agriculture, Taichung, Taiwan, [2]Department of Entomology, National Taiwan University, Taipei, [3]Taiwan, Department of Entomology, National Chung Hsing University, Taichung, Taiwan

Introduction: To maintain the quality of stored rice by reducing the damage from stored-product insect pests, a new apparatus with LED to attract the pests has been developed for this purpose. In this study, we evaluated the efficacy of different monochromatic lights on attracting four dominant stored-product insects, including *Rhyzopertha dominica*, *Sitophilus oryzae*, *Sitotroga cerealella*, and *Cadra cautella*.

Methods: A dodecagon maze with 12 inside-chambers, which a light emitting diode (LED) was installed in each chamber, was used to detect the efficacy of insect attraction under different wavelengths. Eleven LEDs with peak wavelengths at 373, 398, 408, 465, 472, 517, 570, 610, 634, 677 and 715 nm, respectively, were used for producing monochromatic light. Fifty insects were put in the center of the maze and dark adapted for 20 min before the LEDs were turned on to elicit phototactic behavior for 30 min. The number of the insects in each chamber was counted after the test. Each test was 30 replicates. All experimental data were subjected to analysis of variance using SAS and Fisher's protected least significant difference (LSD) at the 5% level of probability.

Results: The most attractive wavelength to *R. dominica* and *C. cautella* was 373 nm; to *S. oryzae* was 408 nm; and to *S. cerealella* was 398 nm.

Conclusions: Attractive wavelengths have been identified for the four dominant species of stored-product insects. The active wavelengths are useful for developing an apparatus which applies phototactic behavior of the insect pests.

POSTER PRESENTATION

Cascading effects of moose browsing on galling insects and their associates on balsam fir

Ken Tabuchi[1], Dan Quiring[1], Kenichi Ozaki[2]

[1]Faculty of Forestry and Environmental Management, University of New Brunswick, Fredericton, N.B, Canada, [2]Hokkaido Research Center, Forestry and Forest Products Research Institute, Sapporo, Japan

Introduction: Mammal browsing influences plant growth and development, which may indirectly affect the abundance and species diversity of insect herbivores. Most previous studies of indirect effects of mammal browsing only examined the abundance of herbivorous insects and did not examine their performance, though effects on performance are important to predict the long term effect of mammal browsing on the herbivorous insect community. We examined the indirect effects of moose browsing on the abundance and performance (survivorship and size of survivors) of P. tumifex and its inquiline.

Methods: We investigated the number of galls per shoot, larval survival rate and the weight of mature larvae of P. tumifex and its inquiline on balsam fir saplings inside and outside of moose exclosures in Newfoundland, Canada.

Results: Moose browsing had a strong, negative impact on the abundance of P. tumifex and its inquiline, presumably by decreasing the number of current year shoots on each sapling outside exclosures. The rate of inquilinism was lower on browsed than on non-browsed plants. In contrast, the weight of mature larvae of both of P. tumifex and the inquiline was weakly but positively related to browsing, due perhaps to the longer needles on browsed plants. There was no effect of browsing on the survival rate of P. tumifex.

Conclusions: Moose browsing caused contrasting indirect effects on abundance and performance of both P. tumifex and its inquiline.

POSTER PRESENTATION

Rapid development of microsatellite markers for *Deladenus siricidicola*, a biological control agent of *Sirex notilio*, using FIASCO enrichment and pyrosequencing

Osmond X.M. Mlonyeni[1], Bernard Slippers[1], Brett P. Hurley[1], Rodrigo J. Ahumada[2], Paula Klasmer[3], Brenda D. Wingfield[1], Michael J. Wingfield[1]

[1]Department of Genetics, Forestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, South Africa, [2]Bioforest S.A, Concepción, [3]Chile, Campo Forestal General San Martín, Estación Experimental Bariloche, Instituto Nacional de Technología Agropecuaria, Negro, Argentina

The woodwasp *Sirex noctilio* and its symbiotic Basidiomycetes fungus, *Amylostereum areolatum*, are invasive pests that cause the most significant damage to *Pinus* spp. in the Southern Hemisphere. The nematode, *Deladenus siricidicola* parasitizes *S. noctilio* and is one of the most important biological control agents of the woodwasp. Currently, nothing is known about the genetic diversity of *D. siricidicola* populations even though such information can be valuable for biological control programs. The aim of this study was to develop microsatellite markers for future use in population studies of *D. siricidicola*. In addition, we test pyrosequencing as a tool to shorten the time needed for microsatellite development. Genomic DNA was enriched for microsatellites using the Fast Isolation by AFLP of Sequences Containing repeats (FIASCO) protocol and products were sequenced using pyrosequencing (Genome Sequencer FLX System™, Roche Diagnostics). The obtained sequences were used to design primers via the webbased program Primer 3 (http://frodo.wi.mit.edu). The pyosequencing data yielded 94 microsatellite containing contigs from which 26 primer pairs were designed. Preliminary analysis indicates extremely little variation amongst the Southern Hemisphere strains. This study demonstrated that pyrosequencing is an effective and fast tool to characterize fragments of microsatellite enriched gDNA, and produced potential markers for population studies of *D. siricidicola*.

POSTER PRESENTATION

Natural enemies associated with *Nipaecoccus viridis* (Newstead) in Khuzestan Province, southwest Iran

Mohammad Saeed Mossadegh, Mehdi Esfandiari, Gholamali Asadeh, Abdolreza Khodaman, Mandana Novin, Valiollah Baniameri

Plant Protection Department, College of Agriculture, Shahid Chamran Univeristy, Ahwaz, Islamic Republic of Iran

Introduction: The mealybug *Nipaecoccus viridis* (Newstead) is one of the major pests of citrus orchards of north Khuzestan, southwest Iran. This pest was first recorded on a sweet lemon tree in 1985 in Ahwaz south of Khuzestan, and then spread rapidly in many citrus orchards in the province.

Methods: A survey for biology as well as natural enemies associated with the mealybug was conducted from 1989 to March 2007 in seven different consecutive projects.

Results: The species recorded belong to the following orders and families: Coccinellidae, Col.: *Hyperaspis polita* Weise, *Nephus includens* (Kirsh), *N.* sp. near *fenestratus* (Sahberg). Encyrtidae, Hym.: *Anagyrus dactylopii* (Howard), *A. agraensis* Sara., *A. diversicornis* Mercet, *A. mirzai* Agarwal & Alam. Cecidomyiidae, Dip.: *Dicrodiplosis manihoti* Harris. The following hyperparasitoids were also recorded: Encyrtidae, Hym.: *Homalotylus quaylei* Timberlake; Signiphoridae, Hym.: *Chartocerus* (*Matritia*) sp. Near *kurdjumovi* (Nikolskaya) and *Pteromalidae*, Hym.: *Pachyneuron muscarum* L.

Conclusion: Although the pest has many natural enemies in the region, but it damages the fruits at early spring due to the low population densities of its natural enemies at this time of the year.

POSTER PRESENTATION

Aquatic bugs (Hemiptera, Heteroptera) of the "Lago Municipal de Cascavel", Paraná, Brazil, as indicators of environmental pollution

Gabriel Simoes de Andrade

Universidade Estadual do Oeste do Paraná, Centro de Ciências Biológicas e da Saúde, Parana, Brazil

Introduction: Aquatic insects are of great environmental interest, both those with only immature stages in this habitat, as those who live there permanently. Some of them are characteristic of lakes or rivers, or both, and in all cases there are species that may be biological indicators of water quality. The first step is the knowledge of representatives from different regions and environments.

Methods: The specimens are being collected in all parts of the lake, which is located in a large area of leisure of the city, with woods and gardens. Usual methods of collection has been used, and the fixing and conservation are made in plastic bottles with alcohol 70%. The identifications are made by the general literature and in some cases, with the help of specialists.

Results: The following species have been found frequently: in Nepomorpha *Belostoma micantulum* Stål, 1858 and *B. oxyurum* (Dufour, 1863) (Belostomatidae), *Notonecta polystolisma* Fieber, 1851 and *Buenoa paranaensis* Jaczewski, 1928 (Notonectidae), *Heterocorixa nigra* Hungerford, 1928 and *Sigara chrostowskii* Jaczewski, 1927 (Corixidae), and in Gerromorpha *Platyvelia brachialis* (Stål, 1860) (Veliidae), *Limnogonus aduncus* Drake & Harris, 1933 and *Halobatopsis platensis* (Berg, 1879) (Gerridae).

Conclusions: All these species were found in large series, showing a good adaptation to local conditions and can be characterized as synantropics. These taxa, specially of Belostomatidae, already have been identified in other Brazilian and South America lakes with features of the present, and can be used as indicators of pollution. The study is being continued with the identification of species of minor occurrence.

POSTER PRESENTATION

The extracts of house dust mite, *Dermatophagoides pteronissinus* (DpE), induce MCP-1, IL-6 and IL-8 in human monocytic THP-1 cells and eosinophilic EoL-1 cells

Ji-Sook Lee[1], Ji-Sun Ryu[1], Joo-Hwan Kim[1], Sang Kyun Koh[2], In Sik Kim[3], Chi-Young Yun[1], Sang-Ho Nam[1]

[1]Department of Biology, Daejeon University, Daejeon, Korea, [2]Republic of, Department of Biology and Department of Microbiology and Biotechnology, Daejeon University, Daejeon, Korea, [3]Department of Biomedical Laboratory Science, School of Medicine, Eulji University, Daejeon, Republic of Korea

Introduction: The house dust mite, *Dermatophagoides pteronissinus* (Pyroglyphidae), is a cosmopolitan guest in human habitation. Dust mites are the most common cause of asthma and allergic symptoms worldwide. In mediating the infiltration of various cells into the skin of patients with atopic dermatitis and psoriasis, pro-inflammatory cytokines such as monocyte chemotactic protein-1 (MCP-1/CCL2), IL-6, and IL-8 (CXCL8) play pivotal roles.

Methods: We investigated the effect of *D. pteronissinus* extract (DpE) on expression of MCP-1/IL-6/IL-8 in the level of both mRNA and protein, and the signal transduction in the human monocytic THP-1 and human eosinophilic EoL-1 cells.

Results: The mRNA and protein expression of MCP-1, IL-6 and IL-8 were elevated by DpE in a time and dose-dependent manner in THP-1 and EoL-1 cells. In addition, the concentration of MCP-1, IL-6 and IL-8 increased in serum of patients with atopic dermatitis, compared with those in normal serum.

Conclusions: These results indicate that DpE can trigger allergic response by increasing the expression of pro-inflammatory cytokines, and may be used as a helpful screening system in drug development for the treatment of atopic dermatitis and other allergic diseases by measuring the effect to inhibit cytokines.

POSTER PRESENTATION

Expression of *Bacillus thuringiensis* subsp. *aizawai* Cry1D toxins in *Escherichia coli*

Hamzah Abdul Aziz[1], Wei Hong Lau[1], Yee How Tan[1], Ahmad Said Sajap[2], Khatijah Yusoff[3]

[1]Department of Plant Protection, Faculty of Agriculture, Universiti Putra Malaysia, Serdang, Selangor, Malaysia, [2]Department of Forest Management, Faculty of Forestry, Universiti Putra Malaysia, Serdang, Selangor, Malaysia, [3]Department of Microbiology, Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia, Serdang, Selangor, Malaysia

Introduction: The most widely used microbial insecticide to date is a product based on *Bacillus thuringiensis,* a spore-forming soil bacterium that produces highly specific insecticidal proteins called Bt toxins during sporulation. In this study, expression of protoxin and active-truncated Cry1D toxin, respectively, *B. thuringiensis* subsp. *aizawai* was carried out in *Escherichia coli*.

Methods: The active and full-length *cry1D* genes were amplified from the genomic DNA of *B. thuringiensis* subsp. *aizawai* and cloned into a TA cloning vector for sequencing. The expression of recombinant Cry1D proteins was carried out in *E. coli* and the proteins were assayed against the larvae of *Spodoptera litura*.

Results: The active and full-length *cry1D* gene were successfully amplified from the genomic DNA of *B. thuringiensis* subsp. *aizawai* and their size was about 1 878 bp and 3 495 bp, respectively. The nucleotide sequence of the *cry1D* genes is very similar to the sequence of *cry1Da1* (accession no.: X54160) and *cry1Da2* gene (accession no.: I76415), with a homology of 100%. In SDS-PAGE analysis, both genes were expressed and their size was about 130 kDa (full-length *cry1D* gene) and 53 kDa (active *cry1D* gene), respectively. The Cry1D protoxin caused 100% mortality to the larvae of *S. litura* after 4 days postinoculation. It induced mortality at a faster rate when compared to the commercial Bt product (Flobac FC*, Denmark), which induced 100% larval mortality after 6 days postinoculation. The active-truncated Cry1D toxin only induced 100% larval mortality after 8 days postinoculation.

Conclusion: We succeeded in expressing active Cry1D toxins in a prokaryotic expression system. It may be useful as an alternative Bt product for insect pest control.

POSTER PRESENTATION

Expression of *Bacillus thuringiensis* subsp. *aizawai* Cry1D toxins in *Escherichia coli*

Hamzah Abdul Aziz[1], Wei Hong Lau[1], Yee How Tan[1], Ahmad Said Sajap[2], Khatijah Yusoff[3]

[1]Republic of, Department of Plant Protection, Faculty of Agriculture, Universiti Putra Malaysia, Serdang, Selangor, Malaysia, [2]Department of Forest Management, Faculty of Forestry, Universiti Putra Malaysia, Serdang, Selangor, Malaysia, [3]Department of Microbiology, Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia, Serdang, Selangor, Malaysia

Introduction: The most widely used microbial insecticide to date is a product based on *Bacillus thuringiensis,* a spore-forming soil bacterium that produces highly specific insecticidal proteins called Bt toxins during sporulation. In this study, expression of protoxin and active-truncated Cry1D toxin, respectively, *B. thuringiensis* subsp. *aizawai* was carried out in *Escherichia coli*.

Methods: The active and full-length *cry1D* genes were amplified from the genomic DNA of *B. thuringiensis* subsp. *aizawai* and cloned into a TA cloning vector for sequencing. The expression of recombinant Cry1D proteins was carried out in *E. coli* and the proteins were assayed against the larvae of *Spodoptera litura*.

Results: The active and full-length *cry1D* gene were successfully amplified from the genomic DNA of *B. thuringiensis* subsp. *aizawai* and their size was about 1 878 bp and 3 495 bp, respectively. The nucleotide sequence of the *cry1D* genes is very similar to the sequence of *cry1Da1* (accession no.: X54160) and *cry1Da2* gene (accession no.: I76415), with a homology of 100%. In SDS-PAGE analysis, both genes were expressed and their size was about 130 kDa (full-length *cry1D* gene) and 53 kDa (active *cry1D* gene), respectively. The Cry1D protoxin caused 100% mortality to the larvae of *S. litura* after 4 days postinoculation. It induced mortality at a faster rate when compared to the commercial Bt product (Flobac FC*, Denmark), which induced 100% larval mortality after 6 days postinoculation. The active-truncated Cry1D toxin only induced 100% larval mortality after 8 days postinoculation.

Conclusion: We succeeded in expressing active Cry1D toxins in a prokaryotic expression system. It may be useful as an alternative Bt product for insect pest control.

POSTER PRESENTATION

Overwintering and cold hardiness of western flower thrips, *Frankliniella occidentalis* (Pergande)

Zhong-ren Lei, Ming-juan Bi

State Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Science, Beijing, China

Introduction: Discovering of *Frankliniella occidentalis* (Pergande) is not long in China, so cold hardiness of *Frankliniella occidentalis* (Pergande) in China and how they can overwinter safely in North of China should be testified through some experiments.

Methods: Put the probe in the type of VM04/100 super-high-low temperature vegetal box , then cooled at 1□/min using a thermoelectric cooling unit until an exotherm corresponding to the release of the latent heat of fusion was registered. The temperature change of insects was gathered□noted and analysed through TC-20 analysis system.

Results: The supercooling point(SCP),freezing point(FP) were tested on western flower thrips, *Frankliniella occidentalis (*Pergande).The lowest temperature of SCP was -23.36±0.93℃ of prophase pupae.The SCP of other stages is pupae < adult < second instar larval < first instar larval < egg. So we can conclude that the fitted overwintering instar of western flower thrips is prophase pupae in Beijing. In certain range SCP gradually lowing through the advanced freezing time extend. But SCP rise if advanced freezing time too long. Pupae can not survive in the winter, estimated by field trials in Beijing with pupae buring. It is suggested that western flower thrips died rapidly near the temperature of SCP. In a word ,the range of cold tolerance ability is prophase pupae > pupae > adult > second instar > first instar > egg.

POSTER PRESENTATION

Overwintering and cold hardiness of western flower thrips, *Frankliniella occidentalis* (Pergande)

Zhong-ren Lei, Ming-juan Bi

State Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Science, Beijing, China

Introduction: Discovering of *Frankliniella occidentalis* (Pergande) is not long in China, so cold hardiness of *Frankliniella occidentalis* (Pergande) in China and how they can overwinter safely in North of China should be testified through some experiments.

Methods: Put the probe in the type of VM04/100 super-high-low temperature vegetal box , then cooled at 1□/min using a thermoelectric cooling unit until an exotherm corresponding to the release of the latent heat of fusion was registered. The temperature change of insects was gathered□noted and analysed through TC-20 analysis system.

Results: The supercooling point(SCP),freezing point(FP) were tested on western flower thrips, *Frankliniella occidentalis*□Pergande□.The lowest temperature of SCP was -23.36±0.93℃ of prophase pupae.The SCP of other stages is pupae < adult < second instar larval < first instar larval < egg. So we can conclude that the fitted overwintering instar of western flower thrips is prophase pupae in Beijing. In certain range SCP gradually lowing through the advanced freezing time extend. But SCP rise if advanced freezing time too long. Pupae can not survive in the winter, estimated by field trials in Beijing with pupae buring. It is suggested that western flower thrips died rapidly near the temperature of SCP. In a word ,the range of cold tolerance ability is prophase pupae > pupae > adult > second instar > first instar > egg.

POSTER PRESENTATION

Developmental changes according to gamma irradiation on the different stages of *Harmonia axyridis* (Coleoptera: Coccinellidae)

Hee Jin Lee[1], Me Ja Seo[1], Eun Jin Kang[1], Hee Bong Seok[1], Dae Hong Lee[1], Chang Wook Jo[1], Cho Rong Park[1], Si Yong Kang[2], Yong Man Yu[1], Young Nam Youn[1]

[1]Dept. of Applied Biology, College of Agriculture & Life Sciences, Chungnam National University, Daejeon, Republic of Korea, [2]Korea Atomic Energy Research Institute, Daejeon, Republic of Korea

The multicolored Asian ladybird beetle, *Harmonia axyridis* (Pallas) (Coleoptera: Coccinellidae), is common to a wide range of natural and agricultural habitats. Applications of gamma irradiation minimized the losses of stored food and the death or failure of emergence in larval and pupal stages. On the other hand, degrade toxin waste as one of alternative to chemical pesticide for both quarantine and sprout control purposes of storage crop pest. So, we have investigated whether gamma irradiation exposed to eggs, lava, pupa and adults of *H. axyridis*. It may be affected the emergence, fertility, fecundity, development period and sex ratio of *H. axyridis*. Some changes of physiological characteristics may be applied to more efficient agents as biological control of several aphids. Insects were exposed to gamma irradiation from 0 to 500 Gy of ^{60}Co depended on their developmental stages. The results showed that the first instar, eggs, third instar, pupae, and adults were more sensitive in order of irradiation dose. And fecundity and fertility of female adults were significantly decreased with increasing gamma irradiation dose at all tested individuals.

POSTER PRESENTATION

Analyses of different elytra color patterns using AFLP in *Harmonia axyridis*

Dae Hong Lee, Eun Jin Kang, Hee Jin Lee, Hee Bong Seok, Chang Wook Jo, Cho Rong Park, Myoung Gi Kang, Mi Ja Seo, Yong Man Yu, Young Nam Youn

Dept. of Applied Biology, College of Agriculture & Life Sciences, Chungnam National University, Daejeon, Republic of Korea

The multicolored Asian ladybird beetle, *Harmonia axyridis*, which demonstrates typical genetic polymorphism in its elytra color patterns. Early studies have color polymorphism in terms of geographical clines while a few investigated temporal populations in Coccinellidae. Nevertheless, note that geographical and temporal morph variation does not always correspond to what is expected from thermal and industrial adaption theories. A recent study of transformation and RNAi of the ladybird beetle, however, there is yet no evidence to indicate the variation is genetic or environmental factors. Here we describe a relatively new molecular fingerprinting technique, amplified fragment length polymorphism (AFLP). Because we think that color polymorphism in Coccinellidae is affected by genetic polymorphism. In total 38 markers were scored from which some markers were polymorphic. Supsequent UPGMA cluster analysis revealed 3 major group of *Harmonia axyridis* populations. But for strains that are more genetically similar, different primer combinations may be need to generate enough polymorphic marker.

POSTER PRESENTATION

Variation of elytra color patterns according to temperatures and photoperiods in *Harmonia axyridis* (Coleoptera: Coccinellidae)

Eun Jin Kang, Hee Jin Lee, Hee Bong Seok, Dae Hong Lee, Chang Wook Jo, Cho Rong Park, Mi Ja Seo, Young Man Yu, Young Nam Youn

Dept. of Applied Biology, College of Agriculture & Life Sciences, Chungnam National University, Daejeon, Republic of Korea

The surface of most coccinellids (particularly the elytra) has characteristic color patterns, which show great variability within many species. Individuals of a species of ladybird often differ from one another in color and pattern. In case of *Harmonia axyridis*, environmental factors, such as temperature or food, can probably influence color and pattern. However, virtually no work has been carried out in the influence of such factor. Therefore, in this study, according to rearing temperature, photoperiod and diet, variation of elytra color patterns were investigated. First instar larva on each color pattern were reared in an incubator at one of two temperatures; 25 and 30℃, under the following photoperiod; L16: D8, L12: D12 and L8: D16 and were provided three species of aphids. And their color patterns of adults were estimated.

POSTER PRESENTATION

Assay of α-amylase in gut and salivary glands of *Eurygaster maura* (Hemiptera: Scutelleridae)

Mohammad Mehrabadi, Ali R Bandani

Department of Plant Protection, University of Tehran, Karaj, Islamic Republic of Iran

Introduction: Among the wheat pest in Iran, genera of *Eurygaster* sp. (Hemiptera: Scutelleridae) is the most economic pest. It's major injury is feeding of wheat seeds. This insect introduces its salivary enzymes into seed and after partially digestion, sucking digested material, therefore identification and assessing of its enzymes is very important.

Methods: The insects were collected from Gorgan wheat farm of Golestan Province, Iran, and maintained on wheat plants in the laboratory at 27 ± 2°C with 14L:10D. Voucher specimens are kept in the Entomological Laboratory, Plant Protection Department, Tehran University Adults were randomly selected and midgut and salivary glands from these individuals were removed by dissection under a light microscope in ice-cold saline buffer (0.006 M NaCl). After dissecting the insects and exploiting of its salivary glands in NaCl, 10 pair of salivary glands were floating in 1000 µl Phosphate buffer and homogenized After hemogenation in standard condition, each sample were separately transferred to 1.5 ml centrifuge tubes and centrifuged at 15000 ×g for 20 min at 4˚C. The supernatants were pooled and stored at -20˚C for subsequent analyses. Amylase activity was measured by dinitrosalicilic acid (DNS) procedures, using soluble starch as substrate. The effect of different ions on α-amylase activity surveyed in the presence of different concentration of chloride salts of Na^+ (5,10,20,40 m mol/L) and K^+,Ca^{2+},Mg^{2+} and ethylenediamine tetraacetic acid (EDTA),sodium dodecyl sulfate (SDS) in concentration (0.5,1,2,4 m mol/L)and urea (0.5,1,2,4 mol/L). Determination of activity in all assessing measured by spectrophotometer based on light absorbent in λ_{max} (OD/min).

Results: Results showed that enzyme activity in salivary glands and guts of adult insects were 0.022 and 0.036 OD/min degrees, respectively. The temperature optimum for enzyme activity was 30-35 c^o, the optimum PH was 6-7. Studying the effect of various ions on α-amylase activity was showed that Na^+ and K^+ ions increased activity only a little. Mg^{2+} decreased amylase activity alittle.Ca^{2+} increased amylase activity. SDS , EDTA a and urea decreased amylase activity.

Conclusions: There were some differences between α-amylase in gut and salivary glands of *Eurygaster maura*, activity of mentioned enzyme in gut is more than salivary glands that could be due to differences of organ's activity.

POSTER PRESENTATION

Assay of α-amylase in gut and salivary glands of *Eurygaster maura* (Hemiptera: Scutelleridae)

Mohammad Mehrabadi, Ali R Bandani

Republic of, Department of Plant Protection, University of Tehran, Karaj, Islamic Republic of Iran

Introduction: Among the wheat pest in Iran, genera of *Eurygaster* sp. (Hemiptera: Scutelleridae) is the most economic pest. It's major injury is feeding of wheat seeds. This insect introduces its salivary enzymes into seed and after partially digestion, sucking digested material, therefore identification and assessing of its enzymes is very important.

Methods: The insects were collected from Gorgan wheat farm of Golestan Province, Iran, and maintained on wheat plants in the laboratory at 27 ± 2°C with 14L:10D. Voucher specimens are kept in the Entomological Laboratory, Plant Protection Department, Tehran University Adults were randomly selected and midgut and salivary glands from these individuals were removed by dissection under a light microscope in ice-cold saline buffer (0.006 M NaCl). After dissecting the insects and exploiting of its salivary glands in NaCl, 10 pair of salivary glands were floating in 1000 µl Phosphate buffer and homogenized After hemogenation in standard condition, each sample were separately transferred to 1.5 ml centrifuge tubes and centrifuged at 15000 ×g for 20 min at 4˚C. The supernatants were pooled and stored at -20˚C for subsequent analyses. Amylase activity was measured by dinitrosalicilic acid (DNS) procedures, using soluble starch as substrate. The effect of different ions on α-amylase activity surveyed in the presence of different concentration of chloride salts of Na^+ (5,10,20,40 m mol/L) and K^+,Ca^{2+},Mg^{2+} and ethylenediamine tetraacetic acid (EDTA),sodium dodecyl sulfate (SDS) in concentration (0.5,1,2,4 m mol/L)and urea (0.5,1,2,4 mol/L). Determination of activity in all assessing measured by spectrophotometer based on light absorbent in λ_{max} (OD/min).

Results: Results showed that enzyme activity in salivary glands and guts of adult insects were 0.022 and 0.036 OD/min degrees, respectively. The temperature optimum for enzyme activity was 30-35 c°, the optimum PH was 6-7. Studying the effect of various ions on α-amylase activity was showed that Na^+ and K^+ ions increased activity only a little. Mg^{2+} decreased amylase activity alittle.Ca^{2+} increased amylase activity. SDS , EDTA a and urea decreased amylase activity.

Conclusions: There were some differences between α-amylase in gut and salivary glands of *Eurygaster maura*, activity of mentioned enzyme in gut is more than salivary glands that could be due to differences of organ's activity.

POSTER PRESENTATION

Determination of gut & salivary pH and comparing of α-Amylase activity in various nymphal stages and adult of *Eurygaster maura* (Hemiptera: Scutelleridae)

Mohammad Mehrabadi, Ali R Bandani

Department of Plant Protection, University of Tehran, Karaj, Islamic Republic of Iran

Introduction: Isolation, studying and identification of insect enzymes and the organs that are resource of them, would be useful to us for more understanding of digestive process in insects. Knowing of this information about economic pests is very valuable and applicable in order to their control. Salivary enzyme entrance of mentioned bugs into the feeding seeds In addition to its direct injury to wheat seeds,causes decreasing of feeding seeds quality, has harmful medicine effects on consumers involved humans.

Methods: The insects were collected from Gorgan wheat farm of Golestan Province, Iran, and maintained on wheat plants in the laboratory at 27 ± 2°C with 14L:10D. Voucher specimens are kept in the Entomological Laboratory, Plant Protection Department, Tehran University. Adults were randomly selected and midgut and salivary glands from these individuals were removed by dissection under a light microscope in ice-cold saline buffer (0.006 M NaCl). Whole *E. maura* nymphs were homogenized in the above mentioned universal buffer and centrifugation carried out as before. The supernatants were pooled and stored at -20˚C for later use. After hemogenation in standard condition, each sample was separately transferred to 1.5 ml centrifuge tubes and centrifuged at 15000 ×g for 20 min at 4˚C. The supernatants were pooled and stored at -20˚C for subsequent analyses. Amylase activity was measured by dinitrosalicilic acid (DNS) procedures, using soluble starch as substrate. Determination of activity measured by spectrophotometer based on light absorbent in λ_{max} (OD/min). PH determinations of salivary glands and midgut were assayed by indicator staining reagent separately.

Results: Studies showed that first part of midgut was slightly alkaline and other three parts were some acidic. α- amylase activity is present in midgut and salivary glands of adult *E. intergriceps* and in whole body of nymphs. Only trace amounts of enzyme activity were detected in the first-nymphal stage (0.008 OD/min), whereas α- amylase activity in second-nymphal stage was 0.025degree of OD/min. In other stages (third to fifth-nymphal stage) reached its highest value (0.036 OD/min). Result determined that the highest activity observed in third to fifth- nymphal stage and the lowest activity in the first nymphal stage.

Conclusions: Because of being the lowest feeding and movement activities in first nymphal stage of *E. maura* against other stages, hence, it is common to be the lowest amylase activity in this stage. After this stage, feeding causes activity of amylase and continues in higher stages. On the other words, these results showed that α-amylase specific activity in the immature stages increased constantly up to third-instar nymph.

POSTER PRESENTATION

Arthropod biodiversity on transgenic cotton in single gene traits, expressing either herbicide tolerance or bollworm resistance (*Cry1Ac*), and in a double gene trait, expressing both herbicide tolerance and bollworm resistance, in South Africa

Tanya Joffe[1], Annette Bennett[2], Neethling Du Toit[3], Erica Du Toit[3], Walter M. Green[4]

[1]School of Agricultural Science/TIAR, University of Tasmania, Hobart, Australia, [2]Inselele Training CC, Centurion, South Africa, [3]Agri-Biotech Research Consultancies CC, Nelspruit, [4]South Africa, Crop and Plant Biotechnology Services CC, Kempton Park, South Africa

This study was aimed at establishing the baseline for insect biodiversity in genetically altered cotton containing single and double gene traits, in Groblersdal (South Africa), over two cotton growing seasons (2003/04 and 2004/05). The purpose was to collect data on arthropod species during the fruiting phase of cotton on a commercial cotton farm, under common management practices for each cotton type (conventional cotton - DeltaOPAL), Bollgard™ (NuOPAL), Roundup Ready™ (DeltaOPAL RR) and Stack gene (NuOPAL RR). Arthropod biodiversity was compared within genetically modified (GM) and non-GM cotton fields after normal spray programs aimed at controlling bollworm populations, to populations found in unsprayed fields. Scouting data from 2003/04 showed that species diversity and richness occurring on GM cotton was similar to that found on conventional cotton, with higher species diversity appearing to be present on Stack gene cotton when monitored by means of sweeping. Pest management strategies differed for each of the GM cotton varieties (Stack gene, Bollgard™ and Roundup Ready™) and this had an effect on the pest and predator populations found during each count. The GM cotton varieties had no obvious negative environmental effect when comparing the arthropod diversity within each field with unsprayed conventional cotton. The results from 2004/05 statistically confirmed that of the previous season. Overall, the highest total number of predators was found on NuOPAL RR during the 2004/05 season. NuOPAL and NuOPAL RR tended to have higher numbers of predators than the sprayed DeltaOPAL and DeltaOPAL RR varieties. The total number of arthropods found on the unsprayed cotton types was similar. In the case of Roundup Ready cotton, fewer arthropods at any specific time was the result of chemical application. A large variety of arthropod species was present on all cotton types evaluated and no trend could be established that these particular species were more prevalent on any particular cotton type. This data could be useful for decision makers interested in developing biosafety regulations for transgenic cotton.

POSTER PRESENTATION

Expression of *Bacillus thuringiensis* subsp. *aizawai* Cry1D toxins in *Escherichia coli*

Abdul Aziz Hamzah[1], Wei Hong Lau[1], Tan Yee How[1], Ahmad Said Sajap[2], Yusoff Khatijah[3]

[1]Department of Plant Protection, Faculty of Agriculture, Universiti Putra Malaysia, Selangor, Malaysia, [2]Department of Forest Management, Faculty of Forestry, Universiti Putra Malaysia, Selangor, Malaysia, [3]Department of Microbiology, Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia, Selangor, Malaysia

Introduction: The most widely used microbial insecticide to date is a product based on *Bacillus thuringiensis,* a spore-forming soil bacterium that produces highly specific insecticidal proteins called Bt toxins during sporulation. In this study, expression of protoxin and active-truncated Cry1D toxin, respectively, *B. thuringiensis* subsp. *aizawai* was carried out in *Escherichia coli*.

Methods: The active and full-length *cry1D* genes were amplified from the genomic DNA of *B. thuringiensis* subsp. *aizawai* and cloned into a TA cloning vector for sequencing. The expression of recombinant Cry1D proteins was carried out in *E. coli* and the proteins were assayed against the larvae of *Spodoptera litura*.

Results: The active and full-length *cry1D* gene were successfully amplified from the genomic DNA of *B. thuringiensis* subsp. *aizawai* and their size was about 1 878 bp and 3 495 bp, respectively. The nucleotide sequence of the *cry1D* genes is very similar to the sequence of *cry1Da1* (accession no.: X54160) and *cry1Da2* gene (accession no.: I76415), with a homology of 100%. In SDS-PAGE analysis, both genes were expressed and their size was about 130 kDa (full-length *cry1D* gene) and 53 kDa (active *cry1D* gene), respectively. The Cry1D protoxin caused 100% mortality to the larvae of *S. litura* after 4 days postinoculation. It induced mortality at a faster rate when compared to the commercial Bt product (Flobac FC*, Denmark), which induced 100% larval mortality after 6 days postinoculation. The active-truncated Cry1D toxin only induced 100% larval mortality after 8 days postinoculation.

Conclusion: We succeeded in expressing active Cry1D toxins in a prokaryotic expression system. It may be useful as an alternative Bt product for insect pest control.

POSTER PRESENTATION

Characterization of nucleopolyhedrovirus and granulovirus of armyworm *Spodoptera litura* (Lepidoptera: Noctuidae) in Malaysia

Wei Hong Lau[1], Said Sajap Ahmad[2], Yusoff Khatijah[3], Manaf Ali Abdul[4], Abdul Samad Noraini[3]

[1]Department of Plant Protection, Faculty of Agriculture, Universiti Putra Malaysia, Selangor, Malaysia, [2]Department of Forest Management, Faculty of Forestry, Universiti Putra Malaysia, Selangor, Malaysia, [3]Department of Microbiology, Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia, Selangor, Malaysia, [4]Department of Cell and Molecular Biology, Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia, Selangor, Malaysia

Introduction: Diseased larvae of *Spodoptera litura* collected from MARDI Research Station in Kelantan, Malaysia exhibited *Wipfelkrankheit* symptom with combinations of whitish and pinkish body colour. Preliminary electron microscopic study conducted on the diseased *S. litura* larvae revealed the presence of two distinct forms of viral occlusion body in the infected tissues of the larvae. In the present study, we attempted to isolate and characterize the different forms of occlusion body (OBs) in the diseased *S. litura* larvae.

Methods: The OBs, virus particles, nucleocapsids and virions were extracted and purified by ultra-centrifugation in a 40-80% (w/w) sucrose gradient. The purified virus components were examined under a TEM. The polyhedrin and granulin genes of both OBs were amplified and sequenced.

Results: The TEM micrograph of isolated preparation revealed two types of OBs that have morphology typical of nucleopolyhedrovirus (NPV) and granulovirus (GV). The NPV is composed of multiple virus particles while the GV is composed of only single virus particle per capsule. Based on the variable number of nucleocapsids enclosed within a virus particle, we confirmed that the NPV belonged to multiple nucleocapsids NPV. The nucleotide sequence analysis of the polyhedrin gene of NPV and granulin gene of GV showed 98% and 81% sequence identity to SpltNPV (accession number: AF037262) and XcGV (accession number: U70069), respectively. Based on the sequence analysis, the local isolates of NPV and GV are placed as a taxon of Group II NPV and Group GV, respectively.

Conclusion: The results presented in this study revealed that the viruses isolated from the diseased larvae of *S. litura* belong to the group of baculoviruses.

POSTER PRESENTATION

Spatio-temporal dynamics of the redlegged earth mite in Western Australia

Robert Smith[1], John Read[2], James Ridsdill-Smith[3]

[1]University of Huddersfield, Huddersfield, United Kingdom, [2]University of Warwick, Warwick, [3]United Kingdom, CSIRO Entomology, W.A, Australia,

The Redlegged Earth Mite (RLEM) *Halotydeus destructor* is an introduced pest of clover pasture in parts of South and Western Australia. RLEM feeds on subterranean clover, a major component of grazing pasture, and causes substantial loss of yield. A long-term study was established at Waroona, south of Perth, during the 1950s. Numbers of RLEM and a competing herbivore, the Lucerne 'Flea' (LF) *Sminthurus viridis*, were sampled on a regular grid of 252 sampling points every three weeks during autumn and winter over a 3-year period to establish baseline dynamics. Numbers of a predator were also counted.

It is known that RLEM form feeding aggregations on plant leaves. Individual mites move only a few metres in their lifetime, yet there are large-scale aggregations of mites over tens of metres. These aggregations must result from population dynamics rather than individual behaviour. The typical aggregation was found by hierarchical mean square analysis to be around 80m x 160m. The locations of aggregations changed between sampling dates.

A non-parametric test of temporal density dependence demonstrated both direct (within generation) and delayed (lag of three generations) density dependence, suggesting a trophic interaction with the predator, modulated by interaction with the competitor.

We tested the hypothesis that the aggregations represent travelling waves of high density moving across the landscape. A U-shaped Mantel correlation plot supported the travelling-wave hypothesis.

- Delayed density dependence suggests that the travelling waves in part result from ecological interactions affecting rates of population increase
- There is some evidence of competition between Redlegged Earth Mite and Lucerne Flea, both of which are predated by another mite (Bdellid).
- High, potential reproductive rate interacts with delayed density dependence and low rates of dispersal to produce travelling waves ('spatial cycles').

POSTER PRESENTATION

Sublethal effects of *Beauveria bassiana* (Balsamo) Vuillemin (Deuteromycotina: Hyphomycetes) on the whitefly *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) under laboratory conditions

Edison Torrado-Leon[1], James Montoya-Lerma[2], Edison Valencia-Pizo[3]

[1]Universidad Nacional de Colombia, Facultad de Agronomía, Cali, Colombia, [2] Universidad del Valle, Departamento Biología, Cali, [3]Colombia, Bayer CropScience, Cali, Colombia

Sublethal effects were evaluated in subsequent generations of whiteflies *Bemisia tabaci* (Gennadius) after exposure of each of the four nymphal stages of the parental generation to the fungus *Beauveria bassiana* (Balsamo) Vuillemin. Examples of such effects include impaired fertility and production of malformations or external variations as well as non-immediate mortality, that is, premature death of later generations. Malformations of the head, legs, wings or abdomen were not observed in adults derived from treated nymphs, nor were negative effects observed in the fecundity and fertility of the descendants of the whiteflies treated with the fungus. However, moulting problems were observed in insects descended from *B. bassiana*-treated whiteflies, the first time this has been reported. Almost 30% of the imagoes resulting from treated nymphs were unable to detach completely from the exuvia. Corrected mortality rates showed a gradual dilution over time.The importance of these findings is analysed in the light of other similar results.

POSTER PRESENTATION

Implementation of an IPM model in tobacco based on the use of a systemic insecticide and the protection of *Nesidiocoris tenuis* as the key predator of the *Traleurodes vaporariorum* white fly

Edison Valencia-Pizo[1], Katerine Valderrama[2], Jaime Granobles[2]

[1]Corporacion Colombiana de Investigacion Agropecuaria, CORPOICA., Research Centre Tibaitata, Bogota, Colombia, [2]Bayer CropScience, Bogota, Colombia

The tobacco is one of the main labour-intensive crops in Colombia, which promotes more than 50,000 direct employments and near to 70,000 indirect employments during the production season, in the optimal producing zones of Huila and Santander departments. The whitefly *Trialeurodes vaporariorum,* definitely is the most limiting pest of tobacco in several producing zones of Colombia, because of its capacity to produce mechanical damage and physiological stress to the tobacco plants. But probably, the most limiting damage caused by whiteflies to the tobacco crop, is related to their capacity to transmit plant viruses, especially of the Geminiviridae familiy, which can produce losses higher than 60%, with whitefly infestations lower than 5% under field conditions. Farmer usually rely on chemical control for the management of the *T. vaporariorum* whitefly, being the pyrethroid, the chloronicotinilic and the growth regulator insecticides the main groups of chemical compounds used against this pest. Normally the control of the whitefly is satisfactory during the early phases of the season (in the seedling trays and during the first 30 days after transplanting). However, as the season progresses, the whitefly control becomes increasingly difficult and very often, growers have to perform more than eight applications until harvest, in order to achieve control and avoid losses. This situation implies an intrinsic risk of development of resistance of the whitefly, especially because there is a limited number of chemical groups with different mechanism of action, suitable for its control under commercial conditions. Regardless of this negative aspect of tobacco production, the crop is also rich in a diversity of beneficial insects (predators and parasitoids), that make a contribution to the crop protection as natural enemies of the main pests. However, the individual contribution of key natural enemies had not being determined. Among insects recognized as predators of *Bemisia* whiteflies, a small group of Hemiptera: Heteroptera belonging to the Anthocoridae, Lygaeidae and Miridae families, represent a significant functional group, suitable for the control of immature as well adult whiteflies in tobacco and other important crops in Colombia. One of the species confirmed in the present study as responsible for an outstanding control of *T. vaporariorum* in tobacco fields in Colombia, is the predatory chinch bug *Nesidiocoris tenuis* (Heteroptera: iridae). This insect represents an extremely interesting study case of applied biological control, considering that the youngest developmental stages of the insect (first and second instar nymphs or N1 and N2) are referred as a pest by some farmers (because of their phytophagous habits). Experiments performed under laboratory conditions, made possible to confirm that the Functional Response of *N. tenuis* feeding on *T. vaporariorum* reached up to 100 first-to-second instar nymphs per day, while consuming up to 60 adult whitefly in the same period of time. Usually foliar application of broad spectrum chemical insecticides, maintain the population of *N. tenuis* far below the average population of its prey, the *T. vaporariorum* whitefly, thus being the predator completely unable to control the pest under the level of the action threshold. Under commercial conditions of pest management, the population relationship between the predator and its prey is of about 2 to 10, expressed as a ratium of 0,2., which implies a high potential of population increase of the whitefly and therefore, a big chance of chemical applications by the farmer. Interestingly, within the IPM model presented here, two applications by drench of the chemical systemic insecticide imidachloprid in the seedling trays (at 1 cc/liter/m2) and to the field between 5 and 8 days after transplanting (at 600 cc/Ha), are enough for maintaining the sucking pest below the action threshold, while allowing a significant population increase of many beneficial insects, as well as the Heteropteran predator, reaching a ratium of 5.0 (a predator/prey relation of 10 to 2, around 50 days after transplanting). As a result of the combined efficacy and control achieved by the chemical systemic insecticide and the predatory Mirid chinch bug, the total number of applications was reduced from an average of 8 in the region to 3 in the experimental fields, including one general treatment of a *Bacillus thuringiensis*-based

bioinsecticide required for the control of the Lepidopteran pest *Heliothis tergemina*. Experiments performed under laboratory conditions with induced-high populations of first and second instar nymphs of *N. tenuis*, were unable to produce a significant damage to the plants exposed, thus posing a serious question to the real potential of this species as pest of tobacco crop. This study represents an important case of an insect with an ambiguous role of herbivore in its initial developmental stages and predator in its latest ones, a characteristic also observed in the case of other predatory Heteropteran chinch bugs, as for example in the family Pentatomidae. The presence of high natural populations of *N. tenuis* in the high land tropical forests surrounding the tobacco producing zones in Santander, suggests that a promising Environmental Service in terms of pest predation might be provided by these forest to the crops. These observations suggest that it may be necessary to develop a more comprehensive and integrated model of pest management, involving not only the crop, but also the periagricultural areas, so far connecting the cultivated lands with the existing natural environments in the main producer regions of Colombia. A model that once validated, could provide a more sustainable approach for IPM, by a rational utilization of natural resources, including the management of arthropod biodiversity in agricultural landscapes.

POSTER PRESENTATION

Studies on comparative feed efficacy of MR_2 variety mulberry leaves treated with vitamin B_6 on *Bombyx mori* (L.) (Lepidopetera: Bombycidae) in relation to cocoon weight and silk traits.

D. Balasundaram, . Selvisabhanayakam, V. Mathivanan

Department of Zoology, Annamalai University, Tamil-Nadu, India

Mulberry leaf (*Morus alba L*) is an exclusive food for silkworm rearing and contributes about 100% of the material for biosynthesis of protein. An experiment was conducted to find out the feed efficacy of *Bombyx mori*. (L.) on control MR_2 leaves treated with vitamin B_6 in order to know the cocoon weight, silk traits, silk quality and quantity. It has been revealed from the present study that the MR_2 varity with vitamin B_6 treated is considered as the most effective feed for silk production rather than the control MR_2 variety. The results are discussed in detail.

POSTER PRESENTATION

Forced copulation in four taxa of Alpine bushcrickets (*Anonconotus* spp).

K. Vahed[1], G. Carron[2]

[1]*Biological Sciences Research Group, University of Derby, Derby, United Kingdom,* [2]*Freshwater Ecology Laboratory (LEBA), University of Geneva, Geneva, Switzerland*

Forced or coercive copulation is known to occur in a variety of insect taxa, but until recently this behaviour had not been recorded in crickets and bushcrickets (Orthoptera: Ensifera). The aim of the present study was to compare the recently documented forced mating behaviour in the Alpine bushcricket *Anonconotus alpinus ghilianii* with that of *A. alpinus alpinus*, *A. pusillus* and *A. baracunensis occidentalis* in both lab. and semi-natural field conditions. In all four taxa, males did not sing to attract females, but instead initiated copulation by "stalking" the female before leaping onto her and using their sharply pointed cercal spurs to maintain a hold on the female's abdomen. In *A. a. ghilianii* and *A. a. alpinus*, the positioning of the male's hind legs appeared to impede the movement of the female's hind legs during copulation. In *A. baracunensis*, the duration of copulation following spermatophore transfer was considerably longer than in the other species. This longer duration of copulation is interpreted as functioning to prolong ejaculate transfer by preventing the female from eating the external portions of the spermatophore. In support of this, male *A. baracunensis* were found to produce a significantly greater ejaculate mass than males of the other *Anonconotus* taxa. Males of all four taxa appeared to be highly unselective when it came to mating and, in the lab., would readily attempt to copulate with other males and nymphs of either sex.

POSTER PRESENTATION

An adapted economic threshold level for the management of bollworm larvae on transgenic cotton in South Africa

Annette Bennett[1], Tanya Joffe[2]

[1]Inselele Training CC., Centurion, South Africa, [2]School of Agricultural Science/TIAR, University of Tasmania, Hobart, Australia

Insect-resistant transgenic cotton (Bt cotton) has been available commercially in South Africa since 1998. Cotton SA has since been continuously involved in the dissemination of information on the benefits for farmers of planting Bt cotton. Besides the environmental benefits from reduced spraying, the associated decreased cost of production, together with improved yield result in greater financial benefits for farmers. Due to a variety of reasons, such as drought and the poor price of cotton on the international market, the production of cotton in South Africa has fallen, however, for many small-scale farmers and dryland commercial farmers, cotton is a preferred choice since it can be cultivated under dryland conditions when few other crops can be planted. The major pest problem on cotton in South Africa is the bollworm complex, made up of the African bollworm *Helicoverpa armigera*, Red bollworm *Diparopsis castanea* and spiny bollworms *Earias biplaga* and *E. insulana*, but with the introduction of Bt cotton, this has been largely eliminated. However, it is vital that farmers continue to scout their cotton and take note of the adapted threshold value for the number of bollworms present on Bt cotton, which is considered to be five or more plants with one or more bollworm larvae present per 24 plants scouted, as opposed to the threshold on conventional cotton of five or more bollworm larvae present per 24 plants scouted. This threshold has been introduced since stress conditions, such as drought, flooding or excessive weeds, can cause some Bt plants to exhibit a lower expression of the Bt gene, resulting in the survival of some larger bollworm larvae on those plants, or larvae may originate from neighbouring weeds or other host plants. Scouting techniques therefore remain essential in both commercial and small-scale farmer setups, with the use of the pegboard system encouraged for illiterate scouts.

POSTER PRESENTATION

Evaluation of the novel insecticide, chlorantraniliprole, applied to the soil for systemic control of lepidopteran pests of vegetables

Thomas P. Kuhar, Helene Doughty

Dept. of Entomology, Virginia Tech Eastern Shore Agricultural Research and Extension Center, Painter, Virginia, United States

Introduction: Application of systemic insecticides through trickle irrigation systems offers several potential advantages over foliar applications, including reduced worker exposure to pesticides, reduced risk to beneficial arthropods, and longer residual control. Chlorantraniliprole (= Rynaxypyr™, Dupont) is a novel systemic insecticide from a new class, the anthranilic diamides. This new class of insecticides activates the insect ryanodine receptors that play a critical role in muscle function. The insecticide has extremely low mammalian toxicity and is a promising new tool for use in food crops such as vegetables.

Methods: Field efficacy experiments and bioassays were conducted in Virginia (USA) on tomatoes, cabbage, and peppers for control of a variety of lepidopteran pests.

Results: Soil-applied chlorantraniliprole provided excellent control of tomato fruitworm (*Helicoverpa zea*) on tomato, European corn borer (Ostrinia nubilalis) on pepper, and a variety of lepidopteran pests on cabbage.

Conclusion: Chlorantraniliprole offers a novel and versatile new insecticide tool for control of lepidopteran pests on vegetable crops.

POSTER PRESENTATION

Reducing food miles: an investigation of gardening by a sedentary caddisfly.

N.L Ings, A.G Hildrew, J. Grey

School of Biological and Chemical Sciences, Queen Mary, University of London, London, United Kingdom

Sedentary macroinvertebrates face a trade-off between the benefits gained from defending food close to their homes and the costs of defence. Therefore, sedentary organisms are likely to be most successful at sites with intermediate food levels and replenishment rates. However, it has been suggested that sedentary grazers such as the caseless caddis larva *Tinodes waeneri* (Trichoptera), which can form a dominant component of the stony littoral community of lakes, may overcome this restriction through manipulating food resources within its feeding territory, *i.e.* gardening.

T. waeneri build galleries of silk bound sediment which were assumed simply to provide protection for the larva. However, it has been postulated that nutrients secreted by larvae might fertilize algae growing on gallery walls providing the larvae with a better quality or quantity of food. We tested this hypothesis by analysing the carbon and nitrogen stable isotope ratios of larvae, their galleries and the biofilm on rocks collected from six lakes spread across a natural nutrient gradient.

We found evidence of nutrient recycling within the *Tinodes* gallery community. Galleries were ^{15}N-depleted compared to the rock biofilm, suggesting that algae on the gallery walls preferentially assimilated ^{14}N from larval excretions that would themselves have been ^{15}N-depleted relative to the larval food source. In addition, mixing models suggest that galleries formed an important carbon and nitrogen source for the larvae. These results provide evidence that *T. waeneri* galleries can act as a garden. This has important implications for community structure and ecosystem function within the littoral of lakes.

POSTER PRESENTATION

Butterflies as environmental indicators for Argentinean Semiarid Chaco

Liliana Didato[1], José Martín-Cano[2] & Andrea Fuster[1]

[1]Facultad de Ciencias Forestales, Univ. Nacional de Santiago del Estero. Sgo. del Estero. Argentina, [2]Departamento de Biología, Universidad Autónoma de Madrid, Spain

Introduction. Semiarid Chaco is a vast region from North Argentina that enlarges until bordering zones. This region is undergoing important transformations during the last years. Forests are being overexploited and great part of these forests is being deforested and replaced by intensive crops. In order to find a balance and a sustainable exploitation it's imperative to have knowledge of the biodiversity and so be able to measure the loss caused by these changes.

Butterflies, due to their colourful look and their well known taxonomy, are one of the easiest animals to watch. On the other hand, butterflies have a high number of species and their high ability to move and ecological requirements get them to be excellent indicators of ecosystem conservation und habitat destruction. This is why they have been chosen as indicators of Chaco Semiarid's modifications.

Material and Methods. Sampling took place during the summertime in the location of Santos Lugares in Alberdi's Department. The method used has been a periodic cover across transects with entomological net and Malaise traps.

Results. Between the most important observed species we emphasize *Ascia manuste* (Pieridae), *Junonia varete hilaris* and *Anartia jatrophae jatrophae* (Nymphalidae), *Libytheana carinenta, Strimon argona* (Lycaenidae) and *Pyrgus alleus* (Hesperiidae).

POSTER PRESENTATION

Cape Ground Squirrel (*Xerus inauris*) influence on invertebrate biodiversity

Corris M. Kaapehi[1], Tharina L. Bird[2], Jim Roth[3] And Jane M Waterman[3]

[1]Department of Agriculture and Nature Conservation, Faculty of Natural Resource Management, Polytechnic of Namibia, Namibia, [2]National Museum of Namibia, Department of Arachnida and Myriapoda, Namibia, [3]Department of Biology, University of Central Florida, Florida, USA

Introduction: The two concepts 'keystone species' and 'ecosystem engineers' are interrelated in that they both refer to the concept of a single or multiple species, having disproportionately large affects on the organization and functioning of ecosystems. Keystone species include species whose effects are direct for example through predator/prey relationships, or indirect through ecosystem engineering by altering succession and composition of ecosystems. Squirrels dig extensive burrow systems that persist year-round. Grass is also removed in the immediate burrow area. We wanted to determine whether Cape ground squirrels (*X. inauris*) are keystone species in terms of their burrowing modifying the habitat to shelter provision and habitat improvement for invertebrates.

Methods: The abundance (how many individuals were trapped) and diversity (number of species) of four invertebrate groups (spiders, beetles, Orthoptera and ants) were compared inside and outside (control) areas occupied by squirrel colonies. Data was collected over two seasons, winter 2007 and summer 2008 in the pro-Namib region of Namibia. Here the winter data is presented.

Results: The four invertebrate groups sampled showed no significant differences in terms of abundance between the colony and control areas. Beetles showed a significantly lower number of species and Orthoptera a significantly higher number of species in the colony areas.

Conclusions: Cape ground squirrels appear to influence the biodiversity of invertebrates at their colonies, but more data is required to make firm conclusions, specifically with regards to seasonal variations.

POSTER PRESENTATION

Cape Ground Squirrel (*Xerus inauris*) influence on invertebrate biodiversity

Corris M. Kaapehi[1], Tharina L. Bird[2], Jim Roth[3] And Jane M Waterman[3]

[1]*Department of Agriculture and Nature Conservation, Faculty of Natural Resource Management, Polytechnic of Namibia, Namibia.*
[2]*National Museum of Namibia, Department of Arachnida and Myriapoda, Namibia.*
[3]*Department of Biology, University of Central Florida, Florida, USA.*

Introduction: The two concepts 'keystone species' and 'ecosystem engineers' are interrelated in that they both refer to the concept of a single or multiple species, having disproportionately large affects on the organization and functioning of ecosystems. Keystone species include species whose effects are direct for example through predator/prey relationships, or indirect through ecosystem engineering by altering succession and composition of ecosystems. Squirrels dig extensive burrow systems that persist year-round. Grass is also removed in the immediate burrow area. We wanted to determine whether Cape ground squirrels (*X. inauris*) are keystone species in terms of their burrowing modifying the habitat to shelter provision and habitat improvement for invertebrates.

Methods: The abundance (how many individuals were trapped) and diversity (number of species) of four invertebrate groups (spiders, beetles, Orthoptera and ants) were compared inside and outside (control) areas occupied by squirrel colonies. Data was collected over two seasons, winter 2007 and summer 2008 in the pro-Namib region of Namibia. Here the winter data is presented.

Results: The four invertebrate groups sampled showed no significant differences in terms of abundance between the colony and control areas. Beetles showed a significantly lower number of species and Orthoptera a significantly higher number of species in the colony areas.

Conclusions: Cape ground squirrels appear to influence the biodiversity of invertebrates at their colonies, but more data is required to make firm conclusions, specifically with regards to seasonal variations.

Morphological dimorphism in carabid beetles living on land snails

Junji Konuma[1], Satoshi Chiba[2]

[1]Department of Zoology, Graduate School of Science, Kyoto University, Sakyo, Kyoto, Japan, [2]Department of Ecology and Evolutionary Biology, Graduate School of Life Sciences, University of Tohoku, Aobayama, Sendai, Japan

Introduction: Morphological dimorphism, known as macrocephalism and stenocephalism, is observed in carabid beetles living on land snails. Macrocephalic type is the beetles whose head is wide enlarged, while stenocephalic type is the beetles whose head is slender elongated. Such dimorphism is not found in the carabid beetles living on insect larvae and earth worms. Why did this dimorphism evolve in the carabid beetles living on land snails?

Methods: We examined the feeding behavior of representative malacophagous carabid beetles, *Damaster blaptoides*. This species is composed of large-headed subspecies and small-headed subspecies, and no intermediate beetle exists in the wild. We developed hybrids between large-headed and small-headed beetles, and intermediate lines in the laboratory. The feeding performance of these beetles was examined experimentally.

Results: Large-headed beetles could readily crush snail shells with their powerful biting, but could not insert their oversized heads into the shells. In contrast, small-headed beetles could insert their heads into the shells for direct predation on snail bodies, but poorly crushed the shells because of their frugal biting. Intermediate beetles had lower performance than large-headed beetles in crushing snail shells, and had lower performance than small-headed beetles in inserting their head into snail shells.

Conclusions: Intermediate beetles had lower performance than large-headed and small-headed beetles in each feeding behavior. This result implies that disruptive selection could occur in the beetle head size. The functional trade-off in feeding behavior would result in morphological dimorphism in carabid beetles living on land snails.

Effects of Break-thru® and an oil emulsion on the efficacy of *Beauveria bassiana* for the control of red spider mite, *Tetranychus urticae* Koch

Celestin M. Gatarayiha, Mark D. Laing, Brendon Neumann, Mike Morris, Ray Miller

[1]University of KwaZulu Natal, School of Biochemistry, Genetics, Microbilogy and Plant Pathology, Pietermaritburg, South Africa, [2]Plant Healty Products (Pty) Ltd., Pietermaritzburg, South Africa, [3]University of KwaZulu Natal, School of Biological and Conservation Sciences, Pietermaritzburg, South Africa

Introduction: The fungus *Beauveria bassiana* has potential use in controlling red spider mite, *Tetranychus urticae*. In this study, Isolate R444 of *B. bassiana* was used to control the pest on cucumbers. Effects of two carriers (Break-thru® and oil emulsion) on the efficacy of the isolate were compared.

Methods: Pure conidia at different concentrations ($5x10^8$; $5x10^7$; $5x10^6$ and $5x10^5$ conidia ml^{-1}) were suspended either in Break-thru® (0.01%) or an oil-based emulsion and sprayed on leaves 2wk after pest inoculation. Two sprays were performed at the interval of 1wk and counts of dead individuals (both motile and egg stages) were made 7d after every spray.

Results: High rate ($5x10^8$ spores ml^{-1}) resulted in the best control where, in average, 85.7 and 59.7 % of adult population were killed in Break-thru® and oil emulsion respectively; similarly 39.8 and 35% of juveniles were killed. In general, there was less mortality of juveniles compared to adults; and no mortality was observed on egg stage for the tested treatments. Break-thru® and oil applied alone did not significantly differ from the untreated control. And when *B. bassiana* was applied in water only the mortality of adult mites was <40%, suggesting that the two surfactants increased the efficacy of the fungus. However, *Beauveria* conidia applied in Break-thru® solution were more efficacious than the mineral oil as measured by greater mortality of mites observed.

Conclusion: Use of Break-thru® as a carrier can be one of the strategies for the efficiency of *B. bassiana* in the management of *T. urticae*.