

Insect Art: Celebrating 50 years of Australian Entomological Research



The WABA Committee and President of the Australian Entomological Society Dr David Yeates (Director, Australian National Insect Collection – ANIC) are proud to present a unique art exhibition featuring important Australian insects to honour significant contributors to Australian entomology including:

- Ian Mackerras (1898–1980) Diptera: Spotted Swamp Fly *Pelecorhynchus nigripennis*
- Ian Common (1917 – 2006) Lepidoptera: undescribed primitive moth from Kangaroo Island, South Australia
- John Lawrence (1934 –) Coleoptera: Rainbow Stag Beetle *Phalacrognathus muelleri*
- Ebbe Nielsen (1950 – 2001) Lepidoptera: Bentwing Swift Moth *Zelotypia stacyi*
- David Rentz (1942 –) Orthoptera: Cooloola Monster *Cooloola ziljan*
- Doug Waterhouse (1916 – 2000) Odonata: Rockmaster damselfly *Dipblebia* sp.

Many of the exhibited artworks are the result of collaboration with ANIC staff over the last six months. Together they form a beautiful collection of original artworks inspired by the dramatic characteristics and colours of Australia's spectacular insects. WABA artists present watercolour, pencil and acrylic paintings as well as ceramic and mixed medium sculpture. All works will be for sale. The exhibition will also offer prints and cards based on the original artworks.

Wildlife and Botanical Artists (WABA)

Established over 14 years ago, WABA is a friendly network of professional and emerging wildlife and botanical artists, based in Canberra, Australia. As a group, WABA has a shared interest in flora and fauna as an important source of inspiration for art and seeks to build bridges between art and science, recognizing that properly valuing our natural environment is key to the growth and sustainability of society. Both art and science must play a part in engaging the broader community.

The WABA website includes an artist gallery displaying works by members. For anyone interested in sponsoring WABA or commissioning works please contact:

Julia Landford, Founding President - 0414 342 839; Glenda Shelley, Vice-President – 0422 405 658; or visit WABA's website at: www.waba.net.au



Stacey Thalden (USA) *Momentary Rest*: Spotted Swamp Fly (*Pelecorhynchus nigripennis*). Acrylic paint and Prismacolor pencil. Photo by Brian McIernon Photography. ©S.THALDEN2014

Welcome

On behalf of the Organising Committee I would like to welcome you to the 2014 Australian Entomological Society Conference. This Conference celebrates the 50th anniversary of the Society, and the Organising Committee has developed a number of special events and presentations to celebrate this important milestone. In particular, the Organising Committee has worked closely with the Wildlife and Botanical Artists Inc. to launch a special exhibition of insect inspired art at the conference. We have chosen to hold the conference in the iconic crucible of Australian science, the Shine Dome, a heritage listed Canberra landmark that is about the same vintage as our Society. With recent civic redevelopment, the Shine Dome now sits adjacent to a vibrant hotel and retail district in New Acton, and is within walking distance of the Australian National University, the National Film and Sound Archive and the National Museum. We hope you will enjoy this celebration of the achievements of Australian entomology over the past half century in our national capital.

David Yeates

President of the Society and Chair of the Organising Committee

Organising Committee

David Yeates (CSIRO National Research Collections Australia) (Chair)

David Rowell (Research School of Biology, ANU)

Ian Naumann (Department of Agriculture, Fisheries and Forestry)

Saul Cunningham (CSIRO Land and Water Flagship)

Alice Wells (Australian Biological Resources Study)

Symposium Conveners

Phylogenomics – a peek over the horizon at big data & emerging methods

Karen Meusemann and David Yeates:
CSIRO National Research Collections
Australia, Canberra, ACT

Information processing in insects

Jocken Zeil: The Australian National
University, Canberra, ACT

How have molecular data supported, enhanced or overturned existing ideas in insect systematics and biogeography

Matt Krosch and Peter Cranston: Centre for
Water in the Minerals Industry (UQ), Brisbane,
QLD; Evolution, Ecology and Genetics,
Research School of Biology, Australian
National University, Canberra, ACT

Australian beetle systematics: a symposium honouring the contributions of John F. Lawrence on his 80th birthday

Adam Slipinski and Rolf Oberprieler: CSIRO
National Research Collections Australia, ACT

Chemical ecology: explaining Australian insect-plant and insect-insect interactions

Martin Steinbauer: La Trobe University,
Melbourne, VIC

Ecosystem services delivered by insects and other invertebrates

Saul Cunningham: CSIRO Land and Water
Flagship, Canberra, ACT

Biological control in the Asia-Pacific Region: highlights from the last 50 years and emerging issues for the future

Bill Palmer and Andy Sheppard: Biosecurity
Queensland, Brisbane, QLD; CSIRO
Biosecurity Flagship, Canberra, ACT

Insects as tools in forensic investigations

James Wallman: University of Wollongong,
NSW

Sally Brown Conference Connections - PO Box 108 Kenmore QLD 4069 Australia
Telephone +61 7 3201 2808 Fax +61 7 3201 2809 - Mobile 0407 178 200

GENERAL INFORMATION

SOCIAL FUNCTIONS

Sunday 28 September:

Welcome Reception 17:00 – 19:00 - Shine Dome, with wines supplied by Lerida Estate
Including the opening of The Wildlife and Botanical Artists Inc. Insect Art exhibition

Monday 29 September

Poster session in the Shine Dome. Drinks and 'nibbles' will be served

Tuesday 30 September:

Conference Dinner at Old Parliament House 18:30 - 22:30. Coaches depart from the Shine Dome and return to University House, QT Canberra and Peppers Gallery Hotel.

The **REGISTRATION DESK** in the Shine Dome will be staffed as follows:

Sunday 28 September from 15:00

Monday – Wednesday from 08:00

INTERNET: Internet access will be available at the Shine Dome Sunday - Wednesday.

SPEAKERS ASSISTANCE: Speakers, please ensure that you take your USB to the Speakers Assistance Desk (beside the registration desk) well before your session so that your presentation can be loaded and checked during morning tea or lunchtime prior to your presentation. Please do not leave this until the last moment.

NAME BADGES: Delegates are requested to wear their name badges at all times during the conference. The committee can be identified by their yellow name badges. The Board of Directors members will have green name badges.

MESSAGES: During conference hours: **Secretariat** Telephone: 0419 025 256 (Jenny Marsden) *Please check the notice board by the Registration Desk regularly for messages.*

TAXI SERVICE: 13 22 27

Things to do in Canberra:

Floriade 13 Sept - 12 October <http://www.floriadeaustralia.com>

National Film and Sound Archive <http://www.nfsa.gov.au>

National Museum of Australia <http://www.nma.gov.au>

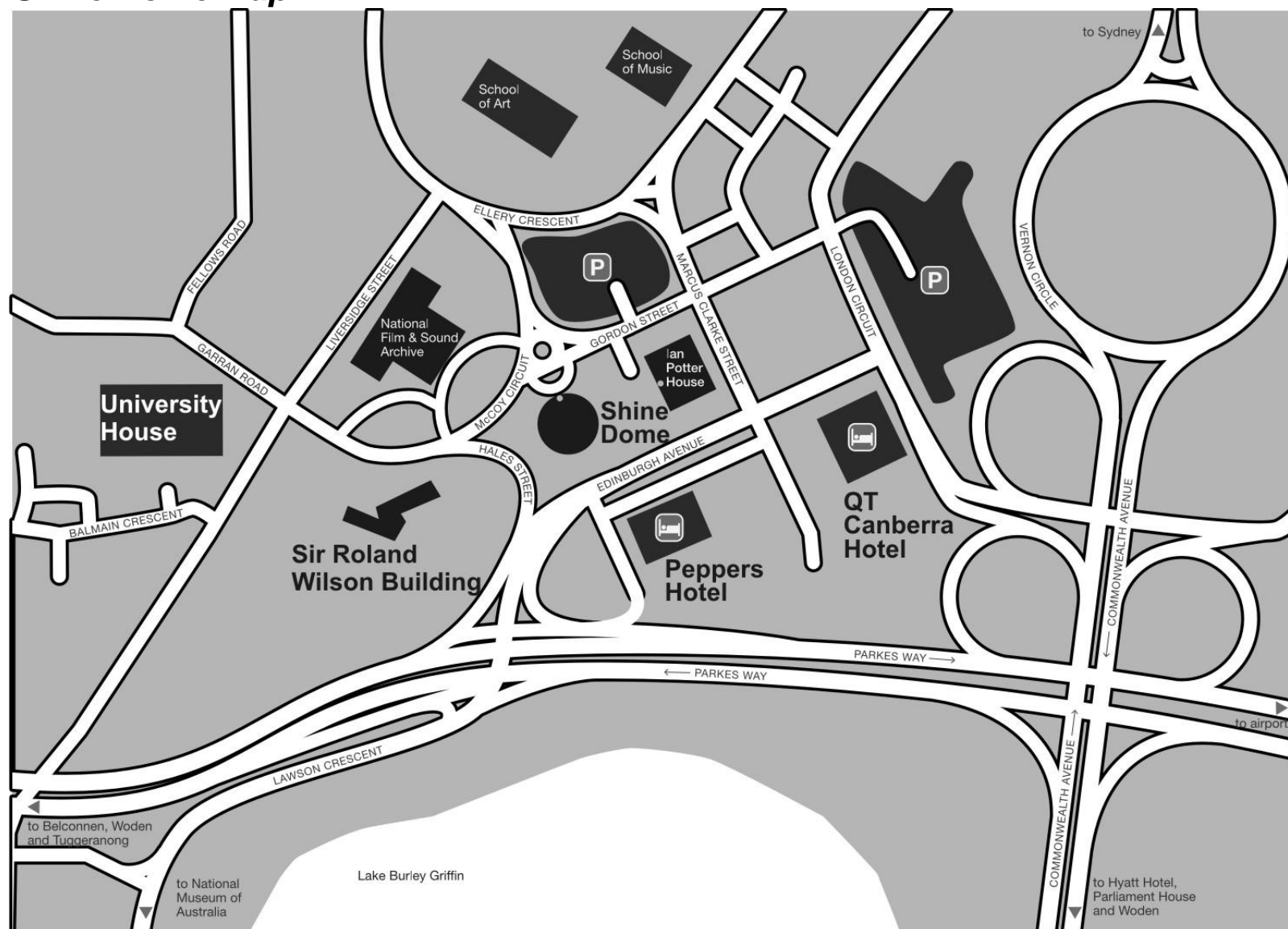
Australian National University <http://www.anu.edu.au>

Dining in Canberra <http://www.outincanberra.com.au/section/dining>

Local restaurants, dining options and other attractions of new the Acton Precinct can be found here <http://www.newacton.com.au/eat/drink>

INSURANCE: the Australian Entomological Society does not accept responsibility for personal accidents, theft and/or damage to the property of conference delegates or accompanying persons.

Shine Dome Map



Biographies – Plenary Speakers



Professor May Berenbaum

Dr. May Berenbaum has had an unparalleled impact on the environmental sciences through a rare combination of path-breaking scientific discovery and influential public engagement. Berenbaum's research transformed the field of chemical ecology with discoveries that provided a genetic basis for the theory of coevolution. Her investigations have encompassed elegant ecological experiments, elucidated proximate physiological mechanisms, included chemical and genetic analyses, and clearly showed the evolutionary consequences of an "arms war" that exists between plants and insect herbivores. Her research has also provided a clear paradigm for understanding the evolution of insect resistance to insecticides. Her work gives a vivid example of how studies in the basic realm of chemical ecology can inform agricultural practices.

Berenbaum has also had a major impact on the environmental sciences through her public engagement work. She is the leading public intellectual for information on insects in the country. She has taken leadership roles in dealing with major insect-related problems that confront us: insects and GM crops, pollinator declines, invasive species, pesticides and resistance, and insect conservation. Her preeminent status in this realm derives in part from her extensive service to the National Research Council of the National Academy of Sciences.

Berenbaum's writing for the public is prolific and highly acclaimed. Berenbaum has written a torrent of lively magazine articles, columns, and three books about insects. Berenbaum is also a very popular and innovative teacher, for which she was recognized by ESA. Berenbaum is a person of remarkable scientific accomplishment, boundless energy, brilliant creativity, and passionate dedication to public understanding of science. She is also inspirational up close as a charismatic, warm, and accessible public figure.



Professor Ryszard Maleszka

Ryszard Maleszka received his MSc and a PhD from the Department of Genetics, University of Warsaw and has done postdoctoral work at the National Research Council of Canada before moving to Australia in 1987. Since 1998 he has been spearheading a research theme called 'From Molecules to Memory' that uses invertebrate model systems to study the genotype to phenotype link, and to understand how epigenetic modifications contribute to environmentally-driven phenotypic plasticity and the maintenance of memory. He is a member of several genomic consortia and advisor to genomic databases. He has published over 100 papers including research and popular articles, reviews and book chapters.



Dr Oliver Niehuis

Dr. Oliver Niehuis is head of the section Biodiversity Genomics and of the Molecular Laboratory at the Center for Molecular Biodiversity Research (zmb) of the Zoological Research Museum Alexander Koenig in Bonn (ZFMK), Germany.

Dr. Niehuis' research interests are focused on insects and in particular on parasitoid and cleptoparasitic Hymenoptera. He is interested in the evolutionary history of insects, in characters that are related to mate or host finding and recognition (e.g., cuticular hydrocarbons, sexual pheromones), and in the evolution of reproductive isolation (e.g., evolution of genic incompatibilities). Oliver's research has a strong molecular component, and he has used genome, transcriptome and exome sequencing as well as QTL mapping to sample suitable markers for phylogenetic inference or to identify genes of traits of major interest.

Dr Niehuis earned his PhD in 2005 at the University of Bonn for his research on the evolutionary history and biogeography of burnet moths (Lepidoptera: Zygaenidae). As a Feodor Lynen research fellow of the Alexander von Humboldt Foundation, he worked for almost four years at the School of Life Sciences at Arizona State University (USA) on the genetics of reproductive isolation in *Nasonia* parasitoid wasps. During a second postdoc at the University of Osnabrück, he gained expertise in target DNA enrichment techniques. Since 2010, Dr Niehuis is head of the Molecular Laboratory at the ZFMK and of the section Biodiversity Genomics. He was major contributor in the *Nasonia* parasitoid wasp genome sequencing project and coordinated the twisted-wing parasite (Strepsiptera) genome sequencing project that set a new standard in the field of phylogenomics. Oliver is a member of the i5K coordinating group, an assemblage of scientists who are united by their aim in fostering the sequencing of non-model arthropod genomes. He also is coordinator of orthology prediction and of the subproject Hymenoptera in the international 1KITE project that seeks to infer reliable insect backbone tree of life.

**AES 2014 Conference - 50th anniversary "Celebrating the next 50 years of Australian Entomology"
Sunday 28 September – Wednesday 1 October 2014 PROGRAM**

Disclaimer: The speakers, topics and times are correct at the time of publishing. In the event of unforeseen circumstances, the organisers reserve the right to alter or delete items from the Conference Program
Key to symbols * (student prize entry) and \$ (CHAEC prize entry)

Time	<i>Sunday 28 September</i>
From 16:00	Registration - posters put up
14:00	CHAEC Meeting
17:00-19:00	Welcome reception including the opening of The Wildlife and Botanical Artists Inc. Insect Art exhibition. Wines supplied by Lerida Estate

MONDAY 29 September

Time	<i>Monday 29 September</i> Ian Wark Theatre Shine Dome	<i>Monday 29 September</i> Sir Roland Wilson Building Room 1.02	<i>Monday 29 September</i> Sir Roland Wilson Building Room 2.02
from 08:00	Registration		
08:30	Opening Ceremony including a presentation from Catriona Jackson - CEO of Science and Technology Australia Chair: David Yeates		
08:40	Housekeeping		
08:45 – 09:30	PLENARY: May Berenbaum - Predicting the future challenges of entomology - lessons from the past		
09:30 - 09:45	<u>Symposium: Chemical Ecology</u> Chair: Martin Steinbauer Paul Cunningham: Using plant odours to control polyphagous pests – could we benefit from a different perspective?	<u>Symposium: Australian beetle systematics - honouring John F Lawrence</u> Chair: Rolf Oberprieler Rich Leschen Advancing Coleoptera Systematics	
09:45 - 10:00		Rolf Oberprieler: The beetle fauna of the Talbragar Fish Bed	
10:00 - 10:30	Morning Tea - Shine Dome	Morning Tea - Shine Dome	Morning Tea - Shine Dome

10:30 - 12:15	Symposium: Chemical Ecology Chair: Martin Steinbauer	Symposium: Australian beetle systematics - honouring John F Lawrence (contd)	Symposium: Information Processing in Insects Chair: Jochen Zeil
10:30 - 10:45	Kevin Farnier*: Host-finding in psyllids: Are <i>Eucalyptus</i> -feeding psyllids anosmic?	Stephen Cameron: Phylogeny of Scarab beetles: A molecular dating analysis reveals diversification trends	Barbara Webb: A computational model of the insect mushroom body can account for ant route memory in complex environments
10:45 - 11:00	Andrew Hayes: Host tree influences on longicorn beetle attack in subtropical <i>Corymbia</i>	Adam Slipinski: Phylogeny and classification of the beetle families classified in the Cerylonid Series (Coleoptera: Polyphaga: Cucujoidea)	
11:00 - 11:15	Rebecca Miller: Hot and Smelly: Thermogenesis and the chemical ecology of pollination in endemic Australian Araceae	Hermes Escalona: Phylogeny and biogeography of Boganiidae (Coleoptera, Cucujoidea)	Jochen Zeil: Visual Homing
11:15 - 11:30	Renae Forbes*: Plant traits influence the functional role of two understory shrubs for native insects	Rich Leschen: Gondwanan Brown Beetles (Coleoptera: Cryptophagidae: Cryptophaginae): We like them	Ken Cheng: Combining sky and Earth: three ant species integrate celestial and terrestrial sources of directional information
11:30 - 11:45	Owen Webb*: Exploiting behaviour to create novel deterrents for the Queensland Fruit Fly (<i>Bactrocera tryoni</i>)	John Marris\$: Flat beetles in a flat land: A review of the Australian Cucujidae (Coleoptera)	Patrick Schultheiss: Searching behaviour in insects
11:45 - 12:00	Martin Steinbauer: Settling down to dine on a dioecious Gondwanan relict: why are psyllid nymphs more abundant at the base of branchlets?	Eric Matthews: A newly constituted Notogean tribe of Tenebrionidae (Coleoptera)	Chloe Raderschall*: Head roll stabilisation in bull ants <i>Myrmecia pyriformis</i> during twilight
12:00 - 12:15	Umar Lubanga*: Chemical Cues, Mate Attraction and Assessment in a Psyllid	Kimberli Pullen / Rolf Oberprieler: Discovering the Australian weevil fauna	
12:15 - 12:30	Simon Lawson: Sex pheromones of cossid moths: emerging pests of Australian and overseas <i>Eucalyptus</i> plantations.	Samuel Brown*\$: Evolution of female secondary sexual structures of New Zealand broad-nosed weevils (Coleoptera: Curculionidae)	
12:30 - 13:30	Lunch - Shine Dome	Lunch - Shine Dome	Lunch - Shine Dome
	<u>Symposium: Chemical Ecology (contd)</u> Chair: Martin Steinbauer	<u>Symposium: Australian beetle systematics - honouring John F Lawrence (contd)</u> Chair: Adam Slipinski	<u>Symposium: Information Processing in Insects (Contd)</u> Chair: Jochen Zeil
13:30 - 13:45	Syed Rizvi*: Effect of <i>Botrytis cinerea</i> -infected leaves and berries of <i>Vitis vinifera</i> on the ovipositional preference and larval performance of <i>Epiphyas postvittana</i>	Sara Pinzon-Navarro: Comparing herbivore guilds: seed-feeding weevils from different continents	Heiner Römer: Auditory information processing in insects under real world conditions
13:45 - 14:00	Alice Del Soccoro: Attract-and-kill for the diamondback moth, <i>Plutella xylostella</i> in canola	Remarks on the symposium by John Lawrence	

14:00 - 14:15	Alex Il'ichev: Survival of oriental fruit moth females under 30-years long mating disruption	Symposium: How have molecular data supported, enhanced or overturned existing ideas in insect systematics and biogeography Chair: Matthew Krosch Matthew Krosch: Symposium overview: the rise and rise of molecular data in insect science	Matthew Symonds: The costs of pheromone signalling in female moths
14:15 - 14:30	Chair: Martin Steinbauer	Andy Austin: Evolution of the Australian parasitoid hymenopteran fauna – a window into the Southern Hemisphere insect biota	Stephen Trowell: Olfactory detection and discrimination: Engineering lessons from an insect
14:30 - 14:45	KEYNOTE Myron Zalucki: From natural history to continental scale perspectives: Contributions of Australian Entomologists to Ecology - a play in three acts	Matthew Krosch: Welcome to the jungle: a Review of (insect) evidence for eastern Australia's major biogeographical barriers to Mesic forest restricted taxa	Rod Peakall: The sexual exploitation of thynnine wasps by deceptive signals emitted from Australian orchids
14:45 – 15:00			Fiorella Ramirez Esquivel*: Miniaturisation in ants: size, number and distribution of antennal sensilla
15:00 - 15:30	Afternoon Tea - Shine Dome	Afternoon Tea - Shine Dome	Afternoon Tea - Shine Dome
	General Contributed Papers Chair: John La Salle	Symposium: How have molecular data supported, enhanced or overturned existing ideas in insect systematics and biogeography (contd) Chair: Matthew Krosch	Symposium: Information Processing in Insects (Contd) Chair: Jochen Zeil
15:30 - 15:45	Guiron Ang*: <i>Ménage à trois</i> : complicated three-way interactions between plant, pest and parasitoid	Michael Shackleton: DNA barcoding reveals hidden diversity among Australia's Trichoptera (Caddisflies)	Misha Vorobyev: Bee colour vision in relation to flowers colours
15:45 - 16:00	Michaela Purcell: A hidden world revealed: using MicroCT scanning to see inside a gall	Mark Blacket: DNA-based identifications reveal multiple introductions of the vegetable leafminer <i>Liriomyza sativae</i> (Diptera: Agromyzidae) into the Torres Strait Islands and Papua New Guinea	
16:00 - 16:15	John La Salle: Advances in managing images of insect specimens in biological collections	Penelope Mills*: Evolution of cryptic species within the Australian gall-inducing scale insect genus <i>Apiomorpha</i> (Sternorhyncha: Coccoidea: Eriococcidae)	Yuri Ogawa: Trichromatic vision in the Australian bull ant

16:15 - 16:30	KEYNOTE Murray Fletcher: The History of the Australian Entomological Society	LI-Xin Eow*: The Molecular Phylogeny of the Fungal Spore-feeding Thrips Subfamily Idolothripinae (Thysanoptera; Phlaeothripidae)	Darrell Kemp: A conceptual framework for the study of coloration in nature
16:30 - 16:45		Yuvarin Boontop*: Signatures of invasion: an integrated approach to revealing the spread of Melon Fly, <i>Bactrocera cucurbitae</i> , (Diptera: Tephritidae) across SE Asia and the West Pacific	Marie Herberstein: Sexual signals for the colour-blind: cryptic female mantids signal quality through brightness
16:45- 17:00		Peter Cranston: Australians in the Andes	Paul Cooper: Can an extra lobe of the cricket salivary gland act as an alternative endocrine transport system?
17:00 – 18:00	Poster Presentations - Shine Dome		
	<i>Free evening – own arrangements</i>		

Tuesday 30 September

Time	<i>Tuesday 30 September</i> Ian Wark Theatre Shine Dome	<i>Tuesday 30 September</i> Sir Roland Wilson Building Room 1.02	<i>Tuesday 30 September</i> Sir Roland Wilson Building Room 2.02
from 08:00	Registration		
08:30	Shine Dome - A history Prof Sue Meek		
08:40	Chair: David Yeates <i>Housekeeping</i>		
08:45 – 09:30	PLENARY: Oliver Niehuis - Inferring deep insect phylogenetic relationships using data from genomes and transcriptomes: research initiatives, methods, results, and prospects		
09:30 - 9:45	<u>Symposium: Biological Control in the Asia-Pacific Region</u> Chair: Bill Palmer KEYNOTE: Andy Sheppard: 100 years of continually successful weed biological control in Australia	<u>Symposium: Phylogenomics - a peek over the horizon at big data</u> Chair: David Yeates David Kainer: The effects of partitioning on phylogenetic inference	
09:45 – 10:00		Karen Meusemann: Four-cluster likelihood mapping - testing for incongruent signal in large phylogenomic datasets	
10:00 - 10:30	Morning Tea - Shine Dome	Morning Tea - Shine Dome	Morning Tea - Shine Dome

10:30 - 12:15	Symposium: Biological Control in the Asia-Pacific Region (contd)	Symposium: Phylogenomics - a peek over the horizon at big data (contd)	Symposium: Information Processing in Insects (Contd)
10:30 - 10:45	Bill Palmer/ Barbara Barratt: IOBC Global and the Asia and Pacific Regional Section (APRS)	Lars Jermiin: <i>AliStat</i> and <i>SymTest</i> : Two Methods for Surveying Phylogenomic Data	Michael Dickinson: Sensory-motor integration in the flight behavior of <i>Drosophila</i>
10:45 - 11:00	Mark McNeill: Biological control of exotic pasture weevil pests in New Zealand agriculture: learning from experience to inform the future.	Michael Woodhams: Mathematically consistent DNA models for time-inhomogeneous mutation	Bruno van Swinderen: Insect attention
11:00 - 11:15		David Yeates: Inferring the relationships of early Dipteran lineages using transcriptomic data	
11:15 - 11:30	Stephen Goldson: Exotic pests and biological control in New Zealand broadacre pasture; success hoisted by its own petard?	Stephen Cameron: Integrating mitogenomic and transcriptomic phylogenetics in insects	Madeleine Beekman: Different bees, different needs – how nest site requirements have shaped the decision-making processes in homeless bees (<i>Apis</i> spp)
11:30 - 11:45	Leigh Pilkington: Biological control past, present and future in the greenhouse industry?	Andreas Zwick: In search of hexapod origins: Capturing phylogenetic signal from serine with 21-amino-acid models	Andy Barron: Choice, decision and uncertainty in honey bees (<i>Apis mellifera</i>)
11:45 - 12:00	Barbara Barratt: The Convention on Biological Diversity 'Access and Benefit-Sharing' protocol: Will it obstruct biological control?	Meng Mao*: Higher level phylogeny of the Hymenoptera inferred from mitochondrial genomes	Yorianta Sasaerila: Effect of shade on the susceptibility of two varieties of <i>Canna edulis</i> Kerr to defoliators
12:00 - 12:15	Mark Hoddle: Biocontrol of Glassy-Winged Sharpshooter in French Polynesia: A Major Success in the South Pacific	Nathan Lo: <i>Blattabacterium</i> function, genome degradation and loss in primitive termites	
12:15 - 12:30		Seraina Klopstein: Directional evolution in hymenopteran morphology	
12:30 - 13:30	Lunch - Shine Dome	Lunch - Shine Dome	Lunch - Shine Dome
	Symposium: Biological Control in the Asia-Pacific Region (Contd) Chair: Leigh Pilkington	Symposium: Phylogenomics - a peek over the horizon at big data (contd) Chair:	
13:30 - 13:45	Matthew Purcell: The role of gall formers as biological control agents of the broad-leaved paperbark tree <i>Melaleuca quinquenervia</i> in Florida USA	Thomas Buckley: Using transcriptomes to reconstruct phylogeny and molecular evolutionary processes in New Zealand insects	
13:45 - 14:00	David Hunter: The use of the fungus <i>Metarhizium acridum</i> to control locusts and grasshoppers	Contributed Papers: Systematics Chair: Andy Austin	
14:00 - 14:15	Don Sands: Rising threats from <i>Arundo donax</i> : Australian contribution to a successful US project	Robert Mesibov: 50 years of new Australian insects: publishing and authorship trends	
14:15 - 14:30	Gurion Ang*: <i>Trichogramma chilonis</i> Ishii: A potential biological control agent of <i>Crocidolomia pavonana</i> in Samoa	Cathy Car: A most ingenious paradox	

14:30 - 14:45	Jacqui Todd: Selection of non-target species for risk assessment of biological control agents: testing a decision-support system	Brian Heterick: Hot Ants – A Taxonomic revision of the genus <i>Melophorus</i> (Hymenoptera: Formicidae)	
14:45 – 15:00	Tao Wang*\$: The effects of temperature on the development and mortality of <i>Eretmocerus warrae</i> (Nauman & Schmidt)	Brad Rundle: An innovative approach promoting entomology and molecular biology to the next generation of scientists	
15:00 - 15:30	Afternoon Tea - Shine Dome	Afternoon Tea - Shine Dome	
15:30 - 15:45	Shengyong Wu: Effects evaluation of entomopathogenic fungus <i>Beauveria bassiana</i> on predatory mite and biological control of their shared pest <i>Frankliniella occidentalis</i>	Contributed Papers: Systematics Chair: David Yeates Jeffrey Skevington: Putting Australian Flower Flies (Diptera: Syrphidae) into a World Phylogenetic Context	
15:45 - 16:00	Chair: Murray Fletcher KEYNOTE Nancy Schellhorn: Arthropods in Agricultural Landscapes: Challenging and Supporting Food and Fiber Production	Andrew Young*\$: A Revision of the Australian Flower Flies (Diptera: Syrphidae)	
16:00 - 16:15		Bryan Lessard: The legacy of Ian Mackerras in Australian Diptera systematics	
16:15 - 16:30		Catherine Byrne: Why the Archiearinae (Geometridae) are no longer considered archaic and recent work on a revision of the montane Tasmanian archiearines.	
16:30 - 17:30	Australian Entomological Society AGM		
18:30 - 22:30	18:30 - 22:30 CONFERENCE DINNER Old Parliament House	18:30 - 22:30 CONFERENCE DINNER Old Parliament House	

Wednesday 1 October

Time	Wednesday 1 October <i>Ian Wark Theatre Shine Dome</i>	Wednesday 1 October Sir Roland Wilson Building Room 1.02	Wednesday 1 October Sir Roland Wilson Building Room 2.02
from 08:00	Registration		
08:40	Chair: David Rowell Housekeeping		
08:45 – 09:30	PLENARY: Ryszard Maleszka - Insect research in the postgenomic era: beyond the DNA sequence		
09:30 - 9:45	<u>Symposium: Ecosystem services delivered by insects and other invertebrates</u> Chair: Saul Cunningham Sarina MacFadyen: Optimizing for multiple benefits requires an understanding of functional connectivity of habitats for ecosystem service providers	<u>Symposium: Insects as tools in forensic investigations</u> Chair: Bryan Lessard KEYNOTE James Wallman: History, accomplishments and challenges of forensic entomology in Australia	
09:45 – 10:00	Yi Feng*: Towards biological control of a generalist insect herbivore: the activities of generalist parasitoids are segregated between crop and adjacent non-crop habitats		
10:00 - 10:30	Morning Tea - Shine Dome	Morning Tea - Shine Dome	Morning Tea - Shine Dome
10:30 - 12:15	<u>Symposium: Ecosystem services delivered by insects and other invertebrates (contd)</u> Chair: Saul Cunningham	<u>Symposium: Insects as tools in forensic investigations (contd)</u> Chair: James Wallman	Student Workshop Dr Tseen Khoo 10:30 - 11:30
10:30 - 10:45	Maarten Van Helden: Soil management and ecosystem services in grapes	Julianne Farrell*: Carrion Café –using insects to determine post mortem intervals in Queensland	
10:45 - 11:00	Philip Barton: Species traits explain contrasting diversity dynamics of beetles and ants at carrion patches	Aidan Johnson: Maggot massing: problems and solutions for the forensic entomologist	
11:00 - 11:15	Manu Saunders: Wild pollinators in almond plantations in the Victorian mallee	Bryan Lessard: Molecular methods in forensic entomology in Australia	

11:15 - 11:30	Katja Hogendoorn: Of bees and burns: the distribution of the green carpenter bee <i>Xylocopa aeratus</i> in relation to fire-history on Kangaroo Island	KEYNOTE Stephen Doggett: Medical Entomology in Australia, 1964-2014	
11:30 - 11:45	Timothy Sutton*: Vulnerability of a fig – pollinator system to climate change		
11:45 - 12:00	Saul Cunningham: Phenology of a bee community in an agricultural landscape near Canberra		
12:00 - 12:15	Phil Carne Prize Presentation Nicholas Fountain-Jones: Examining the effects of distance from mature forest and succession on beetle community recolonisation using species, functional trait and phylogenetic approaches	David Lilly*: Protecting The Future: Understanding Insecticide Resistance In Field Populations Of Bed Bugs In Order To Preserve Insecticidal Control Solutions	
12:15 - 12:30		Kai Dang*: Evolution of <i>kdr</i> -type resistance in <i>Cimex</i> . Who you will be sleeping with in the future?	
12:30 - 13:15	Lunch - Shine Dome	Lunch - Shine Dome	Lunch - Shine Dome
	Contributed Papers: Biosecurity Chair: Anthony Clarke	Contributed Papers: Systematics & ecology Chair: Sarina MacFadyen	Contributed Papers: Ecology Chair:
13:30 - 13:45	Mark Schutze: Requiem for a fruit fly: the end of the road for <i>Bactrocera papayae</i> Drew & Hancock and <i>Bactrocera invadens</i> Drew, Tsuruta, & White (Diptera: Tephritidae). But what does it mean for Australia?	Emily Johnston*: South Australia's Arboviruses: results and methods from the first large-scale FTA® card arbovirus survey	Aidan Hall*: Coevolution between bacterial endosymbionts and their psyllid hosts of the <i>Cardiaspina</i> genus (Hemiptera: Psyllidae)
13:45 - 14:00	Solomon Balagawi: Comparative demography of a specialist and generalist fruit fly: implications for host use and pest management	Geoff Baker: How does landscape management influence <i>Helicoverpa</i> abundance & the risk of Bt resistance ?	Giselle Muschett*: War and Peace: seasonal variation in male conflict in the chameleon grasshopper (<i>Kosciuscola tristis</i>)
14:00 - 14:15	Jaye Newman*: Shape up or ship out: can we alter <i>Bactrocera tryoni</i> (Froggatt) (Diptera: Tephritidae) wing shape to affect sexual performance?	Sarah Tassell*: The impact of the non-native superb lyrebird on Tasmanian invertebrate assemblages	Piotr Trebicki: Climate change and the spread of vector-borne diseases: insight into BYDV and the aphid pathosystem.
14:15 - 14:30	Thilini Ekanayake*: What does Queensland fruit fly, <i>Bactrocera tryoni</i> (Froggatt), do when the sun goes down?	Beatriz Dader*: Impact of UV-A radiation on the performance of aphids and whiteflies and on the leaf chemistry of their host plants	Sohail Qureshi*\$: "Habitat Manipulation" - An option for higher pumpkin yield?
14:30 - 14:45	Olivia Reynolds: Molecular Identification of Immature Parasitoids	Timothy Sutton*: Dispersal and inbreeding in a fig-pollinating wasp and its parasitoid	Tuyet Luong*: Starvation time, recovery and possible Bt detection behaviour of susceptible and resistant <i>Helicoverpa armigera</i> (Hübner) neonates

14:45 – 15:00	Ian Naumann: Technical capacity building for biosecurity in the Asia-Pacific region: Are we making a difference?	Aidan Hall*: Unravelling mummies: using molecular diagnostic tools to explore complex host-parasitoid relationships	Disna Gunawardana: Giant Willow Aphid – a new Aphid on willows in New Zealand
15:00 - 15:30	Afternoon Tea - Shine Dome	Afternoon Tea - Shine Dome	Afternoon Tea - Shine Dome
	<u>Contributed Papers: Biosecurity (Contd)</u> Chair: Leigh Pilkington	<u>Contributed Papers: Systematics and ecology (Contd)</u>	Stephen Doggett: Photography Workshop
15:30 - 15:45	Bernie Dominiak: Revised Fruit Fly Quarantine Distances for Domestic and International Trading	Mackenzie Kwak*: Two birds with one stone: offsetting carbon dioxide emissions and sustaining native insect diversity	
15:45 - 16:00	Alan Flynn: Auckland City of Incursions: Where the show never stops	Sophie Harrison*: Systematics and biogeography of the mygalomorph spider genus <i>Blakistonia</i> (Idiopidae) from semi-arid Australia	
16:00 - 16:15	John La Salle: Extracting rich information from 3D image libraries	Mark Wong*: Exploring Phenotypic Variation in Populations of the Funnel-web Spider <i>Atrax sutherlandi</i> .	
16:15 - 16:45	CLOSING CEREMONY - SHINE DOME Alvin Simmons: Invitation to the 2016 Congress of Entomology, Florida USA Stephen Cameron: Invitation to the 2015 Australian Entomological Society Conference * Student Prize Award * CHAEC Prize Award * Photography and Illustration Prize Awards		

THURSDAY 2 October

<p>Workshop title: DNA target enrichment in phylogenomics - molecular and bioinformatic principles</p> <ul style="list-style-type: none"> • Oliver Niehuis / Manuela Sann - Zentrum für Molekulare Biodiversitätsforschung, Zoologisches Forschungsmuseum Alexander Koenig, Bonn, Germany. • When: Thurs 2 Oct, 9am-5pm. • Where: Research School of Biology, ANU - Gould Meetings Room (Daley Road, Acton, Bldg 116 Rm 246). http://cba.anu.edu.au/news-events/dna-target-enrichment-phylogenomics-workshop
<p>PaDIL workshop</p> <ul style="list-style-type: none"> • Thursday 2 October, 9am-3:30pm • Scarth Room, University House, 1 Balmain Cres, Acton ACT 2601 • Pre-registration required - http://www.pbcrc.com.au/communications/events

POSTER PRESENTATIONS AES 2014

1	Atlas Moth Conservation Network: A new community group to recover a threatened species in the Northern Territory	Michael Braby
2	The effect of temperature on <i>Aphidius gifuens</i> (Hymenoptera: Aphidiidae) and <i>Diaeretiella rapae</i> Hymenoptera:Aphidiidae)	Wenlong Chen
3	Phylogeny of subfamilies Macropsinae and Megophthalminae (Hemiptera: Cicadellidae) from China based on partial DNA data	Renhuai Dai
4	Studying <i>Myzus persicae</i> performance and feeding behaviour, and associated plant viruses under increasing CO ₂	Beatriz Dader
5	From death to dust – using insects to determine post mortem intervals in Queensland	Julianna Farrel
6	A review of necrophagous insects colonising human remains in south-east Queensland	Julianna Farrel
7	Impacts repeated high extreme temperatures on thermal tolerance, metabolism and total protein profile in green peach aphid, <i>Myzus persicae</i> (L.) (Hemiptera: Aphididae)	Behnaz Ghaedi
8	Bush Blitz in Tasmania, summer 2014	Simon Grove
9	Spatial variation in the parasitoid assemblage of a Wattle gall wasp	Marie Henriksen
10	Flying doctors - bees deliver biological control -a new technique for Australian horticulture	Katja Hogendoorn
11	Coexistence of minicircular and a highly rearranged mtDNA molecule suggests that recombination shapes mitochondrial genome organization	Meng Mao
12	From plantings to the paddock: are ground-dwelling beetles and beneficial arthropods moving through fragmented agricultural landscapes?	Katherina Ng
13	Can pre-release supplementation increase the success of Sterile Insect Technique programs for the Queensland fruit fly, <i>Bactrocera tryoni</i> (Froggatt)?	Olivia Reynolds
14	Responses of pest and non-pest fruit flies (Tephritidae: Dacinae: Dacini) to new lures in northern Australia	Jane Royer
15	Morphological comparison of Lord Howe Island Stick Insects originating from the Ball's Pyramid population and the extinct Lord Howe Island population	Sarah Silcocks
16	Biodiversity and ecosystem services for sustainability	Jacqui Todd
17	Long-term monitoring of in-crop aphid populations in south eastern Australia, as a component of a model to predict incidence of <i>Beet western yellows virus</i> in field crops.	Piotr Trebicki
18	The control efficiency of <i>Orius similis</i> (Heteroptera: Anthocoridae) to <i>Frankliniella occidentalis</i> (Thysanoptera:Thripidae)	Prof Junrui Zhi
19	Contrasting success of two introduced <i>Microctonus</i> spp (Hymenoptera: Braconidae) biocontrol agents in Waikato pastures.	Philippa Gerard

POSTER PRESENTATIONS AES 2014 continued

20	The role of abiotic factors for the fluctuation of Jassid (<i>Amrasca biguttula biguttula</i> (Ishida) population on Aubergine (<i>Solanum melongena</i> L)	Muhammad Ali
21	<i>Delicious honey, sticky propolis, productive pollen</i> : Antimicrobial products of the stingless bee nest	Jenny Shanks
22	Cooled propylene glycol preserves DNA of remote field collected insects for next generation sequencing analysis	Hamish Patrick
23	Molecular phylogeny of the Australian jumping plant lice and lerp insects (Hemiptera: Psylloidea) reveals host specificity	Gary Taylor
24	Eucalypt-feeding psyllids use colour to locate the choicest leaves: What looks good must also taste good	Kevin Farnier
25	Native and invasive springtail interactions in a novel ecosystem	Morgan Lythe
26	Studies of the susceptibility of <i>Aedes aegypti</i> from Timor-Leste to synthetic pyrethroids	Stephen Frances
27	Monitoring the fitness and dynamics of <i>Wolbachia</i> -infected <i>Aedes aegypti</i>	Heng Lin Yeap

TABLE OF CONTENTS

ORAL PRESENTATIONS

<i>Ménage à trois</i> : complicated three-way interactions between plant, pest and parasitoid <i>Ang, G.C.K. and Furlong, M.J.</i>	1
<i>Trichogramma chilonis</i> Ishii: a potential biological control agent of <i>Crocidolomia pavonana</i> in Samoa <i>Ang, G.C.K., Uelesen, A., Niko, P., Zalucki, M.P. and Furlong, M.J.</i>	2
Evolution of the Australian parasitoid hymenopteran fauna – a window into the Southern Hemisphere insect biota <i>Austin, A.</i>	3
How does landscape management influence <i>Helicoverpa</i> abundance and the risk of Bt abundance? <i>Baker, G., Tan, C. and Parry, H.</i>	4
Comparative demography of a specialist and generalist fruit fly: implications for host use and pest management <i>Balagawi, S., Drew, R.A.I. and Clarke, A.R.</i>	5
The Convention on Biological Diversity ‘Access and Benefit-Sharing’ protocol: will it obstruct biological control? <i>Barratt, B.I.P. and Brodeur, J.</i>	6
Choice, decision and uncertainty in honey bees (<i>Apis mellifera</i>) <i>Perry, C.J. and Barron, A.B.</i>	7
Species traits explain contrasting diversity dynamics of beetles and ants at carrion patches <i>Barton, P.S.</i>	8
Different bees, different needs – how nest site requirements have shaped the decision-making processes in homeless bees (<i>Apis</i> spp) <i>Beekman, M.</i>	9
Predicting the future challenges of entomology — lessons from the past <i>Berenbaum, M.R.</i>	10
PLENARY SPEAKER	
DNA-based identifications reveal multiple introductions of the vegetable leafminer <i>Liriomyza sativae</i> (Diptera: Agromyzidae) into the Torres Strait Islands and Papua New Guinea <i>Blackett, M.J., Rice, A.D., Semeraro, L. and Malipatil, M.B.</i>	11
Signatures of invasion: an integrated approach to revealing the spread of Melon Fly, <i>Bactrocera cucurbitae</i> , (Diptera: Tephritidae) across SE Asia and the West Pacific <i>Boontop, Y., Clarke, A.R., Cameron, S.L., Krosch, M.N. and Schutze, M.K.</i>	12
Evolution of female secondary sexual structures of New Zealand broad-nosed weevils (Coleoptera: Curculionidae) <i>Brown, S.D.J.</i>	13
Using transcriptomes to reconstruct phylogeny and molecular evolutionary processes in New Zealand insects <i>Buckley, T.R., Dunning, L.T., Dennis, A.B. Sinclair, B.J. and Twort, V.</i>	14
Why the Archiearinae (Geometridae) are no longer considered archaic and recent work on a revision of the montane Tasmanian archiearines <i>Byrne, C. and Throssell, A.</i>	15

Integrating mitogenomic and transcriptomic phylogenetics in insects <i>Cameron, S.L.</i>	16
Phylogeny of Scarab beetles: a molecular dating analysis reveals diversification trends <i>Gunter, N.L., Weir, T., Slipinski, A. and <u>Cameron, S.L.</u></i>	17
A most ingenious paradox <i><u>Car, C.A.</u> and <u>Mesibov, R.</u></i>	18
Combining sky and earth: three ant species integrate celestial and terrestrial sources of directional information <i><u>Cheng, K.</u>, <u>Legge, E.L.G.</u>, <u>Wystrach, A.</u> and <u>Spetch, M.L.</u></i>	19
Can an extra lobe of the cricket salivary gland act as an alternative endocrine transport system? <i><u>Cooper, P.D.</u> and <u>Campos, M.P.</u></i>	20
Australians in the Andes <i><u>Cranston, P.S.</u> and <u>Krosch, M.N.</u></i>	21
Using plant odours to control polyphagous pests – could we benefit from a different perspective? <i><u>Cunningham, P.</u></i>	22
Phenology of a bee community in an agricultural landscape near Canberra <i><u>Cunningham, S.A.</u>, <u>Neave, M. J.</u> and <u>Batley, M.</u></i>	23
Impact of UV-A radiation on the performance of aphids and whiteflies and on the leaf chemistry of their host plants <i><u>Dader, B.</u>, <u>Moreno, A.</u> and <u>Fereres, A.</u></i>	24
Evolution of <i>kdr</i> -type resistance in <i>Cimex</i> : who you will be sleeping with in the future? <i><u>Dang, K.</u>, <u>Toi, C.S.</u>, <u>Lilly, D.G.</u>, <u>Bu, W.</u> and <u>Doggett, S.L.</u></i>	25
Attract-and-kill for the diamondback moth, <i>Plutella xylostella</i> in canola <i><u>Del Socorro, A.</u>, <u>Gregg, P.</u>, <u>Binns, M.</u>, <u>Baker, G.</u>, and <u>Gulliver, S.</u></i>	26
Sensory-motor integration in the flight behaviour of <i>Drosophila</i> <i><u>Dickinson, M.</u></i>	27
Medical entomology in Australia, 1964-2014 <i><u>Doggett, S.</u></i>	28
AES Insect digital macrophotography workshop <i><u>Doggett, S.L.</u> and <u>Zborowski, P.</u></i>	29
Revised fruit fly quarantine distances for domestic and international trading <i><u>Dominiak, D.</u> and <u>Fanson, B.</u></i>	30
What does Queensland fruit fly, <i>Bactrocera tryoni</i> (Froggatt), do when the sun goes down? <i><u>Ekanayake, E.W.M.T.D.</u>, <u>Clarke, A.R.</u> and <u>Schutze, M.K.</u></i>	31
The molecular phylogeny of the fungal spore-feeding Thrips Subfamily Idolothripinae (Thysanoptera; Phlaeothripidae). <i><u>Eow, L.X.</u>, <u>Mound, L.A.</u> and <u>Cameron, S.L.</u></i>	32
Phylogeny and biogeography of Boganiidae (Coleoptera, Cucujoidea) <i><u>Escalona, H.E.</u>, <u>Lawrence, J.F.</u>, <u>Slipinski, A.</u> and <u>Wanat, M.</u></i>	33
Host-finding in psyllids: are <i>Eucalyptus</i> -feeding psyllids anosmic? <i><u>Farnier, K.</u> and <u>Steinbauer, M.J.</u></i>	34

Carrion Café –using insects to determine post mortem intervals in Queensland <i>Farrell, J.F., Whittington, A.E. and Zalucki, M.P.</i>	35
Towards biological control of a generalist insect herbivore: the activities of generalist parasitoids are segregated between crop and adjacent non-crop habitats <i>Feng, Y., Kravchuk, O., Yazdani, M., Sandhu, H., Wratten, S.D. and Keller, M.A.</i>	36
The history of the Australian Entomological Society <i>Fletcher, M.J.</i>	37
Auckland City of Incursions: where the show never stops <i>Flynn, A.R.</i>	38
Plant traits influence the functional role of two understory shrubs for native insects <i>Forbes, R.J. and Steinbauer, M.J.</i>	39
Examining the effects of distance from mature forest and succession on beetle community recolonisation using species, functional trait and phylogenetic approaches <i>Fountain-Jones, N.</i> PHIL CARNE PRIZE WINNER	40
Exotic pests and biological control in New Zealand broadacre pasture; success hoisted by its own petard? <i>Goldson, S.L., Barratt, B.I.P. and Tomasetto, F.</i>	41
Giant Willow Aphid – a new Aphid on willows in New Zealand <i>Gunawardana, D.N., Flynn A.R., Pearson, H.G. and Sopow, S.</i>	42
Coevolution between bacterial endosymbionts and their psyllid hosts of the <i>Cardiaspina</i> genus (Hemiptera: Psyllidae) <i>Hall, A., Johnson, S., Cook, J. and Riegler, M.</i>	43
Unravelling mummies: using molecular diagnostic tools to explore complex host-parasitoid relationships <i>Hall, A., Steinbauer, M., Taylor, G., Johnson, S., Cook, J. and Riegler, M.</i>	44
Systematics and biogeography of the mygalomorph spider genus <i>Blakistonia</i> (Idiopidae) from semi-arid Australia <i>Harrison, S.E., Rix, M.G. and Austin, A.D.</i>	45
Host tree influences on longicorn beetle attack in subtropical <i>Corymbia</i> <i>Hayes, R.A., Piggott, A.M., Smith, T.E. and Nahrung, H.F.</i>	46
Sexual signals for the colour-blind: cryptic female mantids signal quality through brightness <i>Herberstein, M., Barry, K., White, T., Rathnayake, D. and Fabricant, S.</i>	47
Hot Ants – a taxonomic revision of the genus <i>Melophorus</i> (Hymenoptera: Formicidae) <i>Heterick, B., Castalanelli, M.A., Shattuck, S. and Majer, J.</i>	48
Biocontrol of glassy-winged sharpshooter in French Polynesia: a major success in the South Pacific <i>Hoddle, M.S.</i>	49
Of bees and burns: the distribution of the green carpenter bee <i>Xylocopa aeratus</i> in relation to fire-history on Kangaroo Island <i>Hogendoorn, K., Leijs, R. and Glatz, R.</i>	50
The use of the fungus <i>Metarhizium acridum</i> to control locusts and grasshoppers <i>Hunter, D. M. and Peacock, M.</i>	51

Survival of oriental fruit moth females under 30-years long mating disruption <i>Il'ichev, A.L.</i>	52
AliStat and SymTest: two methods for surveying phylogenomic data <i>Jermiin, L.</i>	53
Maggot massing: problems and solutions for the forensic entomologist <i>Johnson, A.P., Mikac, K., Wighton, S. and Wallman, J.F.</i>	54
South Australia's Arboviruses: results and methods from the first large-scale FTA® card arbovirus survey <i>Johnston, E., Toi, C., Weinstein, P., Doggett, S. and Williams, C.</i>	55
The effects of partitioning on phylogenetic inference <i>Kainer, D. and Lanfear, R.</i>	56
A conceptual framework for the study of coloration in nature <i>Kemp, D.J., Herberstein, M.E. and Whiting, M.J.</i>	57
Directional evolution in hymenopteran morphology <i>Klopfstein, S., Vilhelmsen, L. and Ronquist, F.</i>	58
Symposium overview: the rise and rise of molecular data in insect science <i>Krosch, M.N. and Cranston, P.S.</i>	59
Welcome to the jungle: a review of (insect) evidence for eastern Australia's major biogeographical barriers to mesic forest-restricted taxa. <i>Bryant, L.M. and Krosch, M.N.</i>	60
Two birds with one stone: offsetting carbon dioxide emissions and sustaining native insect diversity <i>Kwak, M.L., Forbes, R.J., O'Connor, E., Sandwith, R. and Steinbauer, M.J.</i>	61
Advances in managing images of insect specimens in biological collections <i>Baird, D., Woolston, M., Mantle, B., Fisher, N. and La Salle, J.</i>	62
Extracting rich information from 3D image libraries <i>Anderson, S., Adcock, M., Lovell, D., Mantle, B. and La Salle, J.</i>	63
Sex pheromones of cossid moths: emerging pests of Australian and overseas <i>Eucalyptus</i> plantations <i>Lawson, S.A., Moore, C.M. and Bouwer, M.C.</i>	64
Advancing Coleoptera systematics <i>Leschen, R.A.B.</i>	65
Gondwanan Brown Beetles (Coleoptera: Cryptophagidae: Cryptophaginae): we like them <i>Leschen, R.A.B. and Gimmel, M.L.</i>	66
Molecular methods in forensic entomology in Australia <i>Lessard, B.D., Dowton, M. and Wallman, J.F.</i>	67
The legacy of Ian Mackerras in Australian Diptera systematics <i>Lessard, B.D. and Yeates, D.K.</i>	68
Protecting the future: understanding insecticide resistance in field populations of bed bugs in order to preserve insecticidal control solutions <i>Lilly, D.G., Dang, K., Webb, C.E. and Doggett, S.L.</i>	69
<i>Blattabacterium</i> function, genome degradation and loss in primitive termites <i>Lo, N.</i>	70
Chemical cues, mate attraction and assessment in a psyllid <i>Lubanga, U.K., Seijdhour, F.P., Farnier, K. and Steinbauer, M.J.</i>	71

Starvation time, recovery and possible Bt detection behaviour of susceptible and resistant <i>Helicoverpa armigera</i> (Hübner) neonates	72
<i>Luong, T.T.A., Zalucki, M.P., Cribb, B., Perkins, L.E. and Downes, S.J.</i>	
Optimizing for multiple benefits requires an understanding of functional connectivity of habitats for ecosystem service providers	73
<i>Macfadyen, S., Parry, H. and Schellhorn, N.</i>	
Insect research in the postgenomic era: beyond the DNA sequence	74
<i>Maleszka, R.</i>	
PLENARY SPEAKER	
Higher-level phylogeny of the Hymenoptera inferred from mitochondrial genomes	75
<i>Mao, M., Gibson, T. and Dowton, M.</i>	
Flat beetles in a flat land: a review of the Australian Cucujidae (Coleoptera)	76
<i>Marris, J.W.M. and Ślipiński, S.A.</i>	
A newly constituted Notogean tribe of Tenebrionidae (Coleoptera)	77
<i>Matthews, E. G. and Lawrence, J. F.</i>	
Biological control of exotic pasture weevil pests in New Zealand agriculture: learning from experience to inform the future	78
<i>McNeill, M.R., Barratt, B.I.P., Ferguson, C., Gerard, P., Goldson, S., Hardwick, S., Phillips, C. and Wilson, D.</i>	
50 years of new Australian insects: publishing and authorship trends	79
<i>Mesibov, R.</i>	
Four-cluster likelihood mapping - testing for incongruent signal in large phylogenomic datasets	80
<i>Meusemann, K., Misof, B. and Yeates, D.</i>	
Hot and smelly: thermogenesis and the chemical ecology of pollination in endemic Australian Araceae	81
<i>Miller, R., Farnier, K., Barnes, J., Grant, N., Robinson, S. and Steinbauer, M.</i>	
Evolution of cryptic species within the Australian gall-inducing scale insect genus <i>Apiomorpha</i> (Sternorrhyncha: Coccoidea: Eriococcidae)	82
<i>Mills, P.J. and Cook, L.G.</i>	
War and Peace: seasonal variation in male conflict in the chameleon grasshopper (<i>Kosciuscola tristis</i>)	83
<i>Muschett, G., Herberstein, M.E. and Umbers, K.D.L.</i>	
Technical capacity building for biosecurity in the Asia-Pacific region: are we making a difference?	84
<i>Naumann, I.D., Hossain, Z., Lee, W., Delamoir, S. and Hogan, B.</i>	
Shape up or ship out: can we alter <i>Bactrocera tryoni</i> (Froggatt) (Diptera: Tephritidae) wing shape to affect sexual performance?	85
<i>Newman, J.D., Schutze, M.K. and Clarke, A.R.</i>	
Inferring deep insect phylogenetic relationships using data from genomes and transcriptomes: research initiatives, methods, results, and prospects	86
<i>Niehuis, O.</i>	
PLENARY SPEAKER	
The beetle fauna of the Talbragar Fish Bed	87
<i>Beattie, R.G., Oberprieler, R.G., Cai, C. and Slipinski, S.A.</i>	
Trichromatic vision in the Australian bull ant	88
<i>Ogawa, Y., Narendra, A., Zeil, J. and Hemmi, J.M.</i>	

IOBC Global and the Asia and Pacific Regional Section (APRS) <i>Barratt, B.I.P. and Palmer, W.A.</i>	89
The sexual exploitation of thynnine wasps by deceptive signals emitted from Australian orchids <i>Peakall, R., Bohman, B. and Phillips, R.D.</i>	90
Biological control past, present and future in the greenhouse industry? <i>Pilkington, L. J.</i>	91
Comparing herbivore guilds: seed-feeding weevils from different continents <i>Pinzon Navarro, S.</i>	92
Discovering the Australian weevil fauna <i>Pullen, K.R., Jennings, D. and Oberprieler, R.G.</i>	93
The role of gall formers as biological control agents of the broad-leaved paperbark tree <i>Melaleuca quinquenervia</i> in Florida USA <i>Purcell, M., Pratt, P., Makinson, J., Brown, B., Davies, K., Taylor, G., Giblin-Davis, R. and Scheffer, S.</i>	94
A hidden world revealed: using MicroCT scanning to see inside a gall <i>Purcell, M., Cooper, P., Yeates, D. and Rowell, D.</i>	95
Lablab (<i>Lablab purpureus</i> (L.) Sweet) used for bio-control by native beneficial arthropods in Pumpkins in Queensland Australia <i>Qureshi, S.A., Angove, M., Wilkens, S. and Syeda, S.S.</i>	96
Head roll stabilisation in bull ants <i>Myrmecia pyriformis</i> during twilight <i>Raderschall, C.A., Narendra, A. and Zeil, J.</i>	97
Miniaturisation in ants: size, number and distribution of antennal sensilla <i>Ramirez Esquivel, F., Zeil, J. and Narendra, A.</i>	98
Molecular identification of immature parasitoids <i>Reynolds, O.L., Jenkins, C., Smart, J. and Fell, S.</i>	99
Effect of <i>Botrytis cinerea</i> -infected leaves and berries of <i>Vitis vinifera</i> on the ovipositional preference and larval performance of <i>Epiphyas postvittana</i> <i>Rizvi, S.Z.M., Raman, A., Wheatley, W. and Cook, G.</i>	100
Auditory information processing in insects under real world conditions <i>Römer, H.</i>	101
An innovative approach promoting entomology and molecular biology to the next generation of scientists <i>Rundle, B.J.</i>	102
Rising threats from <i>Arundo donax</i> : Australian contribution to a successful US project <i>Sands, D.P.A., Goolsby, J.A. and Palmer, W.A.</i>	103
Effect of shade on the susceptibility of two varieties of <i>Canna edulis</i> Kerr to defoliators <i>Sasaerila, Y., Tajuddin, T. and Asri, S.</i>	104
Wild pollinator communities in almond plantations and mallee woodlands <i>Saunders, M.E.</i>	105
Arthropods in agricultural landscapes: challenging and supporting food and fibre production <i>Schellhorn, N.A.</i>	106
Searching behaviour in insects <i>Schultheiss, P. and Cheng, K.</i>	107

Requiem for a fruit fly: the end of the road for <i>Bactrocera papayae</i> Drew & Hancock and <i>Bactrocera invadens</i> Drew, Tsuruta, & White (Diptera: Tephritidae). But what does it mean for Australia? <i>Schutze, M.K. and Clarke, A.R.</i>	108
DNA barcoding reveals hidden diversity among Australia's Trichoptera (Caddisflies) <i>Shackleton, M.</i>	109
100 years of continually successful weed biological control in Australia <i>Sheppard, A., Cullen, J. and Palmer, W.</i>	110
Putting Australian Flower Flies (Diptera: Syrphidae) into a world phylogenetic context <i>Skevington, J.H., Young, A.D., Mengual, X., van Steenis, W., van Zuijen, M., Ståhls, G., Hauser, M., Kelso, S. and Thompson, F.C.</i>	111
Phylogeny and classification of the beetle families classified in the Cerylonid Series (Coleoptera: Polyphaga: Cucujoidea) <i>Robertson, J.A., Ślipiński, A. and McHugh, J.V.</i>	112
Settling down to dine on a dioecious Gondwanan relict: why are psyllid nymphs more abundant at the base of branchlets? <i>Steinbauer, M.J., Lubanga, U.K. and Taylor, G.S.</i>	113
Dispersal and inbreeding in a fig-pollinating wasp and its parasitoid <i>Sutton, T.L., DeGabriel, J.L., Riegler, M. and Cook, J.M.</i>	114
Vulnerability of a fig – pollinator system to climate change <i>Sutton, T.L., DeGabriel, J.L., Riegler, M. and Cook, J.M.</i>	115
The costs of pheromone signalling in female moths <i>Symonds, M.R.E., Barling, A., Buttemer, W.A., Cheah, C., Kokko, H. and Umbers, K.D.M.</i>	116
The impact of the non-native superb lyrebird on Tasmanian invertebrate assemblages <i>Tassell, S., Wapstra, E., Richardson, A.M.M. and Barmuta, L.</i>	117
Selection of non-target species for risk assessment of biological control agents: testing a decision-support system <i>Todd, J.H., Barratt, B.I.P., Tooman, L.K. and Malone, L.A.</i>	118
Climate change and the spread of vector-borne diseases: insight into BYDV and the aphid pathosystem <i>Trebicki, P., Nancarrow, N., Freeman, A., Bosque-Perez, N., Yen, A. and Fitzgerald, G.</i>	119
Olfactory detection and discrimination: engineering lessons from an insect <i>Nowotny, T., de Bruyne, M., Berna, A.Z., Warr, C.G. and Trowell, S.C.</i>	120
Soil management and ecosystem services in grapes <i>van Helden, M. and Keller, M.</i>	121
Insect sleep and attention <i>van Swinderen, B.</i>	122
Bee colour vision in relation to flowers colours <i>Vorobyev, M. and Hempel de Ibarra, N.</i>	123
History, accomplishments and challenges of forensic entomology in Australia <i>Wallman, J. F.</i>	124
The effects of temperature on the development and mortality of <i>Eretmocerus warrae</i> (Nauman & Schmidt) <i>Wang, T., Hogendoorn, K. and Keller, M.A.</i>	125
A computational model of the insect mushroom body can account for ant route memory in complex environments	126

<i>Webb, B., Ardin, P., Peng, F., Mangan, M. and Lagogiannis, K.</i>	
Exploiting behaviour to create novel deterrents for the Queensland Fruit Fly (<i>Bactrocera tryoni</i>)	127
<i>Webb, Q., Cunningham, P., Clarke, A. and Furlong, M.</i>	
Exploring phenotypic variation in populations of the funnel-web spider <i>Atrax sutherlandi</i>	128
<i>Wong, M., Woodman, J.D. and Rowell, D.M.</i>	
Mathematically consistent DNA models for time-inhomogeneous mutation	129
<i>Woodhams, M., Sumner, J. and Fernández-Sánchez, J.</i>	
Effects evaluation of entomopathogenic fungus <i>Beauveria bassiana</i> on predatory mite and biological control of their shared pest <i>Frankliniella occidentalis</i>	130
<i>Wu, S., Gao, Y. and Lei, Z.</i>	
Inferring the relationships of early Dipteran lineages using transcriptomic data	131
<i>Yeates, D.K. and Meusemann, K.</i>	
A revision of the Australian Flower Flies (Diptera: Syrphidae)	132
<i>Young, A.D., Skevington, J.H., Thompson, F.C.T., van Steenis, W. and van Zuijen, M.</i>	
From natural history to continental scale perspectives: contributions of Australian Entomologists to Ecology - a play in three acts	133
<i>Zalucki, M.</i>	
Visual homing	134
<i>Zeil, J.</i>	
In search of hexapod origins: capturing phylogenetic signal from serine with 21-amino-acid models	135
<i>Zwick, A.</i>	
POSTER PRESENTATIONS	
The role of abiotic factors for the fluctuation of Jassid (<i>Amrasca biguttula biguttula</i> (Ishida) population on Aubergine (<i>Solanum melongena</i> L)	136
<i>Ali, M., Ashfaq, M., Ashfaq, M., Rana, N., Khalid, S. and Ali, A.</i>	
Atlas Moth Conservation Network: a new community group to recover a threatened species in the Northern Territory	137
<i>Braby, M.F.</i>	
The effect of temperature on <i>Aphidius gifuens</i> (Hymenoptera: Aphidiidae) and <i>Diaeretiella rapae</i> (Hymenoptera:Aphidiidae)	138
<i>Chen, W.</i>	
Studying <i>Myzus persicae</i> performance and feeding behaviour, and associated plant viruses under increasing CO ₂	139
<i>Dader, B., Fereres, A. and Trebicki, P.</i>	
Phylogeny of subfamilies Macropsinae and Megophthalminae (Hemiptera: Cicadellidae) from China based on partial DNA data	140
<i>Dai, R., Li, H. and Li, Z.</i>	
Eucalypt-feeding psyllids use colour to locate the choicest leaves: what looks good must also taste good	141
<i>Farnier, K., Dyer, A.G., Peters, R.A. and Steinbauer, M.J.</i>	
A review of necrophagous insects colonising human remains in south-east Queensland	142
<i>Farrell, J.F., Whittington, A.E. and Zalucki, M.P.</i>	

From death to dust – using insects to determine post mortem intervals in Queensland <i>Farrell, J.F., Zalucki, M.P. and Whittington, A.E.</i>	143
Studies of the susceptibility of <i>Aedes aegypti</i> from Timor-Leste to synthetic pyrethroids <i>Frances, S.P., Morton, C.J. and Pettit, W.</i>	144
Contrasting success of two introduced <i>Microctonus</i> spp (Hymenoptera: Braconidae) biocontrol agents in Waikato pastures <i>Gerard, P.J. and Wilson, D.J.</i>	145
The biology of <i>Dicrodiplosis manihoti</i> (Dip.: Cecidomyiidae) and its interactions with <i>Nipaecoccus viridis</i> (Hem.: Pseudococcidae) <i>Gheibi, M., Hesami, Sh. and Jahromi, S.</i>	146
Bush Blitz in Tasmania, summer 2014 <i>Grove, S.J. and Byrne, C.</i>	147
Spatial variation in the parasitoid assemblage of a Wattle gall wasp <i>Henriksen, M.V., Chapple, D., Chown, S. and McGeoch, M.A.</i>	148
Flying doctors - bees deliver biological control - a new technique for Australian horticulture <i>Hogendoorn, K. and Scott, E.S.</i>	149
Native and invasive springtail interactions in a novel ecosystem <i>Lythe, M.J., Chown, S.L. and McGeoch, M.A.</i>	150
Coexistence of minicircular and a highly rearranged mtDNA molecule suggests that recombination shapes mitochondrial genome organization <i>Mao, M., Austin, A.D., Johnson, N.F. and Dowton, M.</i>	151
From plantings to the paddock: are ground-dwelling beetles and beneficial arthropods moving through fragmented agricultural landscapes? <i>Ng, K., Driscoll, D.A., Lindenmayer, D.B., Macfadyen, S., Lewis, M. and Arnott, A.</i>	152
Cooled propylene glycol preserves DNA of remote field collected insects for next generation sequencing analysis <i>Patrick, H. and Armstrong, K.</i>	153
Can pre-release supplementation increase the success of Sterile Insect Technique programs for the Queensland fruit fly, <i>Bactrocera tryoni</i> (Froggatt)? <i>Reynolds, O.L., Orchard, B., Collins, S. and Taylor, P.W.</i>	154
Responses of pest and non-pest fruit flies (Tephritidae: Dacinae: Dacini) to new lures in northern Australia <i>Royer, J.</i>	155
Delicious honey, sticky propolis, productive pollen: antimicrobial products of the stingless bee nest <i>Shanks, J., Haigh, A., Riegler, M. and Spooner-Hart, R.</i>	156
Morphological comparison of Lord Howe Island Stick Insects originating from the Ball's Pyramid population and the extinct Lord Howe Island population <i>Silcocks, S. and Magrath, M.J.L.</i>	157
Molecular phylogeny of the Australian jumping plant lice and lerp insects (Hemiptera: Psylloidea) reveals host specificity <i>Taylor, G., Fagan-Jeffries, E., Steinbauer, M. and Austin, A.</i>	158

Biodiversity and ecosystem services for sustainability	159
<i>Todd, J.H., Burgess, E.P.J., Barraclough, E.I., Poulton, J., Rheinlander, P., Sorce, M. and Malone, L.A.</i>	
Long-term monitoring of in-crop aphid populations in south eastern Australia, as a component of a model to predict incidence of <i>Beet western yellows virus</i> in field crops.	160
<i>Aftab, M., Trebicki, P., Salam, M.U. and Freeman, A.</i>	
The control efficiency of <i>Orius similis</i> (Heteroptera: Anthocoridae) to <i>Frankliniella occidentalis</i> (Thysanoptera: Thripidae)	161
<i>Zhi, J., Mo, L. and Zhang, J.</i>	

INDEX OF AUTHORS

ORAL PRESENTATIONS

Ménage à trois: complicated three-way interactions between plant, pest and parasitoid

Ang, G.C.K. and Furlong, M.J.

School of Biological Sciences, The University of Queensland, QLD 4072

Three-way (tritrophic) interactions between plants, the herbivores that feed on the plants, and the parasitoids that attack these herbivores, are mediated by herbivore-induced plant volatiles (HIPVs) released upon herbivory. Parasitoids utilize these HIPVs as cues to locate their caterpillar prey and HIPV blends can be learnt to improve foraging efficiency. We tested if parasitoids could exploit learning of host-specific HIPV blends to perform better than naïve conspecifics and investigated if preferences for the HIPV blends released by host and/or non-host herbivore-induced plants varied over time. In olfactometer tests, experienced female *Cotesia glomerata* (Hymenoptera: Braconidae), a parasitoid of the cabbage white butterfly *Pieris rapae* (Lepidoptera: Pieridae), and *Diadegma semiclausum* (Hymenoptera: Ichneumonidae), a parasitoid of the diamondback moth *Plutella xylostella* (Lepidoptera: Plutellidae), preferred plants which had been induced by, or in part by, their host herbivores over non-host-induced plants. Naïve female parasitoids of both species did not discriminate between herbivore-induced plants. This suggests that host prey location is improved with positive oviposition experience, such that not only can an experienced parasitoid discriminate host from non-host, she can also locate hosts within mixed infestations of host and non-host herbivores. However, experienced *C. glomerata* attraction to host-induced plants diminished by the second day after induction (of plants) while experienced *D. semiclausum* attraction to host-induced plants lasted up to three days after induction. We hypothesize that it is beneficial for specialist parasitoids like *D. semiclausum* to retain memory of host-specific HIPVs to maximize foraging efficiency in heterogeneous environments, while generalist parasitoids like *C. glomerata* have more plasticity in the learning of host-specific HIPVs to remain receptive to a broad range of hosts.

***Trichogramma chilonis* Ishii: a potential biological control agent of *Crocidolomia pavonana* in Samoa**

Ang, G.C.K.¹, Uelese, A.², Niko, P.², Zalucki, M.P.¹ and Furlong, M.J.¹

¹School of Biological Sciences, The University of Queensland, QLD 4072; ²Crops Division, Ministry of Agriculture and Fisheries, Nu'u Research Centre, Nu'u, Samoa

The large cabbage moth, *Crocidolomia pavonana* (Lepidoptera: Crambidae) is a major pest of *Brassica* crops in tropical and sub-tropical regions of Africa, Asia and the Pacific. There are no previous reports of effective natural enemies of this pest across this range but in Samoa an arrhenotokous population of the generalist egg parasitoid *Trichogramma chilonis* Ishii (Hymenoptera: Trichogrammatidae) frequently attacks it. This is the first record of *T. chilonis* in Samoa. A three-year field recruitment study showed that although *C. Pavonana* eggs occurred at all times of the year, their abundance was greatest during drier periods. Parasitism of *C. Pavonana* egg masses by *T. chilonis* was variable but the parasitoid was recovered from *C. Pavonana* egg masses at all times of the year, and so it is well established in the major *Brassica* growing regions of the island of Upolu. When partial lifetables were constructed for *C. pavonana*, the rate of egg disappearance (likely due to predation and the physical effects of rainfall) ranged from 0 to 0.839 and the marginal rate of mortality due to *T. chilonis* ranged from 0 to 0.474. When it was present, *T. chilonis* was the major mortality factor affecting *C. Pavonana* eggs in all but one of the recruitment studies. The historical problems surrounding the identity and species status of *T. chilonis* will be discussed and its host range and distribution in the Asia-Pacific region briefly reviewed with consideration of development of *T. chilonis* as a biological control agent of *C. pavonana*. Finally, we will also feature the latest findings on the lepidopteran species included in the host range of *T. chilonis* (diamondback moth, *Plutella xylostella* (Lepidoptera: Plutellidae), common eggfly, *Hypolimnas bolina* (Lepidoptera: Nymphalidae), and an unidentified arctiid moth (Lepidoptera: Arctiidae)), and an interesting tradeoff in sex allocation and progeny size dependent on host egg species.

Evolution of the Australian parasitoid hymenopteran fauna – a window into the Southern Hemisphere insect biota

Austin, A.

Australian Centre for Evolutionary Biology & Biodiversity,
School of Earth & Environmental Sciences, The University of Adelaide, SA 5005

The Australian hymenopteran is clearly highly diverse and contains many unique elements. The drivers for this undoubtedly include southern continental isolation, a diversity of habitats including remnant Gondwanan vegetation, and a flora dominated by *Eucalyptus* and *Acacia* with a number of additional special elements such as the Proteaceae radiation. Analysis of the described parasitoid fauna points to a number of differences in the relative species richness for several families/superfamilies which are difficult to explain. However, even after more than 30 years of ‘modern’ phylogenetic research, the evolution of the fauna for most groups is not well understood. Using a number of exemplar groups from the Evanioidea, Ichneumonoidea and Proctotrupoidea, this presentation will explore their likely origins and biogeography, and outline future research directions that should prove fruitful.

How does landscape management influence *Helicoverpa* abundance & the risk of Bt resistance ?

Baker, G.¹, Tann, C.² and Parry, H.³

CSIRO Agriculture Flagship, ¹P.O. Box 1700, Canberra ACT 2601; ²Locked Bag 59, Narrabri NSW 2390; ³PO Box 2583, Brisbane QLD 4001.

Helicoverpa armigera and *H. punctigera* are major insect pests of cotton in Australia. Transgenic (Bt) cotton, in use since 1996, has effectively reduced the feeding damage caused by *Helicoverpa* and therefore the amount of insecticide applied to fields to control them. However, Bt resistance in *Helicoverpa* remains a major threat to the cotton industry. As part of pre-emptive management strategies to prevent Bt resistance developing in these key and very mobile pests, it is imperative that we understand their population dynamics, especially at large scales.

A grid of pheromone traps has been maintained within an area of approximately 10km radius near Narrabri since 1992. Data from these traps depict major shifts in *Helicoverpa* abundance over time, most notably declines in both species in recent years. At least in *H. armigera*, such decline may be the result of suppression by the wide use of Bt cotton.

Refuge crops (either pigeon pea or non Bt cotton) must be grown by Bt cotton farmers to generate Bt susceptible moths and thus dilute resistance alleles within landscapes. The performance (moth production) of these refuge crops seems likely to have declined in recent years, in part due to greater impact of natural enemies (e.g. pupal parasitoids), probably enhanced by the reduced pesticide use associated with modern cotton farming. Refuge performance is also very patchy within cotton production landscapes, which in turn seems likely to lead to substantial areas being poorly supplied with Bt susceptible moths. Stable isotope signatures (especially C) can be used to help identify likely plant host origins of *Helicoverpa* captured within cotton landscapes. Such analyses suggest that the majority of moths originate from other than the refuge / Bt cotton system. These results will be discussed within a framework of assessing / improving the effectiveness of the current Bt resistance management strategy.

Comparative demography of a specialist and generalist fruit fly: implications for host use and pest management

Balagawi, S.¹, Drew, R.A.I.² and Clarke, A.R.³

¹Elizabeth Macarthur Agricultural Institute, NSW Department of Primary Industries, Private Bag 4008, Narellan, New South Wales 2567; ²International Centre for Management of Pest Fruit Flies, Griffith School of Environment, Griffith University, Nathan, QLD 4111; (3) School of Earth, Environment and Biological Sciences, Queensland University of Technology, GPO Box 2434, Brisbane, Qld 4001.

Knowledge on the demographic consequences of host use provides information which allows understanding of subsequent population dynamics and fitness of phytophagous species. Here, we present results of a comparative study between the specialist fruit fly *Bactrocera cucumis* (French) and the generalist *Bactrocera tryoni* (Froggatt) (Diptera: Tephritidae). Our primary aim was to determine whether their life-history strategies play a role in their current host use patterns. We further aimed to use the life-history data to construct population models that would help determine the sensitive life-history stage(s) that could be targeted for effective field management. The study was conducted under laboratory conditions at $26 \pm 1^\circ\text{C}$ and $65 \pm 10\%$ rH. Eggs collected from laboratory-reared flies were inoculated into organically grown fruits of both primary and alternate host plant cultivars of both fly species. The proportion of survival at all life stages were monitored for all cohorts from the different plant cultivars. Complete life-tables for cohorts of each fly species from the different fruit cultivars were constructed and the key demographic parameters and population models were analysed using the PopTools matrix model computer programme. The results showed that *B. cucumis* had a lower reproductive rate and longer generation time than *B. tryoni*, which had a higher reproductive rate and shorter generation time. The population models revealed that the population growth rate of both species is highly sensitive at the adult reproductive stage, indicating that manipulating the probability of survival at this life stage would most efficiently manage these species. This study showed that insect demographic characteristics play a significant role in their host use patterns as well as their population dynamics and overall fitness. We suggest that any efforts to manage fruit fly population should consider the life-history consequences of host use.

The Convention on Biological Diversity ‘Access and Benefit-Sharing’ protocol: will it obstruct biological control?

Barratt, B.I.P.¹ and Brodeur, J.²

¹AgResearch Invermay, Private Bag 50034, Mosgiel, New Zealand; ²Department of Biological Sciences, University of Montreal, Canada

One of the three objectives of the Convention on Biological Diversity is “the fair and equitable sharing of the benefits” of genetic resources (GRs). It was aimed at businesses such as the pharmaceutical industry which has profited enormously from GR resources taken from countries without consent or any agreement to share benefits. Biological control is at risk of being included in this category and hence subject to an unrealistic level of bureaucracy, despite the fact that it is not a huge, lucrative industry. FAO established a Commission on GRs for Food and Agriculture, and under this they commissioned IOBC to provide scientific advice on the design of an ABS regime that would ensure practical and effective management for collection and use of biological control agents. The IOBC Commission produced a comprehensive document in which it was argued that biological control depends upon reciprocal relationships between countries and biological control agents are exchanged between countries with little or no money changing hands. Biological control was shown to be, for the most part a public good activity with benefits mainly to the public and society, not the implementer. The report was used by FAO to support their Commission and recently, FAO invited IOBC to put together a further document on voluntary codes of conduct, guidelines and best practice for biological control in relation to ABS. This will be incorporated into the FAO commission’s draft document ‘Elements to Facilitate Domestic Implementation of ABS for subsectors of GRs for Food and Agriculture.’ The Nagoya Protocol on ABS provides “a transparent legal framework for the effective implementation of ABS” and was adopted in October 2010. It will enter into force 90 days after ratification by the fiftieth country – this will be 12 October 2014.

Choice, decision and uncertainty in honey bees (*Apis mellifera*)

Perry, C.J.^{1,2} and Barron, A.B.²

¹School of Biological and Chemical Sciences, Queen Mary, University of London. E1 4NS, UK; ²Department of Biological Sciences, Macquarie University, North Ryde, NSW 2109, Australia

Human decision-making strategies are strongly influenced by an estimation of certainty or uncertainty to increase the chances of making a right choice. Humans seek more information and defer choosing when they realize they have insufficient information to make an accurate decision, but whether animals involve estimations of uncertainty in their decision making is currently highly contentious. To explore this issue, we examined how honey bees (*Apis mellifera*) responded to a visual discrimination task that varied in difficulty between trials. Free-flying bees were rewarded for a correct choice, punished for an incorrect choice, or could avoid choosing by exiting the trial (opting out). Bees opted out more often on difficult trials, and opting out improved their success in difficult trials. Bees could also transfer the concept of opting out to a novel task. Our data suggest that bees attempted the difficult trials only when they were more likely to be successful, and otherwise avoided difficult trials. This would imply bees' decision making can be informed by their estimate of success. Data such as this has been considered evidence of basic metacognition in nonhuman animals, and bees' performance was comparable to that of primates in a similar paradigm. We discuss whether these behavioral results prove bees react to uncertainty or whether alternative associative mechanisms can explain these data. To better frame metacognition as a subject for neurobiological investigation, we propose a neurobiological hypothesis for how uncertainty monitoring might occur within the known circuitry of the honey bee brain.

Species traits explain contrasting diversity dynamics of beetles and ants at carrion patches

Barton, P.S.

Fenner School of Environment and Society, The Australian National University, Canberra, ACT 0200

Carrion is an ephemeral and patchy resource that supports a diverse subset of species linked to nutrient cycling and the decomposition process. Many studies have documented changes in the diversity of arthropods at individual carcasses, but few studies that have examined how functional traits of different groups of organisms underpin their responses to carrion patches. We used a carrion addition experiment to compare changes in composition and functional traits of ant and beetle assemblages at carcasses compared with control sites. We found profound changes in beetle assemblage evenness and richness over time, but not ant assemblages. We also found that beetles at carcasses were twice as large and had higher wing loadings than their counterparts at nearby control sites during early decomposition, whereas ants displayed no differences in size. These results provide an example of how the functional traits of opportunist species enable them to exploit rare and dynamic resources. This also shows how large animal carcasses can drive broader biodiversity dynamics across landscapes.

Different bees, different needs – how nest site requirements have shaped the decision-making processes in homeless bees (*Apis* spp)

Beekman, M.

Behaviour and Genetics of Social Insects Lab, School of Biological Sciences A12, University of Sydney, Sydney, NSW 2006.

During reproductive swarming and seasonal migration, a honeybee swarm needs to locate and move to a new nest site. Our current knowledge of swarming and nest site selection in honeybees is based primarily on studies of just one species, *Apis mellifera*. Natural colonies of *A. mellifera* live in tree cavities. The quality of the cavity is often critical to the survival of a swarm. The scouts must search thousands of trees to ensure that they do not settle for a poor cavity when a better one is available. More recently another species of honeybee has been included in studies of nest site selection: the open-nesting dwarf honeybee *Apis florea*. *A. florea* builds a small nest comprised of a single comb suspended from a twig of a shrub or tree in the open. For a cavity-nesting species like *A. mellifera* there is only a limited number of potential nest sites that can be located by a swarm, simply because suitable nest sites are scarce. In contrast, for an open-nesting species like *A. florea* it seems that there is an abundance of shaded twigs that would be equally suitable for building a nest. Here I pull together recent research that shows that the nest site selection processes of *A. florea* and *A. mellifera* have been shaped by each species' nest site requirements. I argue that both species use the same behavioural algorithm, tuned to allow each species to solve their species-specific problem.

Predicting the future challenges of entomology — lessons from the past

Berenbaum, M.R.

PLENARY SPEAKER

Department of Entomology, University of Illinois at Urbana-Champaign, 505 S. Goodwin, Urbana, IL 61801-3795, USA

Predicting the future of anything, even that of a scientific field, is an inherently unscientific enterprise. Entomology as a discipline depends on objective, verifiable facts, whereas forecasting the future is necessarily rife with unverifiable speculation. Notwithstanding, entomologists have attempted to predict the future challenges for their discipline at fairly regular intervals since its beginnings almost 175 years ago. Predictions of entomological challenges in 1908, 1946, 1954, and 1989 have all, remarkably, converged on similar themes: the conceptual challenges of invasive species, loss of biodiversity, and environmentally compatible pest management, and the infrastructural challenges of maintaining entomology as a distinct discipline and securing sufficient public funding for research. In both Australia and the United States, apiculture—the maintenance of the western honey bee *Apis mellifera* for fun and/or profit—provides a case study of the convergence of conceptual and infrastructural challenges and may provide some insights for the next effort to predict future challenges for entomology at large.

DNA-based identifications reveal multiple introductions of the vegetable leafminer *Liriomyza sativae* (Diptera: Agromyzidae) into the Torres Strait Islands and Papua New Guinea

Blacket, M.J.¹, Rice, A.D.², Semeraro, L.¹ and Malipatil, M.B.¹

¹Department of Environment & Primary Industries (DEPI), AgriBio, La Trobe University, Bundoora, Vic. 3083, Australia; ²Northern Australia Quarantine Strategy (NAQS), Department of Agriculture, Cairns, Qld. 4870, Australia.

Leafmining flies (Diptera: Agromyzidae) can be serious economic pests of horticultural crops. Some genera such as *Liriomyza* are particularly problematic with numerous species, some of which are highly polyphagous (wide host range), which can only be confidently identified morphologically from adult males. In the current study DNA barcoding was employed to establish new locality records of the vegetable leafminer fly, *Liriomyza sativae*, from the islands of Torres Strait (Queensland, Australia) and the central highlands of Papua New Guinea (PNG). These records represent significant range extensions of this highly invasive plant pest. Specimens of immature leafminers (from leaf mines) were collected over a five year period during routine plant health surveys in ethanol or on FTA® filter paper cards, the latter proved a reliable means of preserving and transporting insect DNA under tropical conditions. Specimens were identified through sequencing two sections of the Cytochrome Oxidase I (COI) gene and the utility of each was assessed for the identification of species and intra-specific genetic lineages. The current study indicates that multiple haplotypes of *L. sativae* occur in PNG, while a different haplotype is present in the Torres Strait, with genetic regionalisation between these areas apart from a single instance. The DNA barcoding methods employed here not only identified multiple introductions of *L. sativae* but appear generally applicable to the identification of other agromyzid leafminers (Phytomyzinae and Agromyzinae) and should decrease the likelihood of potentially co-amplifying internal hymenopteran parasitoids. Currently, *L. sativae* is still not recorded from the Australian mainland; however, further sampling of leafminer flies from northern Australia and surrounding areas is required, as surveillance for possible *Liriomyza* incursions, as well as to characterise endemic species with which *Liriomyza* species might be confused.

Signatures of invasion: an integrated approach to revealing the spread of Melon Fly, *Bactrocera cucurbitae*, (Diptera: Tephritidae) across SE Asia and the West Pacific

*Boontop, Y.*¹, *Clarke, A.R.*^{1,2}, *Cameron, S.L.*¹, *Krosch, M.N.*³ and *Schutze, M.K.*¹

¹School of Earth, Environmental and Biological Sciences, Queensland University of Technology, G.P.O. Box 2434, Brisbane, Queensland, Australia 4000; ²Plant Biosecurity Cooperative Research Centre, L.P.O Box 5012, Bruce, ACT 2617; ³Sustainable Minerals Institute, University of Queensland, Brisbane, QLD, Australia 4072.

Multidisciplinary approaches greatly enhance our understanding of invasion pathways, particularly via tools that resolve population structure over geographic and temporal scales. This study uses such an approach to investigate population structure in the Melon fly, *Bactrocera cucurbitae*, a widely distributed horticultural pest with a native range including the Indian Subcontinent and Asia. Melon fly has subsequently invaded Africa, the West Pacific, and parts of Oceania. While its population structure is well known in some region, it is poorly understood in SE Asia and the West Pacific.

We used molecular (mtDNA-*cox1*) and morphological data (geometric morphometric wing shape and size; aedeagus morphometrics) to resolve invasive signatures of Melon fly from 13 SE Asian and West Pacific locations. This information is interpreted in relation to historical records of its invasion across the region. We report distinct differences in genetic diversity in SE Asia relative to the West Pacific. Furthermore, wing size, shape and aedeagal length differ between mainland SE Asia and to the West Pacific.

We discuss these data under a hypothesis of multiple and recent introductions from SE Asia into the West Pacific. Greatest diversity in SE Asia suggests this as the origin of Melon fly with dispersal into and across the region. Increased diversity in part of the Pacific supports the notion of multiple introductions to some Islands. These results reinforce the value of integrating multiple data sets to develop a better understanding of dispersal pathways in a serious, invasive pest.

Evolution of female secondary sexual structures of New Zealand broad-nosed weevils (Coleoptera: Curculionidae)

Brown, S.D.J.

Bio-Protection Research Centre, PO Box 85084, Lincoln University, Lincoln 7647, Canterbury, New Zealand

The broad-nosed weevils of the genus *Irenimus* comprise a group of over 70 species which are endemic to New Zealand. The genus is distributed throughout New Zealand in grassland and shrubland habitats, but find their greatest diversity in the alpine regions of the southern South Island. A number of species show remarkable sexual dimorphism in that females frequently show exaggerated structures on the elytra and abdominal ventrites. These structures can be classified into five forms: 1) Tubercles at the top of the elytral declivity; 2) Prolongation of the apex of the elytra; 3) Swelling of the disc of ventrite V; 4) Emargination of the apex of ventrite V; and 5) the posterior margin of ventrite IV produced into a lamina. The evolution of these structures will be discussed in relation to competing hypotheses of mating conflict and oviposition.

Using transcriptomes to reconstruct phylogeny and molecular evolutionary processes in New Zealand insects

Buckley, T.R.¹, Dunning, L.T.², Dennis, A.B.³ Sinclair, B.J.⁴ and Twort, V.¹

¹Landcare Research, Private Bag 92170, Auckland, New Zealand; ²Imperial College London, Silwood Park, Berkshire, SL5 7PY, UK; ³EAWAG, Swiss Federal Institute of Aquatic Science and Technology; 8600 Dübendorf, Switzerland; ⁴Department of Biology, The University of Western Ontario, London, ON N6A 5B7, Canada.

Sequencing of transcriptomes allows phylogenetic analysis based on a large number of gene sequences, in addition to estimation of patterns of selection on protein coding genes. The New Zealand stick insects form two lineages, most closely related to species from New Caledonia, and nested within a large radiation of Australasian species. The New Zealand species are distributed from warm, northern forests to high alpine areas. These geographic distributions and phylogenetic patterns imply that the temperate New Zealand species have evolved from tropical ancestors and therefore have adapted to radically different environmental conditions. The loss of flight has also placed novel metabolic demands on the New Zealand species. Previous Sanger-sequence data sets showed poor phylogenetic resolution among the 10 New Zealand genera and we demonstrate the improved power and limitations of transcriptome-scale data for resolving this radiation. With these same data we also show that selection is widespread in genes encoding metabolic proteins, especially those from the glycolytic pathway. We also describe a parallel study of phylogenetics and molecular evolution in New Zealand orthoptera tree (*Hemideina*) and giant weta (*Deinacrida*).

Why the Archiearinae (Geometridae) are no longer considered archaic and recent work on a revision of the montane Tasmanian archiearines

*Byrne, C.*¹ and *Throssell, A.*²

¹Tasmanian Museum and Art Gallery; ²University of Tasmania

The Archiearinae, a small sub-family of the Geometridae has long been considered to be the most basally derived group in the family; however recent evidence shows that members are relatively derived and that the sub-family is most likely paraphyletic. The distribution of the Archiearinae is amphipolar with two genera and seven species in Tasmania, two genera and three species in the Neotropics in the southern Andes, and two genera and four in the Nearctic and Palaearctic. The subfamily is characterised by alpine adaptations such as melanised cuticle, long hair scales, flash colouration and diurnalism. Several characters have been used to corroborate a basally derived phylogenetic position for the Archiearinae including a reduced tympanum, lack of an accessory tympanum, a very narrow fenestra media and superficial simplistic pupal characteristics. However it is more likely that these are adaptations from a diurnal habit adopted under harsh environmental conditions at high latitudes and altitudes.

The Tasmanian Archiearinae, *Dirce* Prout and *Acalyphes* Turner, are iconic semi-alpine species that live in mountainous areas in Tasmania. On morphological and molecular characters they are most likely not monophyletic and may have affinities with the Australian Nacophorini, a large group of endemic southern Australian species. In this presentation we discuss work on a revision of these genera, which clarifies their nomenclature, phylogenetic relationships and species distributions and includes descriptions of two new species. Immature stages of all new species are illustrated and described. We also elaborate on the global relationships of the Archiearinae in general.

Integrating mitogenomic and transcriptomic phylogenetics in insects

Cameron, S.L.

Earth, Environmental & Biological Sciences, Queensland University of Technology, Brisbane, QLD, Australia.

Whole mitochondrial genomes were the first datasets developed for insect phylogenomics and, to date, the most widely used. Significant volumes of data are available for all orders and a large number of phylogenomics studies have been published at taxonomic levels ranging from interordinal down to within genera. But, with one exception, mitogenome phylogenetic studies of insects have been conducted in isolation from nuclear-gene based studies, limiting their utility and general acceptance. Next-generation sequencing platforms are massively increasing the rate at which mitogenomes are being sequenced, but the pattern of analysing them in isolation from nuclear data persists. The rising tide of RNAseq data provides the capacity to simultaneously collect mitochondrial and nuclear datasets of significant size, however studies to date have not analysed mitogenomic data. The capacity to mine whole, rather than single, mitochondrial genes from current transcriptome datasets and the utility of mitogenomic partitions in improving resolution of nuclear-transcriptome phylogenies will be discussed, primarily with examples from the Lepidoptera. Full, integrative analysis of the evolution of all of their genomes offers tremendous promise for improving our understanding of all aspects of insect evolution.

Phylogeny of Scarab beetles: a molecular dating analysis reveals diversification trends

Gunter, N.L.^{1,2}, Weir, T.³, Slipinski, A.³ and Cameron, S.L.⁴

¹ Department of Zoology, Palacky University, Olomouc, Czech Republic; ²Department of Invertebrate Zoology, Cleveland Natural History Museum, Cleveland, Ohio, United States of America, ³Australian National Insect Collection, CSIRO, Black Mountain Laboratories, ACT, Australia; ⁴Earth, Environmental & Biological Sciences, Queensland University of Technology, Brisbane, QLD, Australia.

Scarabaeidae (chafers, dung beetles etc.) are one of the best recognised, largest (with over 30,000 species and 1,600 genera), and widespread (cosmopolitan distribution) beetle lineages. The phylogeny of the family as a whole has been broadly addressed in major treatments of beetle phylogenetics such as the Hunt (molecular) and Lawrence (morphological) phylogenies of the order, plus multiple studies focused on individual subfamilies but a comprehensive treatment of the family as whole is lacking. We present a new fossil-dated, molecular phylogeny of the family including almost a quarter of extant genera and all major subfamilies plus a complete set of outgroups from other scarabaeoid families. The phylogeny is well resolved, supporting the monophyly of the family and all subfamilies except the Rutellinae, which are paraphyletic with respect to the Dynastinae. We also find significant support for a fundamental split in the family between phytophagous and saprophagous clades as previously proposed. Both clades experience peak diversification 90-110 million years ago, consistent with the period during which angiosperms replace earlier floras to dominate terrestrial ecosystems. Differences in the patterns of diversification for specialist vs generalist scarabs, between phytophagous and saprophagous lineages and the possible drivers of scarab evolution will be discussed.

A most ingenious paradox

Car, C.A.¹ and Mesibov, R.²

¹Department of Terrestrial Zoology, Western Australian Museum, Locked Bag 49, Welshpool DC, Western Australia 6986; ²Queen Victoria Museum and Art Gallery, Launceston, Tasmania 7250.

Millipedes are an ancient group of terrestrial animals with records of specimens from the Silurian period. Of the eight native orders of millipedes found in Australia, Polydesmida is the most speciose. The largest family of Polydesmida, Paradoxosomatidae, is represented by some 170 named species in Australia, but hundreds more are yet to be described. Throughout the family, species are remarkably uniform in general appearance. Despite this similarity of form, there are a number of very clearly defined paradoxosomatid genera in Australia, some with numerous species, found in almost all regions of Australia. They occur in the harshest environments from sea level to mountain tops and from tropical rainforest to deserts. Yet, to date, and perhaps strangely, there are no records of native paradoxosomatids from the Northern Territory, even though the equivalent ecological regions in Africa, South East Asia and South America have high millipede abundance and diversity. In addition, paradoxosomatids are in no sense loyal to Australian habitats: some species thrive equally as well in exotic gardens and plantations as they do in native vegetation. Despite their far-ranging occurrence, interestingly, species typically have very small well defined geographic ranges that overlap very little with the ranges of other species from the same genus. It is not yet clear how these discrete distributions originated and how they are maintained.

Combining sky and earth: three ant species integrate celestial and terrestrial sources of directional information

Cheng, K., Legge, E.L.G., Wystrach, A. and Spetch, M.L.

Department of Biological Sciences, Macquarie University, Sydney, NSW 2109.

Insects typically use celestial sources of directional information for path integration, and terrestrial panoramic information for view-based navigation. But on theoretical grounds, it can be advantageous to use both sources for determining direction. We review 3 cases providing evidence for the integration of celestial and terrestrial cues. Reid et al. (2011) used polarised filters to change the dictates of the sky compass, on nocturnal *Myrmecia pyriformis*. They found compensation for the rotated sky compass, but not full compensation, suggesting that panoramic cues were used as well. Collett (2012) displaced desert ants *Cataglyphis fortis* on their two-legged outbound journey (a stretch in a channel followed by a stretch on open field). After displacement, ants headed in an intermediate direction between the dictates of path integration (celestial compass) and terrestrial cues. We (Legge et al. under review) displaced desert ants *Melophorus bagoti* at a feeder in their natural visually-cluttered habitat prior to their homing journey. The dictates of path integration based on a celestial compass (feeder-nest direction) then conflicted with the dictates of view-based navigation based on the terrestrial panorama (release point-nest direction). Ants headed in a direction intermediate between the dictates of celestial and terrestrial sources of directional information. We conclude that ants can integrate the dictates of celestial and terrestrial information in determining their initial heading.

Can an extra lobe of the cricket salivary gland act as an alternative endocrine transport system?

Cooper, P.D.¹ and Campos, M.P.^{1,2}

¹The Australian National University, Canberra, ACT 0200; ²São Paulo State University, Botucatu, SP, Brazil

Insect hormones have traditionally been considered to be distributed throughout the body either as a result of haemolymph movement or as neurohormones through the various neurohaemal organs. Two of the major producers of hormones are the corpora cardiac and corpora allata in the head segment, near the oesophagus and below the brain. However, the time for hormones to move through an insect body by haemolymph movement may take as long as 2 hours in insects with a mass > 0.5 g. However energy supply for flight and singing that are typical of some of the larger insects occur on the order of 0.5 h. We describe the presence of a pair of lobes of the thoracic salivary glands in the head that are located surrounding the retrocerebral complex (corpora cardiac, corpora allata, hypocerebral ganglia) in the cricket, *Teleogryllus commodus* Walker (Orthoptera:Gryllidae). These lobes are present in both genders and in instars with head capsule widths of 0.1 mm. Serotonergic nerves innervate the lobes, similar to thoracic lobes, indicating that secretion may be under nervous control,. However, the presence of adipokinetic hormone is found only in the ducts of the glands of these lobes, suggesting that water-soluble hormones may be transported from the head directly to the thorax through the salivary gland duct system. We suggest that these lobes may constitute a new method for the movement of hormones from the head into the rest of the insect body.

Australians in the Andes

Cranston, P.S.¹ and Krosch, M.N.²

¹Evolution, Ecology and Genetics, Research School of Biology, Australian National University, Canberra, ACT 0200; ²Centre for Water in the Minerals Industry, Sustainable Minerals Institute, The University of Queensland, Brisbane, QLD 4072.

Molecular population genetic studies on selected Australian Chironomidae (Diptera) have revealed subtle, fine-scale barriers isolating populations (deeply divergent mitochondrial lineages, perhaps equating to species) in discrete refugia. In eastern Australia these were inferred to be due to Miocene age vicariance related to endemism in habitat fragmentation. Similarly orientated studies in New Zealand's South Island and Patagonian South America also showed several highly divergent (2.0–10.5%) lineages of late Miocene–Pliocene age within each taxon. However, these were not geographically localized, lacking endemism and several lineages were widespread.

Molecular phylogenetic studies testing the gondwanan vicariance hypothesis to explain austral patterns in diverse groups of Chironomidae have given us with additional data. This relates especially to taxa distributed across the central-southern Andes. This extensive mountain chain runs the length of South America, and divides the continental watershed into waters flowing west into the Pacific from those east-flowing into the South Atlantic Ocean. Chironomidae, as aquatic insects with larvae developing in lotic waters and with short-lived adults would be expected to show population divergence across the catchment given such an 'obvious' vicariant barrier. However no evidence was found for genetic partitioning on the basis of slope of the ranges – the Andes at this latitude formed no barrier to west-east dispersal. We discuss some possible explanations of this unexpected results.

Using plant odours to control polyphagous pests – could we benefit from a different perspective?

Cunningham, P.

School of Earth, Environmental and Biological Sciences, Queensland University of Technology, Brisbane, QLD 4001.

Research into using plant odours to attract or deter herbivorous insects generally begins with great optimism and ends with scientists banging their heads against a brick wall. This may be partly because we are not giving enough consideration to the way insects perceive plant odours in nature, and the evolutionary forces that shape their responses towards host plants. In this talk, I will take a closer look at olfaction in polyphagous insects, drawing on my behavioural research on the moth, *Helicoverpa armigera*, and recent work on the tephritid fruit fly, *Bactrocera tryoni*. I propose that what we see as polyphagy could equally be viewed as a form of specialization (in *H. armigera*, towards flowering hosts, and in *B. tryoni*, towards ripe fruits), and that this alternative perspective may help in our selection of volatiles to be used in lures. In support of this, I will present results from my behavioural studies on adult *B. tryoni*, showing how these flies are strongly attracted to suites of volatiles that are associated specifically with fruit ripening. Finally, I will present initial results from my collaborative work with the University of Stockholm, Sweden, where we are aiming to link behavioural studies on insect olfaction with optical imaging of the insect antennal lobe. By studying the mechanism behind the behavior we hope to get a new insight into why these insects prefer some volatile blends over others. This could lead to a novel way of designing odour lures for controlling some of the world's worst insect pests.

Phenology of a bee community in an agricultural landscape near Canberra

Cunningham, S.A.¹, Neave, M. J.¹ and Batley, M.²

¹CSIRO Land and Water Flagship, Box 1700, Canberra, ACT 2601, Australia; ²The Australian Museum, Sydney, New South Wales, Australia

There is increasing recognition that the ecosystem service of crop pollination, provided by wild bees, is important to many crops, including broadacre crops grown in Australia such as canola and faba beans. Maximising the benefits from wild pollinators requires an understanding of their patterns of abundance in time and space in managed landscapes. We surveyed bees over a 5 year period at a single location near Canberra, which was adjacent to cropped paddocks and 500m from suburban housing development. Bees were collected using a blue vane trap, which attracts bees with a visual stimulus only. We collected 1880 individuals comprising 28 species. Halictid bees dominate, accounting for 92% of individuals. Four of the five most abundant species were in the genus and *Lassioglossum*, in particular *L. cognatum* (32%) and *L. clelandi* (27%) and *L. lanarium* (13%). Both species richness and abundance typically peaked in October-November, with a secondary peak in February-March. The only large bees (intertegular span >2mm) were from the families Apidae or Megachilidae, and were more abundant later in the season (after January). We examined species-specific phenologies for the six most abundant species. *L. clelandi* has a clear single peak in the early part of the season (Sept-Oct). In contrast *L. hemichalceum* (February-March) and *Apis mellifera* (March) had clear single peaks late in the season (after January). The remaining three (*L. cognatum*, *L. lanarium*, *H. sphecooides*) had bimodal patterns of abundance, with an early and late peak, and a low point in January. In addition to these seasonal patterns we observed that trapping rates were lower in periods of higher rainfall, probably reflecting reduced opportunities for flight.

Impact of UV-A radiation on the performance of aphids and whiteflies and on the leaf chemistry of their host plants

Dader, B., Moreno, A. and Fereres, A.

Instituto de Ciencias Agrarias-Consejo Superior de Investigaciones Científicas (ICA-CSIC), Calle Serrano 115 dpdo., 28006 Madrid, Spain.

UV radiation regulates a multitude of plant chemistry processes and morphogenesis. Besides, UV radiation directly plays a major role on insect fitness and indirectly affects their success via changes in plant chemistry. In this study, we hypothesize that UV is central to the trophic relationships between the two key pests *Myzus persicae* Sulzer (Hemiptera: Aphididae) and *Bemisia tabaci* Gennadius (Hemiptera: Aleyrodidae) and their hosts pepper (*Capsicum annuum* L.) and eggplant (*Solanum melongena* L.).

Potted peppers and eggplants were exposed from seed to supplemental UV-A. At a 10- and 4-true leaf stage for peppers and eggplants, respectively, plants were infested by aphids and whiteflies. Insect pre-reproductive period, offspring and growth rates were calculated as well as host plant chemistry. Effects on plant chemistry and growth (stem height, leaf area and dry weight) were monitored over 7 and 12 weeks for pepper and eggplants, respectively. At intervals leaf material was also harvested and analyzed for secondary metabolites, soluble carbohydrates, amino acids, proteins and photosynthetic pigments.

Both plant species responded to UV with shorter stems. In pepper, there were higher leaf secondary metabolites, amino acids, total content of protein and sucrose in response to UV. For eggplants, chemistry was unaffected by UV exposure except for photosynthetic pigments. Our results demonstrate consistent but species-specific effects showing that pepper is sensitive to UV but eggplants appear more tolerant. UV exposure increased aphid population growth in parallel to pepper leaf sugars and amino acid content. Conversely, for whitefly, UV-A radiation had negative effects on insect performance with longer pre-reproductive period and a lower larval number. Our results demonstrate species-specific responses highlighting direct negative effects on whitefly and indirect positive effects of UV-A radiation on aphids via plant chemistry.

Evolution of *kdr*-type resistance in *Cimex*: who you will be sleeping with in the future?

Dang, K.^{1,2}, Toi, C.S.¹, Lilly, D.G.¹, Bu, W.² and Doggett, S.L.¹

¹Department of Medical Entomology, Pathology West, ICPMR, Westmead Hospital, Westmead, NSW, 2145, Australia; ²Institute of Entomology, Nankai University, Tianjin, 300071, China.
Email: Stephen.Doggett@health.nsw.gov.au

An understanding of the resistance mechanisms within bed bugs (Hemiptera: Cimicidae: *Cimex* spp.) is essential in order to develop effective control strategies. To date, knockdown resistance (*kdr*) investigations have largely been limited to modern strains of *Cimex lectularius* L. (common bed bug) within the USA. No research has been undertaken on museum specimens, which may give insights on when *kdr* resistance evolved, or on disparate *C. lectularius* populations outside the USA. No data is available on *kdr* in the tropical bed bug, *Cimex hemipterus* (F.) Investigations on *kdr* mechanisms were undertaken on modern and museum Australian *C. lectularius*, as well as on *C. hemipterus* collected around the world.

For *C. lectularius*, both the V419L and L925I mutations were identified, however a novel putative *kdr* mutation, I936F, was found in specimens dating back to 1994. This mutation has largely disappeared from modern bed bug strains, only showing in one Adelaide strain. Insecticide efficacy investigations suggest that this strain is more susceptible than those possessing other *kdr* mutations, which may account for its low frequencies today.

For *C. hemipterus*, none of the strains possessed the *C. lectularius* *kdr* mutations, however *C. hemipterus* had one (L1014F) or both of two (M918I and L1014F) novel putative *kdr* mutations.

The investigations revealed that there have been waves of *C. lectularius* invading Australia with different *kdr* mutations, with weakly resistant strains being replaced with more resistant strains. The *kdr* mutations in *C. hemipterus* clearly evolved independently from *C. lectularius*, which demonstrates the concomitant insecticide pressures that have induced the development of resistance. This information could be a portent for the future; with treatment failures and an over reliance on certain products, bed bugs with even a greater level of resistance may evolve in the future. Such research reinforces the need for an IPM approach to bed bug management.

Attract-and-kill for the diamondback moth, *Plutella xylostella* in canola

Del Socorro, A.¹, Gregg, P.¹, Binns, M.¹, Baker, G.², and Gulliver, S.³

¹University of New England, Armidale, NSW 2351; ²South Australian Research and Development Institute, Urrbrae, SA 5064; ³AgBitech Pty Ltd, Toowoomba, QLD 4350.

We have previously developed an attractant based on synthetic plant volatiles targeting the adults of the noctuid pests *Helicoverpa* spp., and the product (Magnet®) has been registered for cotton, sweet corn and green beans. With funding from the Grains Research and Development Corporation (GRDC) and AgBitech Pty Ltd, we investigated the feasibility of attract-and-kill as a novel approach to manage the diamondback moth, *Plutella xylostella* (Lepidoptera: Plutellidae) in canola. A small-scale field trial conducted on forage rape at Victor Harbor, SA in 2013, demonstrated that the attract-and-kill using Magnet® and the insecticide spinetoram (Success Neo®) worked for this species. It also showed that pheromone traps can be used to monitor DBM numbers in treated and control plots. Following this, we conducted a large-scale field trial involving aerial application of more than 600 ha of pre-flowering canola at Cummins, SA which showed a major reduction in DBM adult numbers in treated fields in comparison with the untreated and distant control fields.

Sensory-motor integration in the flight behaviour of *Drosophila*

Dickinson, M.

Division of Biology and Bioengineering, Caltech, Pasadena, CA, USA 91125

To generate complex behaviours, insects must integrate information on different spatial and temporal scales. On a fast scale, the nervous system must transform sensory information into a set of motor commands to modify behaviour on a moment-by-moment basis. Over longer time scales, insects must modify their behavioural responses to sensory stimuli to produce context-appropriate actions. Exhibiting the correct actions over space and time is essential for generating complex behavioural sequences such as those involved in courtship or food search. My laboratory has been using the fruit flies as a model system for studying sensory motor integration on these different temporal scales. A common strategy for maintaining a straight course is to measure the rate of rotation and steer in such a way to maintain that rate at zero. In such a system, the addition of an integral term depending on past values of the sensory input is needed to eliminate steady-state error. Consistent with this principle, the optomotor responses of flies follow a time course exhibiting integration of the motion input. To investigate the cellular basis of this effect, we have performed whole-cell patch-clamp recordings and calcium imaging. Our results suggest that calcium accumulation in cell terminals provides a biophysical mechanism for implementing integration. When searching for food, odour provides useful information to over long distances whereas visual cues are only useful at close range. We have developed automated techniques for tracking the behaviour of flies in wind tunnels to study how they integrate olfactory and visual cues. Our results show that flies use an iterative set of reflexes to accurately follow odour plumes. In addition, contact with attractive chemicals induces a behavioural state change so that the fly becomes attracted to small visual objects. This odour-induced visual salience serves to guide the fly to the source of the odour.

Medical entomology in Australia, 1964-2014

Doggett, S.

Department of Medical Entomology, CIDMLS, Pathology West, Westmead Hospital, Westmead, NSW 2145.

Australia has had a rich history in the field of Medical Entomology, in both practical and applied research, particularly over the last 50 years, which has placed the nation on the world stage.

Innovations in taxonomy has seen the change from the classical taxonomists, including Marks, Dobrotworsky and Lee (mosquitoes), Kettle, Dyce and Debenham (ceratopogonidae) and ticks (Roberts), to the development of proteomics (including Bryan, Sweeney and Foley on mosquitoes), to modern molecular based taxonomy (Beebe again on mosquitoes).

The emphasis of research over the last 50 years in Medical Entomology has focused on mosquitoes due to their nuisance biting and propensity to transmit infectious agents. This includes the mapping of malaria vectors (Sweeney and colleagues), mosquito biology (notably Russell & Kay), investigations into mosquito borne disease, surveillance and vector competence (most notably Marshal, Mackenzie & colleagues, Cloonan, Russell & colleagues, and van den Hurk), saltmarsh mosquito management (Dale and Easton in runnelling, Whelan and Muller in practical control), constructed wetlands design to minimise vectors (Russell and Webb), repellents (Frances), and to modelling (Williams).

In more recent years, many of the research initiatives relating to Dengue and the control of its main vector, *Aedes aegypti*, have been led by Ritchie and colleagues, with the development of such innovations as lethal and biodegradable ovitraps, and new surveillance technology. More recently, Gates Foundation money has been provided to Scott and colleagues to investigate the use of the intracellular bacteria, *Wolbachia*, to minimise Dengue transmission.

Outside of mosquitoes, researchers such as Tovey have investigated dust mites, while various workers have examined ticks in their impact upon human morbidity (Graves on rickettsia, Russell *et al.* on Lyme disease, van Nunen on mammalian meat allergies). Geary has led the way in providing a world class pathology service and was the first to employ disinfected maggots for wound debridement. Finally, I have proudly worked with a team who were the first in the world to develop an industry standard to combat the global bed bug resurgence.

This presentation will focus on the Medical Entomology researchers, their research and achievements, during the 50 year history of the Australian Entomological Society.

AES Insect digital macrophotography workshop

Doggett, S.L.¹ and Zborowski, P.²

¹Department of Medical Entomology, CIDMLS, Pathology West – ICPMR, Westmead Hospital, Westmead NSW 2145. ²

Ever wanted to take great insect close up shots but were not able to quite capture that ‘golden moment’? Insect photography is one of the most challenging forms of photography, requiring highly specialised equipment and a thorough understanding of photographic technique. Quality insect photographs are essential for taxonomic purposes and a great image has huge educational benefits by displaying the beauty of the miniature world only seen by a select few.

A 1.5hr insect macrophotography workshop will be held in conjunction with the 50 year anniversary of the Australian Entomological Society, conducted by two highly published and award winning insect photographers, Paul Zborowski and Stephen Doggett.

The workshop will enable you to capture better pictures. Learn from the basic to the advanced. Basic topics include; photographic theory, composition, macro equipment, the use of flash, selecting the right tripod, to proper studio and field techniques.

More advanced topics include photostacking, hi-speed photography, to cross polarisation (for those beetle lovers who hate reflections). A quick overview of digital post processing will be provided so that you can get the best out of the image that you have captured.

Various digital images will be displayed with an explanation of how they were captured.

It will be possible to see and use a range of macro equipment and so bring your insects and memory card (compact flash or SD card).

Revised fruit fly quarantine distances for domestic and international trading

Dominiak, D.¹ and Fanson, B.²

¹New South Wales Department of Primary Industries, 161 Kite Street, Orange, NSW 2800 Australia.
E-mail: bernie.dominiak@dpi.nsw.gov.au; ²School of Life and Environmental Sciences, Deakin University,
Geelong, VIC 3216, Australia

Background: After the loss of area freedom for Queensland fruit fly, the current suspension distance is 15 km, an area covering 707 sq km. This rule was devised in the early 1990's when the underlying science was lacking. This large suspension zone cause significant environmental and economic impacts on growers and exporters. Given the advances in technology, data storage and statistical analyses, it is timely to review past outbreak records and evaluate the merits of the current suspension distance.

Methods: We reviewed the trapping records of wild flies from 48 incursions in the New South Wales portion of the Fruit Fly Exclusion Zone between 2002 and 2010. The exponential, normal, shifted normal, inverse square and Cauchy distributions were used to model the actual distributions and to calculate suspension distances. Several risk standards were used to estimate appropriate levels of protection.

Results: The mean dispersal of wild flies generally ranged between 200 to 500 m. The exponential model fitted the data best and predicted a suspension zone of about 4 km. This equates to a suspension area of about 50 sq km, compared to the current 707 sq km or a reduction of 93% of the area required to be treated for market access.

Conclusion: The new methods used here for calculating suspension zones indicate that, based on area, the current suspension zones could be dramatically reduced. The amount of pesticides entering the food chain or the environment could be reduced by up to 93%, or the carbon footprint could be reduced by 93%. These new methods are currently being considered as a trade standard for Australia domestic trade. Once a reduction is accepted domestically, the challenge will be to gain international recognition of this new science to justify less punitive international trade agreements.

What does Queensland fruit fly, *Bactrocera tryoni* (Froggatt), do when the sun goes down?

Ekanyake, E.W.M.T.D.¹, Clarke, A.R.^{1,2} and Schutze, M.K.^{1,2}

¹School of Earth, Environmental and Biological Sciences, Science and Engineering Faculty, Queensland University of Technology, Brisbane, Australia; ²Plant Biosecurity Cooperative Research Centre, Bruce, Australian Capital Territory, Australia

Bactrocera tryoni, the Queensland fruit fly (Qfly), is Australia's worst horticultural pest insect. While much is known of its mating system from small cage laboratory studies, little is known about how the sexes come together to mate at dusk. In replicated, large field cage mating studies, we asked: i) does Qfly exhibit 'landmarking' behaviour by using tall trees as mate-rendezvous sites; and ii) do males establish lek territories prior to female arrival, as has been routinely inferred for this species. For each of seven replicates, 125 sexually mature virgin males and females were released prior to dusk in a 7 X 7 X 4 m field cage containing two tall (2.7 m) and two short (2.0m) artificial trees. Five-minute counts of individual flies and mating pairs on trees were made, along with recording instances of male-male aggression and male calling (wing vibration and pheromone release)behaviour. Ninety-nine percent of all mating pairs across replicates (n = 85) occurred on tall trees; only 1% of couples were recorded from short trees. The proportion of individual females in tall trees prior to dusk was greater than that of males ($60 \pm 3\%$ vs $40 \pm 3\%$), but within ten minutes of dusk males arrived in large numbers such that they dominated females ($68 \pm 5\%$ vs $32 \pm 5\%$). Among those males, most 'called' ($88 \pm 5\%$) but few engaged in male-male aggressive behaviour ($12 \pm 5\%$). The preference for tall trees is supportive of Qfly using a 'land-marking' system to initially bring the sexes together. The greater number of females at mating sites before dusk, with little male-related territorial behaviour prior to courtship, questions the long-held view that Qfly has a lek-based mating system.

The molecular phylogeny of the fungal spore-feeding Thrips Subfamily Idolothripinae (Thysanoptera; Phlaeothripidae).

Eow, L.X.¹, Mound, L.A.² and Cameron, S.L.¹

¹Earth, Environment & Biological Sciences School, Science & Engineering Faculty, Queensland University of Technology, GPO Box 2434, Brisbane, QLD 4001; ²CSIRO Entomology, GPO Box 1700, Canberra, ACT 2601.

The subfamily Idolothripinae (Thysanoptera; Phlaeothripidae) contains over 700 species of presumably spore-feeding thrips, closely associated with dead plant materials in the tropics and subtropics. A traditional tribal classification of the 80 recognized genera within this subfamily consists of two tribes and nine subtribes. The classification is based on eight morphological characters that only provide relationship hypotheses for four out of the nine subtribes, while the rest are uncertain. Furthermore, difficulties in taxonomy exist where diagnostic characters commonly overlap between genera. The aim of this study is to estimate a phylogeny of the Idolothripinae using molecular data. Five genes (mitochondrial cytochrome oxidase I, Histone 3, Tubulin-alpha I, 18S rDNA and 28S rDNA) were sequenced for 39 species. Together with data from GeneBank, the dataset represented all nine subtribes and 30 genera. The concatenated dataset was analysed using Bayesian inference and Maximum Likelihood. The implication of this molecular inference on the traditional classification system based on morphology will be discussed. The phylogenetic framework provided here is important to give insights for issues revolving around morphological characters are not always adequate in taxonomic or classification resolution, and also facilitate the study of evolutionary history of the tube-tailed thrips (Thysanoptera, suborder Tubulifera).

Phylogeny and biogeography of Boganiidae (Coleoptera, Cucujoidea)

Escalona, H.E.¹, Lawrence, J.F.¹, Slipinski, A.¹ and Wanat, M.²

¹CSIRO, Australian National Insect Collection, GPO Box 1700, Canberra, ACT 2601, Australia; ²Museum of Natural History, University of Wrocław, Sienkiewicza, Wrocław, Poland.

The phylogeny of the cucujoid family Boganiidae is inferred for the first time based on an analysis of 102 morphological characters (70 adult and 32 larval), utilizing the parsimony phylogenetic software TNT. The analysis resulted in a monophyletic Boganiidae placed in Cucujoidea and divided into two main clades, Boganiinae and Paracucujinae, each clade was supported by a series of synapomorphies. The Boganiinae genera recognized were *Afroboganium* Endrödy-Younga & Crowson and *Boganium* Sen Gupta & Crowson, while Paracucujinae includes *Paracucujus* Sen Gupta & Crowson, *Metacucujus* Endrödy-Younga & Crowson, *Athertonium* Crowson new placement and the New Caledonian *Dzumacium caledonicum* gen. n., sp. n. New specimen data and biological information for the Australian taxa are summarized with overviews on biogeography, the relationships of Boganiidae with the fossil jurassic beetle *Parandrexia* Martynov (Parandrexidae) are discussed. Two new species of *Boganium*, primarily from the Australian Malle are described: *B. malleense* sp. n. and *B. medioflavum* sp. n., new host records for *Boganium* include *Eucalyptus gracilis* F. (Myrtaceae). Adults and larvae of *Paracucujus rostratus* Sen Gupta & Crowson are redescribed, having been collected in male cones of the cycad *Macrozamia riedeli* (Gaudich) when the inflorescence is shedding pollen. *Athertonium parvum* Crowson is redescribed and *Athertonium williamsi* sp. n. described from coastal New South Wales. Host records for *Athertonium* include *Syzygium smithii* (Poir.) Nied. (= *Acmena smithii* (Poir.) Merr. & L. M. Perry), *Rhodomyrtus psidioides* (G. Don) Benth and *Waterhousia floribunda* F. Muell. B. Hyland in the Myrtaceae, *Elaeocarpus obovatus* G. Don and *E. reticulatus* Sm. in the Elaeocarpaceae, *Caldcluvia paniculosa* F. Muell. Hoogl. in the Cunionaceae, *Toona ciliate* M. Roem in the Meliaceae and *Cryptocarya microneura* Meisn. in the Lauraceae. The host plant associations of *Dzumacium* remain unknown.

Host-finding in psyllids: are *Eucalyptus*-feeding psyllids anosmic?

Farnier, K. and Steinbauer, M.J.

Department of Zoology, La Trobe University, Kingsbury Drive, Melbourne, VIC. 3086

Psyllids are well represented in the Southern hemisphere and especially in Australia where there are approximately 366 described species in 58 genera. The greatest number of species occurs on *Acacia* and *Eucalyptus* hosts. Although eucalyptus psyllids accept novel plant species, their endemic host range is generally restricted to a very limited number of eucalypts. Unfortunately, the means by which eucalyptus psyllids locate their host(s) vegetationally diverse forests has not been investigated.

Earlier work conducted with Northern hemisphere species suggests that, like some aphids, psyllids rely on olfaction to migrate between alternate seasonal hosts. Despite electrophysiological evidence suggesting that psyllid sensilla perceive a limited range of volatile plant compounds (i.e. green leaf volatiles and terpenoids), behavioural confirmation of olfaction-driven attraction to host plants remains scarce.

We studied the chemical profile of oil and headspace samples of the leaves of three *Eucalyptus* species (i.e. *E. globulus*, *E. camaldulensis*, *E. kitsoniana*) utilized by four different species of psyllid (*Ctenarytaina eucalypti*, *C. bipartita*, *Anoeconeossa bundoorensis* and *Glycaspis brimblecombei*). We found quantitative and qualitative differences in terpenoid composition between species suggesting that volatile metabolites may provide olfactory cues specific to preferred host. We also examined psyllid responses to host odours in Y-tube olfactometer bioassays. Surprisingly, none of the species tested exhibited chemotaxis toward host odours suggesting that psyllids do not rely on olfaction to orient to different *Eucalyptus* species.

Potential alternate functions of olfaction in psyllids, including the possibility that other plant traits provide more reliable host location cues will be addressed. The limitations of the studies of host alternating Hemiptera will also be discussed.

Carrion Café –using insects to determine post mortem intervals in Queensland

*Farrell, J.F.*¹, *Whittington, A.E.*² and *Zalucki, M.P.*¹

¹The University of Queensland, Brisbane, Qld 4072; ²The University of Florida, Gainesville FL32610, USA.

Forensic entomology and necrophagous insect succession have been extensively studied in southern Australia, however long-term data describing insect taxa associated with decomposition are scarce in northern and sub-tropical Australia. A succession study of the invertebrates associated with carrion in south-east Queensland was conducted over two years to investigate seasonal and annual variation. Colonisation, successional patterns, species diversity, relative abundance of sarcosaprophagous insects, and their potential as forensic indicators were investigated. Data were collected from 64 pig carcasses (*Sus scrofa*) decomposing in open grassland and timbered peri-urban habitats at a field site on the western Darling Downs.

Caloglyphus berlesei (Acari) outnumbered all other necrophagous invertebrates, however the Calliphoridae and Sarcophagidae (Diptera) are the most useful forensic indicators in terms of specimens observed, collected and reared from the carcasses. The primary colonisers of the carcasses varied seasonally, and seven calliphorid (blow fly) and four sarcophagid (flesh fly) species were identified as forensically significant for the region. The most important calliphorids and sarcophagids from a forensic viewpoint were *Calliphora augur*, *C. stygia*, *Chrysomya megacephala*, *Sarcophaga impatiens*, *S. aurifrons*, *S. froggatti* and *S. praedatrix* because they indicated clear seasonal preferences and bred in the pig carrion. The suites of species occurring as primary and secondary invaders in Queensland are quite different to those recorded in southern and Western Australia. The implication is that succession data generated elsewhere in Australia could not be reliably used for post mortem interval estimations in Queensland.

Comparative data were collected on an opportunistic basis from road-kill, farmed livestock carcasses in the region, and from human remains in the Queensland Health Forensic and Scientific Services mortuary in Brisbane. Similar succession patterns and dominant species were observed over a range of vertebrate remains in south-east Queensland.

Towards biological control of a generalist insect herbivore: the activities of generalist parasitoids are segregated between crop and adjacent non-crop habitats

Feng, Y.¹, Kravchuk, O.¹, Yazdani, M.¹, Sandhu, H.², Wratten, S.D.³ and Keller, M.A.¹

¹School of Agriculture, Food & Wine, University of Adelaide SA 5005, Australia; ²School of the Environment, Flinders University, PO Box 2100 Adelaide SA 5001, Australia. ³Bio-Protection Research Centre, PO Box 85084, Lincoln University, Lincoln 7647, New Zealand.

Theory predicts that niche partitioning plays a key role in the coexistence of similar species. Specifically, a spatially heterogeneous competitive environment can facilitate species' coexistence when intrinsic differences between competing species are insufficient to general specific niches for species. We hypothesise that in an agro-ecosystem, natural enemies that attack the same hosts can co-exist through partitioning between crop and non-crop habitats, so native vegetation adjacent to crops in an agroecosystem may not always be the source of natural enemies that are active in crops. We experimentally measured the parasitism rate of larval *Epiphyas postvittana* (Walker) (Lepidoptera: Tortricidae) in both vineyards and the adjacent vegetation at six and eight sites in two consecutive years. Potted plants infested with young larval *E. postvittana* were placed in a vineyard and the adjacent vegetation for two weeks. These larvae were then recovered and reared in the laboratory to measure parasitoid diversity and parasitism rates. Moreover, local leaf rollers were regularly collected at each experimental site to assess their natural population and related parasitoids. Parasitised hosts were then identified using a PCR-based protocol to determine the parasitoids' host. Our results support species-specific niche partitioning between competing parasitoids in crop and adjacent non-crop habitats. The parasitoid *Therophilus unimaculatus* (Turner) (Hymenoptera: Braconidae) was most active in non-crop native vegetation, whereas *Dolichogenidea tasmanica* (Cameron) (Hymenoptera: Braconidae) parasitised the most larvae in the vineyards. A number of biotic and abiotic factors in vineyard ecosystems including the plants, cyclic seasonal change, landscape characteristics, alternative hosts, host density and abiotic factors present in the vineyards and the adjacent vegetation habitats can contribute to generate spatial niche differences between vineyards and the adjacent natural habitats. These can facilitate the coexistence of parasitoids species that competing for the same hosts.

The history of the Australian Entomological Society

Fletcher, M.J.

Orange Agricultural Institute, Forest Road, Orange, NSW 2800

In this presentation, I will chart the history of our Society from early attempts to establish a national entomological society which first occurred in the 19th century and continued until the 1960s when meetings of entomologists attending ANZAAS conferences in 1962 and 1964 resolved to form an Entomological Society of Australia. The Society was formally launched in Hobart on 17 August 1965. I will highlight the visionaries of the time who ensured that the fledgling society would be a truly national society even extending into the international community by hosting the International Congress of Entomology in 1972 and 2004. I will look at the evolution of the society's publications, its awards and some of the controversial issues into which it has delved. I will conclude with an explanation of why after 49 years we are up to Volume 53 of our Journal, up to Volume 50 of our newsletter but only celebrating the 45th Annual General Meeting.

Auckland City of Incursions: where the show never stops

Flynn, A.R.

Ministry for Primary Industries, PO Box 2095, Auckland 1140, New Zealand

Not surprisingly for a large city, Auckland features significantly as a locality for records of New to New Zealand organisms. Auckland's airport and sea port process large volumes of passenger and commodity traffic, there is a high density of facilities receiving containerised imports, it is home to the international mail centre and numerous private vessels arrive from Australia, neighbouring pacific islands and further afield. In the last 32 years there have been approximately 170 new insect records reported to the Ministry, 94 (55%) from Auckland. This is an average of three per year. This presentation reviews an historical selection of these insect incursions, discusses similarities and lessons learnt.

Plant traits influence the functional role of two understory shrubs for native insects

Forbes, R.J. and Steinbauer, M.J.

Department of Zoology, La Trobe University, Melbourne, VIC 3086, Australia

Plant traits linked to their nutritional quality influence the abundance and species richness of insects they support. Numerous studies have shown that nitrogen is essential for herbivorous insects. However, herbivore performance is likely optimised by the acquisition of multiple macro-nutrients. Defence mechanisms such as degree of sclerophylly (leaf toughness) and concentrations of plant secondary metabolites (e.g. phenols) determine nutritional quality by defining the balance between beneficial and antagonistic dietary elements. We measured concentrations of five macro-nutrients (N, P, K, Ca, Mg) as well as total phenol contents of two understory shrubs (*Cassinia arcuata* and *Daviesia ulicifolia*) to study their relative contributions to the abundance and diversity of insects on each plant. *C. arcuata* is a member of the Asteraceae family (non-legume) while *D. ulicifolia* belongs to the Fabaceae family (leguminous species). *C. arcuata* supported 2709 insects belonging to 203 species whilst *D. ulicifolia* supported 847 insects belonging to 152 species. The leaves of *C. arcuata* are small, have short lifespans and are low in nitrogen and phenols. Conversely, *D. ulicifolia* leaves are larger, have long lifespans (tough leaves) and are higher in nitrogen and phenols. The traits of *C. arcuata* fit those of an early colonising species whereas those of *D. ulicifolia* better fit those of a climax species. Insect abundance and species richness on *D. ulicifolia* was best explained by phenol content and canopy volume, whilst canopy volume alone best explained insect abundance and species richness on *C. arcuata*. In native woodlands, the primary functional role of *C. arcuata* is as a shelter plant while the functional role of *D. ulicifolia* is as a food and shelter plant.

Examining the effects of distance from mature forest and succession on beetle community recolonisation using species, functional trait and phylogenetic approaches

Fountain-Jones, N.

PHIL CARNE PRIZE WINNER

How mature forest impacts adjacent disturbed forest, or "forest influence", is a poorly understood ecological concept that is important for sustainable forest management worldwide. Forest influence enables mature forest adapted species to recolonise adjacent disturbed forest by providing suitable conditions and habitat and sources populations for re-establishment. Beetles have been found to be responsive to forest influence effects, yet the mechanisms that underlie re-colonisation by old-growth adapted species are largely unknown. Forest influence is likely to change as forest succession proceeds, but little is also known about how beetle communities respond to forest succession, what forces are important, and to what extent beetle communities recover and become comparable to mature forest.

Here I will demonstrate that forest influence is important for beetle communities as it alters the successional trajectory of adjacent logged forest, and provides suitable conditions over time for beetle species to recolonise, including species considered mature forest indicators. Furthermore, using a novel combined species abundance, functional trait and phylogenetic approach, I explore the multidimensional forces driving beetle community successional change and how it differs between beetle trophic groups. I illustrate that the sets of traits responding to succession varies according to trophic position, as does the environmental and evolutionary forces that shape them. The recovery of functional trait and phylogenetic composition is also dependent on trophic group and in some instances trait and phylogenetic community recovery precedes species recovery.

Exotic pests and biological control in New Zealand broadacre pasture; success hoisted by its own petard?

Goldson, S.L.¹, Barratt, B.I.P.² and Tomasetto, F.¹

¹AgResearch Lincoln, Private Bag 4749, Christchurch 8140, New Zealand; ²AgResearch Invermay, Private Bag 50034, Mosgiel, New Zealand

This contribution examines the implications of and possible reasons for, the extraordinary susceptibility of New Zealand's broad-acre pastures to invasive exotic insect species that have so often become severe pests. This propensity is usually attributed to a lack of biotic resistance that arises from species-paucity found in New Zealand's large area of improved grasslands. These pastoral ecosystems areas comprise very incomplete transplants of European grassland plant species. In the same vein, this same lack of biotic resistance may also provide an explanation as to why introduced classical biological agents (parasitoids) have been so successful. It can indeed be reasonably argued that there is a good representation of New Zealand's native fauna in these transplanted ecosystems thereby creating biodiversity. However, these species may not comprise the mix of generalist predators, spiders and parasitoids usually found in the pest species' native ranges and irrespective, the question remains as to why exotic invasive species are so successful in New Zealand pastures. Finally all is not well in pasture biological control environment. In spite of the outstanding (and celebrated) biological control successes of invasive weevil species in the pastoral ecosystem, there is now emerging evidence that at least some may be short-lived. Such loss of susceptibility of pests to biological control agents is indeed a very rare event, but the literature does indicate that there are certain ecological and behavioural settings that predispose towards it. The contribution discusses how these factors have converged in New Zealand pastures. These ideas stand to be tested and comprise a number of working hypotheses.

Giant Willow Aphid – a new Aphid on willows in New Zealand

Gunawardana, D.N.¹, Flynn A.R.¹, Pearson, H.G.² and Sopow, S.³

¹Ministry for Primary Industries, PO Box 2095, Auckland 1140; ²Ministry for Primary Industries, PO Box 14018, Christchurch 8544; ³SCION (New Zealand Forest Research Institute), Private Bag 3020, Rotorua 3046

Giant Willow Aphid, *Tuberolachnus salignus* (Hemiptera: Aphididae) was first detected in Central Auckland in late December 2013 on crack willow. At the same time it was reported from Northland and picked up in MPI's High Risk Site Surveillance programme in South East Auckland. One of the largest aphid species, its hosts are various species of Salicaceae, willow (*Salix* spp.) and poplar (*Populus* spp.). Although its distribution is almost cosmopolitan wherever willows are grown, this is the first record in Australasia. Since its first detection in Auckland, *T. salignus* has been reported from both North and South Islands. New Zealand host records include *Salix alba* varieties, *S. fragilis*, *S. matsudana*, *S. humboldtiana*, *S. caprea*, *S. babylonica* and *Populus nigra*. Giant willow aphid forms dense colonies on the trunk and branches of hosts and can adversely impact the growth of trees. Colonies can produce large amounts of honeydew that attracts honeydew feeders such as ants and wasps. As this aphid is a recent arrival, understanding its behaviour in a new environment, host preference and management options are key areas that require study. Its biology, potential pest status, current distribution and hosts in New Zealand will be presented.

Coevolution between bacterial endosymbionts and their psyllid hosts of the *Cardiaspina* genus (Hemiptera: Psyllidae)

Hall, A.¹, Johnson, S., Cook, J. and Riegler, M.

Hawkesbury Institute for the Environment, University of Western Sydney, Locked Bag 1797, Penrith NSW 2751, Australia

Insects are one of the most diverse animal groups and one of the keys to their success is their associations with microorganisms. Understanding how insect hosts and their associates have coevolved is important to understanding their adaptive potential or limitations. Obligate vertically transmitted endocellular symbionts represent the most intimate associations and have been described in a number of insects. Psyllids are sap-feeding insects belonging to the hemipteran suborder Sternorrhyncha. They are known for their intimate interactions with bacterial endosymbionts. *Candidatus Carsonella ruddii* is the primary obligate endosymbiont of psyllids, while *Arsenophonus* is a genus of bacteria described in a range of arthropods and can be either vertically or horizontally transmitted. This study aimed to test the phylogenetic congruence of both bacteria with the phylogeny of their psyllid hosts, by using mitochondrial and nuclear host genes and at least two bacterial genes. We also aimed to test the current taxonomic classification of this significant genus of eucalypt psyllid by constructing its phylogeny. We have found that there is a lack of genetic support for the current classification of this genus, and a more comprehensive phylogenetic analysis of the *Cardiaspina* genus is required. *Candidatus Carsonella ruddii* has been found with 100% prevalence in all species of the *Cardiaspina* genus tested and appears to have a phylogeny congruent to that of its host supporting the idea of long-term cospeciation with the host. Unexpectedly, *Arsenophonus* also has 100% prevalence in almost all *Cardiaspina* species screened. This makes the genus *Cardiaspina* an ideal system in which to compare phylogenetic congruence with the insects of a vertically transmitted primary symbiont and a secondary symbiont shown in other insect groups to be transmitted both vertically and horizontally. For the first time, we have tested such coevolutionary relationships at the lowest taxonomic level (between species) in the Psylloidea superfamily.

Unravelling mummies: using molecular diagnostic tools to explore complex host-parasitoid relationships

Hall, A.¹, Steinbauer, M.², Taylor, G.³, Johnson, S.¹, Cook, J.¹ and Riegler, M.¹

¹Hawkesbury Institute for the Environment, University of Western Sydney, Bourke Street, Richmond, NSW 2753; ²Department of Zoology, La Trobe University, Melbourne, Victoria, Australia; ³Earth and Environmental Sciences, University of Adelaide, South Australia, Australia

Understanding insect predator-prey networks is extremely important to understanding population dynamics and thus has broad implications in ecosystem functioning, as well as for applications such as in biological control. Parasitoids play a major role in terrestrial food webs given their capacity to influence the population dynamics of their hosts. Host-parasitoid relationships are complex due to the diverse interactions with insect host species and also between different parasitoid species. The ways in which parasitoids interact with each other can alter their community structure and determine their impact on host populations. Recent years have seen a rise in the use of molecular diagnostic techniques for the investigation of parasitoid-parasitoid interactions. Our study aimed to use DNA barcoding and multiplex PCR approaches to investigate host-parasitoid and parasitoid-parasitoid relationships for the first time in psyllids (Hemiptera: Psyllidea). We have used the *Cardiaspina* genus of psyllids, commonly found in large numbers on several eucalypt hosts throughout Australia, as our study system. Four species of the genus collected from sites in Adelaide, Canberra and Western Sydney were included in our investigation. DNA barcoding and morphological characterisation has been used to assess the diversity and host specificity of parasitoid species for these psyllid hosts over a large geographic range. DNA extracted from mummies (parasitised psyllid nymphs) was subjected to multiplex PCR to investigate the relationships between parasitoid species. We describe, for the first time using DNA barcoding, the parasitoid complexes associated with four host psyllid species. Considering previous morphology-based descriptions on the diversity of parasitoids in the *Cardiaspina* genus, we have found a surprisingly low diversity. Multiplex PCR with species specific cytochrome B primers on parasitised nymphs and mummies has enabled us to describe the interactions between a primary parasitoid and a facultative hyperparasitoid both belonging to the prominent psyllid parasitoid genus of *Psyllaephagus* Ashmead (Hymenoptera: Encyrtidae), as well as a known hyperparasitoid in the *Cardiaspina* genus *Coccidoctonus psyllae* Riek (Hymenoptera: Encyrtidae).

Systematics and biogeography of the mygalomorph spider genus *Blakistonia* (Idiopidae) from semi-arid Australia

Harrison, S.E.¹, Rix, M.G.^{1,2} and Austin, A.D.¹

¹Australian Centre for Evolutionary Biology and Biodiversity, School of Earth and Environmental Sciences, The University of Adelaide, Adelaide S.A. 5005, Australia; ²Department of Terrestrial Zoology, Western Australian Museum, Perth W.A. 6106, Australia

Australian mygalomorph spiders are diverse at both the generic and species levels, with many species regarded as short-range endemics and some listed as threatened by conservation agencies. The putatively Gondwanan family Idiopidae, in particular, has radiated throughout the continent and occurs in most temperate, mesic and arid zones. All nine genera and 114 described species are endemic to the continent. They are dispersal-limited, have long life-cycles, and have adopted a cryptic burrowing lifestyle. The genus *Blakistonia* Hogg is well-defined and is known to occur in South Australia and neighbouring states (Queensland, Victoria, and Western Australia), with three described species. This study will examine the systematics, evolutionary history and phylogeography of *Blakistonia*. The aim is to use molecular methods to develop a multi-locus dataset to explore relationships within the genus, and to reconcile the resulting molecular phylogenies with morphology, in particular that of adult males which are traditionally used to diagnose species. Phylogeographic analyses will cast light on evolutionary processes, allowing us to explore biogeographic barriers in mesic versus arid biomes, and to develop a framework for revising the taxonomy of the genus. Preliminary CO1 mtDNA data already show interesting genetic structuring among specimens from different localities, and morphological analysis has revealed a number of distinctly different male palpal morphologies, suggesting a number of undescribed species currently exist in South Australia.

Host tree influences on longicorn beetle attack in subtropical *Corymbia*

Hayes, R.A.¹, Piggott, A.M.^{2,3}, Smith, T.E.^{1,4} and Nahrung, H.F.^{1,5}

¹Forest Industries Research Centre, University of the Sunshine Coast; ²Institute for Molecular Bioscience, University of Queensland; ³Department of Chemistry & Biomolecular Sciences, Macquarie University; ⁴Horticulture and Forestry Science, Agri-Science Queensland, Department of Agriculture, Fisheries and Forestry; ⁵Faculty of Science, Health, Education and Engineering, University of the Sunshine Coast

Plant secondary chemistry mediates the ability of herbivores to locate, accept and survive on potential host plants. We examined the relationship between attack by the beetle *Phoracantha solida* (Coleoptera: Cerambycidae) and the chemistry of the secondary phloem (inner bark) of two differentially attacked plantation forestry taxa, *Corymbia variegata* and its hybrid with *C. torelliana*. We hypothesised that this differential rate of attack may relate to differences in secondary chemistry between the taxa. We used spectrophotometric and chromatographic methods to examine the secondary chemistry of the bark. We found differences in the bark chemistry of the taxa, both with respect to phenolic compounds and terpenoids. We could detect no difference between bored and non-bored *C. variegata* trees (the less preferred, but co-evolved host). Hybrid trees were not different in levels of total polyphenols, flavanols or terpenes according to attack status, but acetone extracts were significantly different between bored and non-bored trees. Variations in the bark chemistry explain the differential attack rate between *C. variegata* and the hybrid hosts.

Sexual signals for the colour-blind: cryptic female mantids signal quality through brightness

Herberstein, M., Barry, K., White, T., Rathnayake, D. and Fabricant, S.

Department of Biological Sciences, Macquarie University, NSW 2109, Australia
E-mail: marie.herberstein@mq.edu.au

Visual crypsis is thought to evolve through the significant selective pressure imposed by predators. However, effective intraspecific communication between the sexes may require greater detectability. Here we investigate the extent of crypsis in the false garden mantid *Pseudomantis albofimbriata*, as perceived by prey (i.e. bees), predators (i.e. birds) and mates (i.e. male mantids). Our results provide evidence of partial visual conspicuousness in an otherwise highly cryptic animal. Male mantids are inconspicuous to prey, predators and conspecifics – that is, they are chromatically and achromatically cryptic. Females are chromatically cryptic to potential receivers, but their abdomens are achromatically conspicuous to prey, predators and conspecifics. Females in good condition (and therefore with more eggs) had brighter abdomens than females in poor condition and males had a significant preference for these good-condition females during simultaneous choice tests. Our results suggest males use female abdominal brightness as a sexual signal for mate choice in this system. We further propose that female mantids use the only channel available to them for conspecific communication, while also minimizing their conspicuousness to predators and prey. Our study demonstrates a novel compromise in the trade-off between sexual and natural selection in a classically cryptic insect.

Hot Ants – a taxonomic revision of the genus *Melophorus* (Hymenoptera: Formicidae)

*Heterick, B.*¹, *Castalanelli, M.A.*², *Shattuck, S.*³ and *Majer, J.*¹

¹Department of Environment and Agriculture, Curtin University, GPO Box U1987, Perth WA 6845, Australia;

²Terrestrial Zoology, Western Australian Museum, Locked Bag 49, Welshpool DC, WA 6986, Australia;

³C/o CSIRO Ecosystem Sciences, PO Box 1700, Canberra, ACT 2601, Australia'

The taxonomic revision of the endemic Australian formicine genus *Melophorus* ('furnace ants'), using morphological analysis and molecular markers, is here discussed. Formicine ants are readily characterised by the acidipore on the gaster, which directs a spray of formic acid against enemies. Morphological analysis has uncovered 93 recognizable taxonomic units tentatively placed in seven species-groups. Most of these taxa are undescribed. Molecular analysis, using the mitochondrial gene COI and the nuclear genes histone 3 (H3), rhodopsin (LR), abdominal-A (AA), and Wingless (Wg) has been performed on over 50 of these units. Individual gene trees for the COI, CYTB, LR, AA and Wg genes have been produced, but a final composite tree incorporating multiple genes is still in progress. In practice, bar-coding using COI has been found to be most informative.

In all, 46 taxonomically recognisable units have successfully produced molecular signals, but not all of these ants have produced signals for all genes, and hence some taxonomic units cannot be represented on a comprehensive gene tree. Additionally, not all morphologically distinctive *Melophorus* were available for sequencing. All five genes show homogeneity, with the basal groups (the *M. bagoti* clade, the *M. aeneovirens* clade and the *M. potteri* clade) being well supported. Some nine species are strongly attested in these three clades. Less strongly supported clades with weaker signals may indicate more closely related complexes where evolutionary pressures continue to impact on the worker genotype. While most nominated morphospecies appear to be monophyletic for the terminal clades, which represent members of the *M. ladius* species-group, the phylogenetic signal for some ants is weak, particularly for species within the *M. fieldi* complex. Hence, taxa like *Melophorus turneri* and its allies are rendered polyphyletic on gene trees, despite uniform morphologies and the fact

Biocontrol of glassy-winged sharpshooter in French Polynesia: a major success in the South Pacific

Hoddle, M.S.

Department of Entomology, University of California, Riverside, CA 92521 USA

Glassy-winged sharpshooter (GWSS), *Homalodisca vitripennis* (Hemiptera: Cicadellidae), an insect native to the southeast USA and northeast Mexico has successfully infiltrated several island groups in the South Pacific, including, French Polynesia (1999), Hawaii (2004), Easter Island (2005), and the Cook Islands (2007). It was likely moved into these vastly separated areas via the trade in live plants. In French Polynesia, populations of this xylem feeding bug reached extraordinary densities and it was unintentionally spread throughout most major island archipelagos via the movement of infested plants that likely harbored GWSS egg masses laid on the underside of leaves. In 2004, a classical biological control program targeting GWSS with the mymarid egg parasitoid, *Gonatocerus ashmeadi*, was initiated. A total of 13,786 parasitoids were released at 27 sites on the island of Tahiti between May and October 2005. Within seven months GWSS populations had been reduced by >90%. *G. ashmeadi* tracked the GWSS invasion front in French Polynesia colonizing widely disparate islands (separated by ~1,400 km of ocean) without deliberate human assistance within 10 months of its release which strongly suggested this natural enemy was being introduced into new islands via the movement of live plants that bore parasitized GWSS egg masses. *G. ashmeadi* was accidentally introduced into Hawaii, Easter Island, and possibly the Cook Islands as well. This movement of *G. ashmeadi* throughout numerous South Pacific islands strongly suggested that at this time there were major biosecurity failures to prevent the unwanted inter-island movement of plants and insects in this region. The invasion of GWSS through French Polynesia provided an ideal opportunity to assess factors affecting establishment of *G. ashmeadi*. Detection on new islands was always in close vicinity to major air or seaports and occurred when GWSS densities of ~ 7 nymphs per minute of sweeping were detected.

Of bees and burns: the distribution of the green carpenter bee *Xylocopa aeratus* in relation to fire-history on Kangaroo Island

*Hogendoorn, K.*¹, *Leijs, R.*² and *Glatz, R.*^{1,2,3}

¹The University of Adelaide, School of Agriculture, Food and Wine, Adelaide SA 5005; ²South Australian Museum, North Terrace, Adelaide SA 5000; ³D'Estrees Entomology & Science Services, PO Box 17, Kingscote SA 5223.

The green carpenter bee *Xylocopa aeratus* has a disjunct distribution in bushland around Sydney and on western Kangaroo Island (KI). Extinction of the species in Victoria and mainland South Australia is thought to have resulted from a combination of habitat clearing and large-scale bushfires. Here, we investigate the possible effects of large-scale bushfires on the occurrence of this iconic bee by analysing its current distribution on KI against fire history. We focus on the outcomes of a large bushfire that burnt most of Flinders Chase National Park (FCNP) in 2007.

On KI, *X. aeratus* depends on two types of nesting substrate, which are intricately but differentially related to fire history: large, dead *Banksia* trunks that can be re-used for several generations, and dead flower-spikes of *Xanthorrhoea* that are more ephemeral.

We surveyed western KI for active nests and nesting substrate, and combined these data with earlier surveys and historical collection data. Bees had recolonised much of FCNP using *Xanthorrhoea* spikes after fire. Now, most of these have fallen and suitable *Banksia* will not be available for a significant time. Stable populations were only found in areas that had been unburnt for a long time (≈ 40 -85 years), where old *Banksia* were abundant. We conclude that fire can cause local extinction of carpenter bees through: (a) complete burns of isolated patches; (b) frequent burns (<20 years apart), which can prevent seeding and regrowth of large *Banksia*; (c) burns of large vegetated areas, which synchronise the widespread loss of both substrates, and results in regeneration on time scales that don't support *X. aeratus* populations. To conserve *X. aeratus* on KI, fire managers should: (a) refrain from prescribed burns where *X. aeratus* exists; (b) refrain from frequent burning of unoccupied habitat with suitable *Banksia*; (c) relocate active nests during winter from areas targeted for prescribed burning.

The use of the fungus *Metarhizium acridum* to control locusts and grasshoppers

Hunter, D. M. and Peacock, M.

BASF Agricultural Specialties, Australia

The search for alternatives to the widespread use of chemicals to control locusts and grasshoppers (Orthoptera: Acrididae) has led to the development of the mycoinsecticide Green Guard®, having the active ingredient *Metarhizium acridum* (Hypocreales: Clavicipitaceae). Green Guard has been used in large-scale control operations in Australia with over 100,000 ha treated since operational use began in 2000. The main uses have been on organic farms or in environmentally sensitive areas. During the more than 10 years of operational use, we have learned a great deal about what is required to maximize the effectiveness of *Metarhizium* for locust control. We have found that when you apply *Metarhizium*, some locusts are sprayed directly but the grass protects some, so that an important source of infection is locusts picking up *Metarhizium* from the vegetation, allowing a lower initial dose to be applied. Under the very hot conditions (maxima 37-42°C) of summer in the inland, Green Guard has been shown to cause >90% mortality of locusts within 6-10 days. Against locusts and grasshoppers in milder conditions during spring, mortality is often slightly less (80%) and occurs more slowly (2 weeks or so). While the longer period for mortality means that applications are usually against the nymphal stage, there has been successful spraying of adults. During April 2007, dense swarms of the oriental migratory locust near rivers in East Timor were sprayed with Green Guard and by two weeks after treatment, few locusts remained. During 2010 and 2011, locusts in Uzbekistan and Georgia were sprayed with a water mix formulation of Green Guard: mortality reached 75-90% in 10-14 days. What has been learned with formulation, application and use of Green Guard is being applied to other biological control agents such as *Beauveria bassiana* and *Bacillus thuringiensis* as part of moving towards an increasing use of biological control in IPM programs against a wide variety of pests.

Survival of oriental fruit moth females under 30-years long mating disruption

Il'ichev, A.L.

Department of Environment and Primary Industries, Biosciences Research Division, Tatura,
Victoria 3616, Australia

Identification of the sex pheromone structures revolutionised our understanding of insect olfactory orientation. Commercial production of the sex pheromones made new methods of monitoring and pest control possible. Since then, it has been demonstrated for many insect species that the release of large quantities of sex pheromone into a target crop (termed “mating disruption”) could disrupt mate location and prevent or delay mating, reducing egg fertilisation and pest damage. Sex pheromone mediated mating disruption (MD) is now a widely-used tool of Integrated Pest Management systems in Australian horticulture. MD has been used for over 30 years to control oriental fruit moth (OFM) *Grapholita molesta* (Busck) (Lepidoptera: Tortricidae) in stone fruit orchards in Northern Victoria. However, some OFM populations had survived under long-term MD and substantial damage can be detected in these stone fruit orchards. MD applications in orchards are designed to disrupt male moths, when the real goal is to reduce the female’s ability to reproduce. Our study indicated that OFM females are capable of detecting their own sex pheromone and that sex pheromone exposure change their behaviour and advances female calling by ca. 2 hours. Also, high concentration of the artificial sex pheromone for MD could repel OFM females and they could avoid the effect of MD by moving outside the treated area to seek mates. It would be very important to check whether the volume and structural composition of sex pheromone changed in the pheromone gland of OFM females under long-term exposure to MD. Recently it was demonstrated, that antennal sensitivity of OFM females to sex pheromone exposure could stimulate abnormal mating behaviour, and suggested, that MD may initiate a secondary mechanism that affects the mating behaviour of

AliStat and SymTest: two methods for surveying phylogenomic data

Jermiin, L.

CSIRO Land & Water, Canberra, Australia

Phylogenetic studies of insect evolution are often conducted using model-based phylogenetic methods and phylogenomic data. When such studies are done, it is often assumed that the data are sufficiently complete (i.e., they contain enough unambiguous characters to allow the ‘true’ tree to be inferred reliably) and have evolved under globally stationary, reversible, and homogeneous (SRH) conditions. Methods to survey whether this is the case are available but they are not widely used in studies of insect evolution. I present two new programs for doing so. AliStat measures the completeness of multiple sequence alignments using four metrics, allowing users to decide which sites and/or sequences to retain in a final alignment. SymTest implements the matched-pairs tests of symmetry, marginal symmetry, and internal symmetry, allowing users to survey multiple sequence alignments for evidence of evolution under non-SRH conditions. The merits of AliStat and SymTest will be illustrated using published data from studies of insect evolution.

Maggot massing: problems and solutions for the forensic entomologist

Johnson, A.P.¹, Mikac, K.¹, Wighton, S.² and Wallman, J.F.¹

¹School of Biological Sciences, University of Wollongong, NSW 2522, Australia; ²Cordeaux Heights, NSW 2526, Australia.

Study of the remarkable temperatures generated by maggot masses and how they affect maggot growth is critical for validating and refining the use of maggot development to estimate the minimum time since death in murder investigations. In this talk, we highlight the problems associated with the phenomenon of maggot massing and offer relevant solutions that can be used in both research and casework.

Massing of maggots of two forensically important blowfly species, *Chrysomya rufifacies* and *Calliphora vicina*, were studied to quantify both the heat produced in masses of different sizes and the corresponding impact on an individual maggot's growth. Results suggest that mass size affects temperature generation and maggot growth rate; however the level of impact is species dependent. We have also traced the movement of individual maggots within a mass to determine the heat exposure of the individual compared to the maximum heat generated within the overall mass. In addition, we report on the types of bacteria present in carrion, and the heat associated with them when maggots are present compared to when they are absent. Ultimately, the results of this study will refine minimum death time estimates in cases where maggot mass heating has occurred.

South Australia's Arboviruses: results and methods from the first large-scale FTA® card arbovirus survey

Johnston, E.¹, Toi, C.², Weinstein, P.^{1,3}, Doggett, S.² and Williams, C.^{1,3}

¹School of Pharmacy and Medical Sciences, University of South Australia, North Terrace, Adelaide, SA 5000;

²Medical Entomology, Centre for Infectious Disease Microbiological Laboratory Services, Westmead Hospital, Westmead, NSW 2145; ³Sansom Institute for Health Research, University of South Australia, Adelaide, SA 5000

Every year in Australia, over 6000 people become infected with a mosquito-borne virus (arbovirus) including Ross River virus (RRV) and Barmah Forest virus (BFV), among others. The most prevalent of these viruses is RRV which causes prolonged symptoms of fatigue, muscle soreness and polyarthritic joint pain and costs Australians tens of millions annually in diagnosis, prevention and treatment. Approximately 250 cases of human infection are reported every year in the state of South Australia. Our ability to determine the spatial distribution of RRV risk has been constrained by limitations in the accuracy of human case data and the logistic and economic challenges of conducting large-scale arbovirus surveys. A modern development has capitalized on the nectar-feeding behaviour of mosquitoes to collect arboviruses on nucleic acid-preserving cards (FTA® cards), thus streamlining the virus surveillance process. We adapted this technique to an existing mosquito surveillance program and conducted the first ever large-scale arbovirus survey in South Australia. During four months of the peak virus season (January-April 2014), we set CO₂-baited EVS light traps at 100 locations around South Australia with a honey-baited FTA® card inside. After collection, mosquitoes were kept in a humid environment and given one week to feed on the honey-soaked card. Cards were then tested for arboviruses using a nested PCR. We made 23 virus detections from around South Australia including 11 of RRV, 5 of BFV and 3 of Stratford virus (not previously reported from South Australia). This level of detection suggests that our low-budget method is highly sensitive at detecting infectious mosquitoes. In this presentation, we report on our methods, the resulting detections, the spatial distribution of the detections, the mosquitoes associated with the detections and explore the implications of our method and findings.

The effects of partitioning on phylogenetic inference

Kainer, D.¹ and Lanfear, R.^{1,2}

¹Research School of Biology, Division of Evolution, Ecology and Genetics, The Australian National University, Canberra, ACT 0200, Australia; ²National Evolutionary Synthesis Center, Durham, North Carolina, USA

In this study we investigate the effects of partitioning on phylogenetic inference. Partitioning is a commonly used phylogenetic method that aims to accommodate variation substitution patterns among sites. Most phylogenetic studies use one of a small number of approaches to choose a partitioning scheme: no partitioning, partitioning by gene and codon position, or optimising a partitioning scheme using the BIC or the AICc. But despite partitioning's popularity, there have been few systematic studies of its effects on phylogenetic inference, and there have been no studies that compare different approaches to partitioning across many datasets. In this study, we applied four partitioning schemes to each of 34 publicly available empirical datasets, and compared the topologies, branch lengths, and branch support estimated with each scheme in a maximum likelihood framework. We find that the choice of partitioning scheme almost always affects tree topology, particularly when partitioning is omitted. Most notably, we find occasional instances where the use of a sub-optimal partitioning scheme produces highly supported but incorrect nodes in the tree. Branch lengths and bootstrap support are also affected by the choice of partitioning scheme, sometimes dramatically so. We discuss the reasons for these effects and make some suggestions for best practice.

A conceptual framework for the study of coloration in nature

Kemp, D.J., Herberstein, M.E. and Whiting, M.J.

Department of Biological Sciences, Macquarie University, Sydney, Australia

The world in color presents a dazzling dimension of phenotypic variation. Interest in color is burgeoning due to the increased accessibility of spectrometers coupled with heightened appreciation of how animals view color differently to humans. However, biologically-accurate appraisals of color are challenged by the complexities of reconstructing how spectral information is perceived, integrated and processed in the brains of viewers. Color research requires a marriage between two schools of enquiry, termed top-down and bottom-up. Top-down studies are broadly motivated to use color traits to examine ecological and/or evolutionary processes, and often performed by non-color specialists using novel species. Bottom-up enquiry, on the other hand, seeks to understand the visual and perceptual basis of color signal reception in well-characterized model systems. Reconciling these two schools is critical because bottom-up insights generate the intellectual and analytic basis for top-down studies, which in turn may validate key bottom-up principles. I present a conceptual framework for color research that emphasizes the need for unification and reciprocity among these parallel schools of enquiry. The framework is developed by classifying the key top-down research questions (spectral/physical, perceptual distance and discriminatory) and integrating them with the concepts and tools of bottom-up knowledge. I briefly outline the important empirical challenges, designed to assist researchers avoid the pitfalls and mistakes apparent in some existing literature.

Directional evolution in hymenopteran morphology

Klopfstein, S.^{1,2}, *Vilhelmsen, L.*³ and *Ronquist, F.*²

¹The University of Adelaide, North Terrace, Adelaide, SA 5005, Australia; ²Department of Biodiversity Informatics and Genetics, Swedish Museum of Natural History, Box 50007, SE-104 05 Stockholm, Sweden;

³Department of Entomology, Natural History Museum of Denmark, Universitetsparken 15, DK-2100 Copenhagen Ø, Denmark

Directional evolution has a large impact on shaping the morphological, ecological and molecular diversity of life. But standard substitution models assume stationarity of the evolutionary process over the time scale examined, an assumption that is often not met by real data and which hinders the inference of directionality in the first place. We here present a simple, non-stationary model for binary characters which assumes that the state frequencies at the root differ from the equilibrium frequencies of the homogeneous evolutionary process along the rest of the tree. The model is implemented in MrBayes 3.2 and offers a reversible-jump algorithm for testing directional versus stationary evolution. Simulations show that correctly inferring directionality based on data from extant taxa only is strongly dependent on the evolutionary rate, the shape of the tree, relative branch lengths, and the number of taxa. Accounting for directionality improves tree inference and even facilitates correct rooting of the tree at suitable evolutionary rates, i.e., between about 0.1 and 0.5 expected substitutions between root and tips. Applying the model to hymenopteran presence -- absence data of wing veins, muscles, and sclerites, we find high support for a trend towards reductions in the former two, while stationarity cannot be ruled out for sclerites. Adding fossil and time information in a total-evidence dating approach results in more precise estimates not only of the ancestral state at the root of the tree, but also of the divergence times. Our model relaxes the assumption of stationarity by adding a minimum of additional parameters and is thus well suited to study evolutionary modes in datasets of limited size, in contexts where evolution is suspected to not yet have reached an equilibrium state.

Symposium overview: the rise and rise of molecular data in insect science

Krosch, M.N.¹ and Cranston, P.S.²

¹Centre for Water in the Minerals Industry, Sustainable Minerals Institute, The University of Queensland, Brisbane, QLD 4072; ²Evolution, Ecology and Genetics, Research School of Biology, Australian National University, Canberra, ACT 0200.

Molecular techniques and technologies have exploded in use across the varied research streams in biology over the last several decades. The world of insects certainly has not been immune and the dramatic increase in knowledge stemming from molecular entomological studies has had wide-ranging impacts globally. From the development of model systems for exploring genomic structure and function in *Drosophila*, to helping understand biogeographical patterns, to contributing to taxonomic and biodiversity knowledge, the applications of molecular data to insects have been far-reaching. The current -omics revolution promises to expand the horizons of molecular research in insects even further. This symposium will explore current research in which molecular data has contributed significantly to hypotheses derived from other data types. Talks span a wide range of molecular applications – from assessing evolution across landscapes, taxonomy and systematics, invasion biology, and diagnostics – and showcase the impact molecular data can have in entomology.

Welcome to the jungle: a review of (insect) evidence for eastern Australia's major biogeographical barriers to mesic forest-restricted taxa.

Bryant, L.M.¹ and Krosch, M.N.²

¹School of Earth, Environmental and Biological Sciences, Queensland University of Technology, Brisbane 4000, Australia; ²University of Queensland, Centre for Water in the Minerals Industry, St Lucia, Brisbane 4072, Australia.

The influence of climatic changes occurring since the late Miocene on Australia's east coast mesic forest ecosystems has received significant attention over the past 15-20 years. In particular, the impact of the dramatic shift from widespread mesic forest to a much drier landscape in which remnant mesic forest was isolated in small refugia intersected by grassland and open woodland has long intrigued ecologists and biogeographers. From the early recognition of common zones where avian subspecies distributions were consistently separated, to the first studies of intraspecific mitochondrial DNA divergences across these zones, to more recent multi-locus molecular analyses, many researchers have been fascinated by the drivers, processes and effects of the major biogeographical barriers that intersect mesic forest refugia along the east coast. Nevertheless, there remain substantial knowledge gaps and inconsistencies in our understanding of these barriers, particularly in relation to their geographical extent, inception and duration. This has had an often profound impact on the interpretation of biological patterns. Here we review evidence reported from insect studies for the major east coast dry habitat barriers and discuss phylogeographical patterns and divergence times. We show that patterns and tempo in many insect taxa contradict the accepted dogma for many of these barriers. Appropriate sampling remains essential to detect subtle patterns and we identify several key research areas for future exploration.

Two birds with one stone: offsetting carbon dioxide emissions and sustaining native insect diversity

Kwak, M.L.¹, Forbes, R.J.¹, O'Connor, E.², Sandwith, R.² and Steinbauer, M.J.¹

¹Department of Zoology, La Trobe University, Melbourne VIC 3086; ²Greenfleet, Level 3, 520 Collins Street, Melbourne, VIC 3000.

Revegetation plantings of native tree species are established by Greenfleet to offset anthropogenic CO₂ emissions. Unlike commercial eucalypt plantations, Greenfleet plantings are not monocultures of economically valuable species, but comprise polycultures of species and genotypes indigenous to the locality to be revegetated. Since Greenfleet forests seek to mimic the pre-existing vegetation, there is a high likelihood that they are effective ways to sustain native insect diversity; however this has never been tested. Light trap sampling of Lepidoptera, Coleoptera and Hemiptera was undertaken to assess insect diversity in paired Greenfleet and remnant forests between December 2013 and February 2014. Coleoptera and Hemiptera were less abundant in Greenfleet forests compared to remnants. Conversely, the abundance of Lepidoptera was higher in Greenfleet forests compared to remnant forest. The richness of species of Coleoptera was higher in remnants compared to Greenfleet forests. The richness of species of Lepidoptera and Hemiptera did not differ between Greenfleet and remnant forests. Our research indicates that Greenfleet forests can play a significant role in sustaining native insect biodiversity. We discuss the factors (diversity of tree species, age of planting and climatic conditions) apparently linked to differences in insect diversity between Greenfleet and remnant forests.

Advances in managing images of insect specimens in biological collections

Baird, D.¹, Woolston, M.¹, Mantle, B.², Fisher, N.² and La Salle, J.¹

¹Atlas of Living Australia, CSIRO National Facilities and Collections, GPO Box 1700, Canberra, ACT 2601;

²Australian National Insect Collection, CSIRO National Facilities and Collections, GPO Box 1700, Canberra, ACT 2601

The Atlas of Living Australia has developed a suite of tools to manage, discover and display images within the Atlas, including >92,000 images of insects and over 5000 images of type specimens. These include a Collection Explorer which will enable searching by collection or taxon, as well as an Imaging Tool for managing images, annotating and tagging images, measuring specimens (or parts of specimens) within images, creating sub-images, and creating and exporting image albums. This tool will also provide the ability to view the detail in high resolution images by zooming and panning within an image. A key component of this work will be to provide better tools and workflow for uploading images from collections.

Extracting rich information from 3D image libraries

Anderson, S.¹, Adcock, M.¹, Lovell, D.¹, Mantle, B.² and La Salle, J.³

¹CSIRO Digital Productivity and Services Flagship, GPO Box 664, Canberra, ACT 2601; ²Atlas of Living Australia, CSIRO National Facilities and Collections, GPO Box 1700, Canberra, ACT 2601; ³ Australian National Insect Collection, CSIRO National Facilities and Collections, GPO Box 1700, Canberra, ACT 2601

Creating high quality image libraries is only the first step in the process of unlocking the information in biological collections. This project will create the ability to place digitised 3D insect specimens in a web-based viewer that will enable visualisation of and interaction with specimens. The viewer will display a specimen alongside scale information, and the user can rotate, zoom and pan around the specimen to view it from any position. A user can take real-world measurements from a specimen, with these measurements represented visually using a coloured line. Measurements can be straight point-to-point lines, multi-segmented lines, or curved lines. The measurement values are previewed in real-time and can be recalled at any time. A user can also highlight an area of interest on a specimen, and label it. This can be used to bring attention to something, but also to take surface area measurements. Information extracted from these annotations will be stored in such a manner that it can be used for other purposes, for example feeding into a morphological character matrix.

Sex pheromones of cossid moths: emerging pests of Australian and overseas *Eucalyptus* plantations

Lawson, S.A.¹, Moore, C.M.² and Bouwer, M.C.³

Department of Agriculture, Fisheries and Forestry, Ecosciences Precinct and University of the Sunshine Coast, GPO Box 267, Brisbane, QLD 4001; (2) School of Biological Sciences, The University of Queensland, St Lucia Campus, Brisbane, Queensland 4072; (3) Forestry and Agricultural Biotechnology Institute, University of Pretoria, Private bag X20, Hatfield 0028, South Africa.

Moths in the family Cossidae are significant pests of various crops and forest trees around the world. In Australia, the giant wood moth (*Endoxyla cinereus* and other *Endoxyla* spp.) and Culama wood moth (*Culama australis*) have been recorded as pests in *Eucalyptus* plantations in the tropics, subtropics and temperate regions. The giant wood moth is a primary pest, and infestations of this species in plantations of *Eucalyptus grandis* in NSW in the 1970's led to widespread plantation failures. Culama wood moth is a widely distributed secondary pest of eucalypts, and can cause significant damage to wood quality following initial attack by other borer species. Overseas, two native cossid moths have emerged as pests of eucalypt plantations: *Chilecomadia valdiviana* in Chile, and *Coryphodema tristis* in South Africa. Management of cossids using insecticides is problematic and not cost-effective on a plantation scale. Female-produced sex pheromones are well-known for many cossid moths overseas and have been used to effectively reduce moth populations in some crops. Concurrent work in Australia and South Africa identified the major components of the pheromone blends of *C. australis* and *C. tristis*, with each blend successfully tested in the field for attractancy to male moths. Both these species belong to the subfamily Cossinae and use 14 Carbon acetates as the primary components, differing in the placement and stereochemistry of the double-bond along the carbon chain. Blends of E-10 and Z-10 tetradecenyl acetate varying from 40:60 to 60:40 and at different doses were tested against *C. australis* in southeast Queensland and northwest Tasmania, and found to be highly effective in attracting males. Despite a considerable amount of effort at elucidation, the pheromone blend of *E. cinereus* remains unknown. Potential use of these pheromones as management methods in eucalypt plantations is discussed.

Advancing Coleoptera systematics

Leschen, R.A.B.

Landcare Research, New Zealand Arthropod Collection, Private Bag 92170, Auckland, New Zealand,
leschenr@landcareresearch.co.nz

John F. Lawrence is well-known as a leading authority of beetles. On this occasion of his 80th birthday, some of John's most significant achievements are highlighted and how his activities as a scientist, teacher, mentor, collaborator, and friend has, and continues, to leave an indelible mark on Coleoptera classification and taxonomy and those who study beetles.

Gondwanan Brown Beetles (Coleoptera: Cryptophagidae: Cryptophaginae): we like them

Leschen, R.A.B.¹ and Gimmel, M.L.²

¹Landcare Research, New Zealand Arthropod Collection, Private Bag 92170, Auckland, New Zealand, Email: leschenr@landcareresearch.co.nz; ²Department of Biology, Faculty of Education, Palacky University Hnevotinska 3, CZ-75515, Olomouc, Czech Republic, Email: phalacrid@gmail.com

The family Cryptophagidae is a worldwide group with cryptic habits. There are few taxonomic specialists and the beetles are small, brown and often confused with other fuzzy beetles in collections. Taxonomic study requires careful dissections, patience and verve. One student of the group, Tapan Sen Gupta, never published on cryptophagids and instead dealt mainly with look-a-likes now in Erotylidae. All said, we like them, maybe as a form of self-punishment and self-denial to work on other charismatic groups that could attract funding. The gondwanan Picrotini were defined by Roy Crowson (1980) and have been treated in larger family-group reviews and systematic studies by John Lawrence. The Juan Fernandez species were revised (Leschen and Lawrence 1993) and a catalogue of the tribe has been published (Leschen and Gimmel 2012). We are revising the genera and recognize 22 genera with 13 genera described as new from Australia, Papua New Guinea, New Zealand, and South America (Chile, Ecuador). Several members of Picrotini depart from primitively fungal feeding habits to feeding on fern spores (*Cryptothelypteris* Leschen & Lawrence) or plant pollen (some *Ostreacryptus* Leschen). Most members are flight-capable, but several lack hind wings (e.g., *Picrotus* Sharp (New Zealand), *Neopicrotus* Leschen (Chile and Australia), *Thortus* Broun (New Zealand), or contain species that are both winged and apterous (e.g., *Ostreacryptus*). Gigantism occurs in the apterous genus *Thortus* with most mainland New Zealand species rather small (ranging from 1.5 to 2.0 mm) and one species from the subantarctic Auckland Islands with a length of 3 mm. Features of the group which that are used to define generic limits include the pronotal margins with a glabrous space, pronotal tumidities, evaporative areas that are associated with glandular ducts and pores, postcoxal lines, connation of the abdominal ventrites, and abdominal spiracle diverticulae and texture.

Molecular methods in forensic entomology in Australia

Lessard, B.D.¹, Downton, M.² and Wallman, J.F.³

¹Australian National Insect Collection, CSIRO Ecosystem Sciences, Canberra, ACT 2601, Australia; ²Centre for Medical and Molecular Bioscience, University of Wollongong, NSW 2522, Australia; ³School of Biological Sciences, University of Wollongong, NSW 2522, Australia

Correct identification of the insects that feature in forensic investigations is fundamental to all subsequent inferences from these creatures, especially in regard to the minimum time since death. Flies of forensic importance, which are the primary tools of forensic entomologists, are often difficult to identify, both as adults and immatures. In particular, the larvae of many species are poorly known morphologically.

Modern molecular methods have powerful applicability to the identification of forensic Diptera, especially when only larvae are available for analysis (and they may have been degraded or moribund). Such techniques were pioneered in Australia in the early 2000s. This talk summarises the molecular methods and especially the gene regions that have been utilised thus far in the analysis of the Australian blowfly and flesh fly fauna and the opportunities that exists for future research. Problems inherent in the close evolutionary affinities of some native species are highlighted.

The legacy of Ian Mackerras in Australian Diptera systematics

Lessard, B.D. and Yeates, D.K.

Australian National Insect Collection, CSIRO, Black Mountain, Clunies Ross Street, Canberra, ACT, 2601.

Dr Ian Mackerras significantly contributed to our understanding of the evolution and taxonomy of the Australian Diptera. During his phenomenal career he had published over 130 scientific papers and even served as a Major in the Australian Army Medical Corps, where he would give soldiers vials for specimen collection in the battle fields. Mackerras had a passion for the Diptera, especially the horse flies (Diptera: Tabanidae), having developed a robust morphology-based classification system for the entire family that is still valid and used today. Mackerras had extensively revised the majority of the Australian horse fly genera, with all but one genus, *Dasybasis*, being revised before his passing. The genus *Dasybasis* is now currently being revised using an uncompleted manuscript originally written by Mackerras, along with supplementary descriptions and a taxonomic key to all 70+ species that will be published in honour of the late scientist. This will ultimately complete the baseline taxonomy of the Australian horse flies which Mackerras initially started some 60 years ago. In addition, recent molecular data has confirmed the utility of Mackerras' original classification scheme based on morphology alone, as well as validating key evolutionary predictions that were made by Mackerras in the 1960's. The legacy of Mackerras still lives on today through his robust taxonomic descriptions, intuitive classification schemes and forward evolutionary thinking which will continue to benefit future students and researchers to come.

Protecting the future: understanding insecticide resistance in field populations of bed bugs in order to preserve insecticidal control solutions

Lilly, D.G., Dang, K., Webb, C.E. and Doggett, S.L.

Department of Medical Entomology, Westmead Hospital, University of Sydney and Pathology West – ICPMR
Westmead, Westmead, NSW 2415, Australia.

Research around the world examining the efficacy of insecticides against bed bugs (Hemiptera: Cimicidae: *Cimex* spp.) has presented a broad spectrum of results, often with significant discrepancies despite evaluating identical active ingredient(s). This is reflected in the field, with failures being common with products otherwise reported as efficacious in laboratory tests. The variability in laboratory trials may be due in part to differences in experimental methodology, however it is more likely a result of inherent variations in resistance profiles of the bed bug strains used. Resistance profiling on *C. lectularius* in Australia has previously revealed the existence of resistance to pyrethroid insecticides and that multiple resistant mechanisms exist in field populations. To further investigate the correlation of these results to modern field populations of bed bugs, a program to collect and screen field specimens was initiated. To date, over 40 bed bug strains (of both *C. lectularius* and, to a lesser extent, *C. hemipterus*) have been collected from across Australia and successfully colonized. To screen for resistance, a dose of 2.5 g/L deltamethrin in acetone applied at a rate of 1 µL/bug was set as the discriminating value, with mortality recorded at 24 hours post application. This dose is equivalent to approximately 7,500x and 50x the LD₅₀ values respectively of presently maintained susceptible and resistant *C. lectularius* laboratory strains. Twenty adult bed bugs of mixed sex and age in two replicates of ten were used for the bioassays. Results indicated a broad spread in the magnitude of resistance, covering <10% to 100% mortality. These findings complement concurrent research, which indicates variable patterns of resistance mechanisms are present across the country. The results have important implications for product manufacturers and registration authorities in ensuring that a product is as effective at controlling bed bugs in the field as the laboratory.

***Blattabacterium* function, genome degradation and loss in primitive termites**

Lo, N.

School of Biological Sciences, The University of Sydney, Australia

The low levels of nitrogen in wood means that termites feeding on this substrate must find ways of obtaining and conserving this element. *Blattabacterium cuenoti* is an intracellular bacterium found in specialized bacteriocytes of the fat body of cockroaches and the primitive termite *Mastotermes darwiniensis*. The bacteriocytes are found adjacent to uric acid containing cells (urocytes), and it was long thought that the function of the bacterium was to convert uric acid (an end product of nitrogen metabolism) back into usable nitrogen products for the host. The absence of genes encoding uricases in all *B. cuenoti* genomes thus far sequenced was, therefore, unexpected. One hypothesis to explain this absence is that gut bacteria are responsible for recycling uric acid, and that the breakdown product urea is transported back to the fat body where *B. cuenoti* converts it into essential amino acids for its host. I will examine the evidence for this hypothesis as well as alternative hypotheses on uric-acid degradation in cockroaches and termites. I will then compare the *B. cuenoti* genomes thus far sequenced and discuss the connection between social behaviour and the degradation and eventual disappearance of the *B. cuenoti* genome during the evolution of termites.

Chemical cues, mate attraction and assessment in a psyllid

Lubanga, U.K.¹, Seijthour, F.P.², Farnier, K.² and Steinbauer, M.J.²

¹Department of Zoology, La Trobe University, Melbourne, Australia; ²Chemical Ecology Group, Keele University, Keele, United Kingdom.

Australian is home to over 10% of the world psyllid fauna most of which are host specific for plant families including; Myrtaceae, Fabaceae and Casuarinaceae, which represent a significant component of Australia's forest fauna. Currently, Australian research on psyllid reproductive behaviour especially the mechanisms that facilitate aggregation and enhance reproductive success lags behind global research partly due to lack of severe psyllid related plant diseases. However, the unpredictable fluctuations in abundance and behaviour with in Psylloidea implies that it is vital that the reproductive behaviour and the underlying mechanism of the Australian psyllid fauna be studied.

This study aimed to understand the reproductive behaviour and communication signals of a Psyllid; *Aacanthocnema dobsoni* (Hemiptera: Triozidae). *A. dobsonii* endemic to Australia, feeds on *Allocasuarina verticillata*, is multivoltine throughout its range and overwinters as adults and nymphs. It can be found in very high numbers (e.g. 80-120 nymphs per branchlet) which is when chlorosis of host branchlets may be visible. Females may live up to 60 days, can lay up to 420 eggs and appear to be receptive to males throughout this period. Y-tube olfactometer bioassays results show no significant differences in male and female responses to offered odorants produced by conspecific females and males. Gas chromatography-mass spectrometry analyses indicate quantitative and qualitative gender, age and mating status based difference in cuticular hydrocarbons profiles. Bioassays using freshly killed females and males with or without cuticular hydrocarbons show that males spend significantly more time searching and trying to mate with freshly killed females with intact cuticular hydrocarbon profiles compare freshly killed females with cuticular hydrocarbons removed.

These results indicate that *A. dobsoni* may not rely on chemical signals for long range mateattraction/searching. However, cuticular hydrocarbons may act as cues used in close range mate recognition and assessment.

Starvation time, recovery and possible Bt detection behaviour of susceptible and resistant *Helicoverpa armigera* (Hübner) neonates

Luong, T.T.A.¹, Zalucki, M.P.¹, Cribb, B.¹, Perkins, L.E.¹ and Downes, S.J.²

¹The University of Queensland, QLD 4071; ²CSIRO Entomology, Australian Cotton Research Institute, Narrabri, NSW 2390

Although physiological resistance of *Helicoverpa armigera* (Hübner) (Lepidoptera: Noctuidae) to Bt crops has been looked for in many studies, there is no convincing evidence that field resistance has developed. Nevertheless, higher numbers of surviving larvae than expected have been found in the field from time to time. It has been suggested that a behavioural component, specifically the avoidance of the toxin, can contribute to larvae surviving on Bt-toxin expressing plants. This type of avoidance behaviour in a toxic environment has been described as a type of resistance. If such behavioural differences in a Bt and non-Bt environment exist, then they should be considered as a potential basis for adaptation to Bt toxin by *H. armigera*. If larvae can detect Bt toxin and bigger neonate larvae can go without food for a longer time, they can move further and would be more likely to locate less toxic plant parts.

Here we determine whether *H. armigera* larvae can detect Bt toxin on artificial diet and leaves. We investigate the effect of initial larval size on time to starvation, as well as recovery from a period of food deprivation. How larvae respond to food deprivation may lead to differences in survival and how far neonates can move to find a suitable feeding site. These experiments were conducted with both *H. armigera* resistant and susceptible strains.

There was no strong evidence that neonates could detect Bt-toxin based on their survival after 6 days. However, where larvae were released did affect survival; they did better when first released on non-Bt sides of two-diet treatments. Neonates seemed to move less when released on non-Bt diets and initial experiments over the first 24h of life suggest they abandon Bt cotton leaves more readily than conventional cotton.

Optimizing for multiple benefits requires an understanding of functional connectivity of habitats for ecosystem service providers

Macfadyen, S.¹, Parry, H.² and Schellhorn, N.²

¹CSIRO Agriculture Flagship, Clunies Ross St., Canberra ACT 2601, Australia; ²CSIRO Agriculture Flagship, Dutton Park Brisbane, Brisbane QLD 4001, Australia

Recent declines in biodiversity in agricultural landscapes have increased interest in the link between biodiversity and ecosystem services. Synergies between agricultural productivity and biodiversity conservation can be achieved if an understanding of ecosystem services leads to a change in management practice that intentionally supports greater biodiversity. Research efforts to date have focussed on understanding how land-use choices (i.e. what crops we plant, where) impacts species richness and abundance within those habitat-patches. However, the functional connectivity of habitat-patches across space and time influences the ability of an agricultural landscape to support ecosystem service provision. For some species the right habitats may be present in agricultural landscapes but still “isolated” due to management factors going on at the field, farm and landscape-scale. Natural pest control is an example of an important ecosystem service, which may directly contribute to productivity on farms, and is delivered by a range of highly mobile invertebrate predators and parasitoids (natural enemies). Meta-analyses have shown that natural enemies generally display a positive response to greater landscape complexity (especially the amount of non-crop vegetation), but pests show no consistent relationships. Our own work in mixed grain production landscapes has investigated where these species are found throughout the cropping year, and the frequency of movement between crop and non-crop habitat-patches. We have been using our findings to suggest ways that habitat-patches can be better managed to facilitate movement of natural enemies but impede movement of pests.

Insect research in the postgenomic era: beyond the DNA sequence

Maleszka, R.

PLENARY SPEAKER

Research School of Biology, The Australian National University, Canberra ACT 0200

Insect genomics has already produced a massive amount of raw data that generated attractive and often unexpected experimental opportunities for both academic researchers and biotechnologists. With the publication of dozens of genomic drafts and with large datasets energizing much of basic research, how is the insect community participating in this windfall? What benefits are flowing from the genomic projects of *honey bees*, *ants*, *wasps*, *termites* and *aphids* with their auxiliary and potent *dot.com* bioinformatics, genes-on-a-chip, and cutting edge proteomics?

Genomics is challenging entrenched views on the evolution of complex systems and is helping us to better understand and solve some of the most puzzling problems in biological sciences. It is apparent that evolutionary forces have given rise to a remarkable variety of organisms by utilising a surprisingly small number of protein coding genes. Humans, nematodes and insects have comparable number of protein-coding genes suggesting that both developmental and behavioural complexities cannot be explained in terms of an increased protein coding capacities of diverse organisms in different phyla. These data highlight our ignorance of biological complexity and the manner in which it is instantiated during evolution. One line of genome-inspired research that is promising to deliver important clues to the question of how a limited number of genes can generate a virtually unlimited organismal and behavioural complexity is *epigenomics*.

In purely biochemical terms, epigenomics deals with various types of chemical ‘decorations’ such as DNA methylation or abundant chromatin proteins modifications that provide instructions about the proper location and timing of selective gene activation. These modifications, often referred to as “epigenetic”, may last through cell divisions for the duration of the cell's life, but may also persist through generations even though they do not involve changes in the underlying DNA sequence of the organism. This vast field, driven by a deluge of raw sequencing data is revealing a very complex portrait of epigenomic dynamics operating at multiple levels, interacting with each other and remaining in a constant flux. *But how do we evaluate what these chemical modifications mean in a functional context? How environment is linked to the genome and how external cues are translated into cellular responses via epigenomic changes? When do these changes go above threshold and guide organisms into another direction, such as an alternate developmental trajectory? How does malfunctioning of epigenetic mechanisms result in diseases?*

This is an area in which excellent progress can be made by reducing complexity to manageable components using relevant models with measurable phenotypic endpoints. One such organism is a social honey bee, *Apis mellifera*, an emerging and valuable system to investigate epigenomes and their role in the interplay with cellular signalling, adult differentiation and behaviour. Our progress in delineating the role of epigenetic mechanisms in controlling conditional phenotypes in this species has already provided important clues to understanding effects of diet and environment on development and predispositions to complex behavioural traits.

Higher-level phylogeny of the Hymenoptera inferred from mitochondrial genomes

Mao, M., Gibson, T. and Dowton, M.

Centre for Medical Bioscience, School of Biological Sciences, University of Wollongong, Wollongong, NSW, 2522, Australia

Higher-level hymenopteran relationships remain unresolved in both morphological and molecular analyses. In this study, we present the most comprehensive analyses of hymenopteran relationships based on 48 mitochondrial (mt) genomes. One complete and two nearly complete mt genomes representing three hymenopteran superfamilies were newly sequenced. We assessed the influence of inclusion/exclusion of 3rd codon positions, alignment approaches, partition schemes and phylogenetic approaches on topology and nodal support within the Hymenoptera. The results showed that the topologies were sensitive to the variation of dataset and analytical approach. However, some robust and highly supported relationships were recovered: the Ichneumonomorpha was monophyletic; the Trigonalioidea + Megalyroidea and the Diaprioidea + Chalcidoidea were consistently recovered; the Cynipoidea was generally recovered as the sister group to the Diaprioidea + Chalcidoidea. In addition, the monophyletic Aculeata and Proctotrupomorpha were recovered in some analyses. Several gene rearrangements were detected in each of the three newly sequenced mt genomes. Specifically, the *Ibalia leucospoides* mt genome harbors a large inversion of a gene block from *trnE* to *trnS₂*. Inverted, duplicated A+T rich regions were detected in the *Ibalia leucospoides* mt genome, which probably played an important role during the formation of the large gene block inversion via recombination.

Flat beetles in a flat land: a review of the Australian Cucujidae (Coleoptera)

*Marris, J.W.M.*¹ and *Ślipiński, S.A.*²

¹Entomology Research Museum, Bio-Protection Research Centre, PO Box 85084, Lincoln University, Lincoln 7647, New Zealand; ²CSIRO Ecosystem Sciences, GPO Box 1700, Canberra, ACT 2601, Australia.

The Cucujidae is a small family of characteristically strongly flattened beetles, consisting of four described genera: *Cucujus*, *Palaestes*, *Pediacus* and *Platysus*. We present an overview of the world cucujid fauna, its biology and biogeography. The Australian fauna is discussed, including the first species of *Pediacus* from the region, which was recently-described, and current taxonomic research on *Platysus*.

A newly constituted Notogean tribe of Tenebrionidae (Coleoptera)

Matthews, E. G. and Lawrence, J. F.

The South Australian Museum, North Terrace, Adelaide, SA 5000

The tribe Trachelostenini Lacordaire, 1859 currently has the rank of family and contains just the genus *Trachelostenus* Solier, 1851 of southern Chile. It is proposed to return it to tribal status in the subfamily Tenebrioninae and to broaden its scope to include the genera *Myrmecodema* Gebien, 1943 of central Chile and *Leaus* Matthews and Lawrence, 1992 of Tasmania and north Queensland. Evidence is presented to support these changes.

Biological control of exotic pasture weevil pests in New Zealand agriculture: learning from experience to inform the future

*McNeill, M.R.*¹, *Barratt, B.I.P.*², *Ferguson, C.*², *Gerard, P.*³, *Goldson, S.*¹, *Hardwick, S.*¹, *Phillips, C.*¹ and *Wilson, D.*³

¹AgResearch, Lincoln Science Centre, Private Bag 4749, Christchurch 8140, New Zealand; ²AgResearch, Invermay Agricultural Centre, Private Bag 50034, Mosgiel 9053, New Zealand; ³AgResearch, Ruakura Research Centre, Private Bag 3123, Hamilton, New Zealand.

Exotic grasses and legumes form the mainstay of New Zealand pastoral agriculture but are susceptible to a wide range of native and exotic invertebrate pests. For exotic pests, escape from natural enemies, few competitors and favourable environmental and climatic conditions mean that populations can quickly reach densities that reduce pasture productivity and persistence and hence impose a financial cost on producers. Impacts include direct effects caused by acute pest outbreaks resulting in production losses or chronic pest infestation that cause insidious effects on pasture persistence. Three high impact exotic pasture pests are the lucerne weevil (*Sitona discoideus*), Argentine stem weevil (*Listronotus bonariensis*) and clover root weevil (*S. obsoletes*) (all Coleoptera: Curculionidae). Biological control of these weevils has been a keystone component of their management in New Zealand with the introduction of three parasitoids of the genus *Microctonus* (Hymenoptera: Braconidae), *M. aethiopoides* (Moroccan and Irish strains) and *M. hyperodae*. Quarantine studies and subsequent field research on target and non-target impacts have been critical to informing biological control theory and developing guidelines for future introductions. As part of integrated pest management strategies, biological control has been shown to reduce the impacts of these weevil species, and crucial to raising the profile of biological control amongst farmers. However, emerging issues of climate and land use change, the role of endosymbionts in arthropod biology and the broad acre use of insecticides will impact on the effectiveness of biological control. This will produce as yet unrealised benefits and costs to agricultural systems and it is important that research capability is positioned to respond to these emerging issues.

50 years of new Australian insects: publishing and authorship trends

Mesibov, R.

Queen Victoria Museum and Art Gallery, 2 Invermay Road, Launceston, Tasmania 7248, Australia

Australian Faunal Directory data were used to create a new, publicly available dataset, nai50, which lists 18318 species and subspecies names for Australian insects described in the period 1961-2010, together with associated publishing data. The number of taxonomic publications introducing the new names varied little around a long-term average of 70 per year, with ca 420 new names published per year during the 30-year period 1981-2010. Within this stable pattern there were steady increases in multi-authored and 'Smith in Jones and Smith' names, and a decline in publication of names in entomology journals and books. For taxonomic works published in Australia, a publications peak around 1990 reflected increases in museum, scientific society and government agency publishing, but a subsequent decline is largely explained by a steep drop in the number of papers on insect taxonomy published by Australia's national science agency, CSIRO. The oral presentation will include data on the taxonomic productivity of selected entomologists.

Four-cluster likelihood mapping - testing for incongruent signal in large phylogenomic datasets

Meusemann, K.^{1,2}, Misof, B.² and Yeates, D.¹

¹Australian National Insect Collection, National Research Collections Australia, CSIRO National Facilities and Collections, Clunies Ross Street, Acton, ACT 2601; ²Zoologisches Forschungsmuseum A. Koenig, Zentrum für Molekulare Biodiversitätsforschung, Adenauerallee 160, 53113 Bonn, Germany

“Four-cluster Likelihood Mapping” (FcLM) was introduced in the 1990's and tests for (incongruent) signal that is not necessarily obvious from common tree reconstruction methods or split networks with multiple taxa. FcLM was recently implemented in RAxML and is now applicable for large-scaled datasets. We illustrate the utility of the method using a recent example from insect phylogenetic relationships. The relationship among Odonata (damselfly- and dragonflies), Ephemeroptera (mayflies) and Neoptera are investigated testing for the long debated "Palaeoptera" hypotheses using a dataset with 1478 orthologous single copy genes from the 1KITE project (www.1kite.org).

In addition, we can discriminate potential phylogenetic from other confounding signal by applying FcML on datasets, but with phylogenetic signal removed using different permutation approaches. Confounding signal can lead to erroneously support and might be due to such factors as (1) unevenly distributed missing data and (2) compositional heterogeneity along with non-stationary substitution processes within a dataset. We expect this method to be useful in phylogenetic research, however there is still plenty room for improvement in the method and its application at various phylogenetic levels.

Hot and smelly: thermogenesis and the chemical ecology of pollination in endemic Australian Araceae

Miller, R.¹, Farnier, K.², Barnes, J.³, Grant, N.³, Robinson, S.³ and Steinbauer, M.²

¹Department of Geography and Resource Management, University of Melbourne, Burnley Campus, Richmond, Victoria 3121, Australia; ²Department of Zoology, La Trobe University, Melbourne, Victoria 3086, Australia;

³School of Biological Sciences, University of Wollongong, Wollongong, NSW 2522, Australia.

Thermogenesis, a trait usually associated with mammals and birds, also occurs in some flowers. Thermogenesis in flowers is assumed to be important in the pollination biology of these species, by enhancing scent volatilisation, and/or providing a thermal reward to insect pollinators. Despite the ecological significance of thermogenesis in plant-pollinator interactions, little is known about its prevalence in the Australian flora. Further, the pollination and chemical ecology of Australian Araceae – the family in which thermogenesis is most reported – is little documented. We report findings on two endemic Australian arums, the rare *Typhonium eliosurum*, and *Alocasia brisbanensis*. We characterised heat generation in different floral tissues, identified insects visiting during male and female phases of flowering, and characterised floral volatiles during different stages of anthesis. *Alocasia brisbanensis* showed negligible thermogenic capacity, whereas tissues on the *T. eliosurum* spadix heat for several days. Heating in *T. eliosurum* is associated with a strong unpleasant odour characterised by typical constituents of dung-like aromas in other Aroideae, including indole and skatole, which are strongly correlated with dung beetle pollination in that subfamily¹. By contrast, the sweet scent of *A. brisbanensis* inflorescences was dominated by ionones and ionols. Insects most commonly associated with *T. eliosurum* were Diptera, of the family Sphaeroceridae, whereas two families of small beetles, Nitidulidae and Staphylinidae dominated collections from *A. brisbanensis*. In the latter species, differences in scent during anthesis were found, as were differences in the suite of insect visitors across its geographic range.

Evolution of cryptic species within the Australian gall-inducing scale insect genus *Apiomorpha* (Sternorhyncha: Coccoidea: Eriococcidae)

Mills, P.J. and Cook, L.G.

The University of Queensland, St. Lucia, QLD 4072.

The Australian gall-inducing scale insect genus *Apiomorpha* has considerable chromosome variation ranging from $2n=4$ to c.192. The three well-studied species groups: the *A. minor* species group, the *A. munita* species-complex and the *A. pharetrata* species-complex. The chromosome variation within each of these groups is correlated with cryptic species, which also sometimes differ in gall morphology, host use and molecular (allozymes and DNA sequences) data. Although the two identified cryptic species within the *A. pharetrata* species-complex can be differentiated on the basis of non-overlapping chromosome differences, this is not possible for the other two species-complexes. Cryptic species within the *A. munita* species-complex have been identified using allozymes and host use differences whereas cryptic species within the *A. minor* species group exhibit a combination of molecular, host use and chromosome differences. Here we report on additional cryptic species within *Apiomorpha*.

War and Peace: seasonal variation in male conflict in the chameleon grasshopper (*Kosciuscola tristis*)

Muschett, G.¹, Herberstein, M.E.¹ and Umbers, K.D.L.^{2,3}

¹Macquarie University, Department of Biological Sciences, NSW 2109; ²University of Wollongong, School of Biological Sciences, NSW 2522; ³University of Western Australia, Centre for Evolutionary Biology, WA 6008

While common, contests among animals are costly and seldom escalate to physical combat. Among Orthoptera, grasshoppers are known for their overall passive nature, but males of the chameleon grasshopper (*Kosciuscola tristis*) present an interesting exception. *K. tristis* males frequently engage in fierce fights over access to females. Fights include biting, grappling and mandible displays. Initial observations suggested that fighting occurred more frequently later in the season. The aim of our study was to assess whether there was any variation in fighting behaviour across the compressed Australian alpine season. We quantified how fighting related to male traits, female quality and male copulation success. We set up mating arenas similar to field scenarios which consisted of 5 males to 1 female and observed all aspects of behaviour for one hour. We also complemented our experiments with behavioural observations in the field. Our results showed seasonal variation in overall mating behaviour. Males were quicker to mate and mated for longer early in the season than later in the season. Confirming our initial observations, we found that males fought more often later in the season than early in the season. We discuss these data relative to seasonal fluctuations in sex ratio, female quality and mating opportunities.

Technical capacity building for biosecurity in the Asia-Pacific region: are we making a difference?

Naumann, I.D., Hossain, Z., Lee, W., Delamoir, S. and Hogan, B.

Plant Health Policy Branch, Biosecurity Plant Division, Australian Government Department of Agriculture,
GPO Box 858, Canberra ACT 2601.

The Australian Government Department of Agriculture is currently responsible for several programmes operating in the Asia-Pacific region and designed to develop technical capacity to support biosecurity systems. These programmes include (a) workshops and publications to develop understanding of the principles and global frameworks that support biosecurity, and (b) activities to enhance skills in performing surveillance, undertaking credible diagnostics, managing reference specimens, maintaining pest information systems, analysing risk and dealing effectively with phytosanitary threats. Data and case histories from recent workshops and capacity-building activities involving 18 south and south-east Asian countries indicate that the programmes are indeed making a positive difference. These programmes appear to be successful in the short term, but how should we go about measuring ‘success’ in the longer term? Indeed, how do we estimate scientific and technical proficiency across multiple disciplines and across culturally diverse countries at various stages of economic development?

Shape up or ship out: can we alter *Bactrocera tryoni* (Froggatt) (Diptera: Tephritidae) wing shape to affect sexual performance?

Newman, J.D.¹, Schutze, M.K.¹ and Clarke, A.R.^{1,2}

¹School of Earth, Environmental and Biological Sciences, Queensland University of Technology, G.P.O. Box 2434, Brisbane, Queensland 4001; ²Plant Biosecurity Cooperative Research Centre, L.P.O Box 5012, Bruce, ACT 2617.

Subtle changes in morphology may significantly impact insect fitness, and the relative contribution of genes, environment, and their interaction to such variation is the subject of ongoing research. The true fruit flies (F. Tephritidae) are a group for which subtle morphological variation is well documented, especially the shape of wings which are functionally important for flight and, for many species, courtship. However, mechanisms governing variation in tephritid wing shape remain to be fully understood.

We tested if Queensland fruit fly, *Bactrocera tryoni*, wing shape significantly changed following larval rearing on: i) different diets at a single temperature (guava, avocado, or tomato; 27°C); or ii) different developmental temperatures on a single diet (17°C, 22°C, or 27°C; guava). Wings of 30 males and 30 females were subjected to geometric morphometric shape analysis to evaluate differences in wing shape among treatments. Mating trials following different rearing conditions were conducted to test for any relationship between wing shape and male mating success.

There was a significant difference in wing shape among flies reared on different diets and temperatures. For the diet study, the greatest difference in wing shape was observed between guava reared males and all other diet treatments, especially between guava and avocado. For the temperature study, wing shape of *B. tryoni* reared at 17°C was significantly different to those reared at 22°C and 27°C. A significant difference in wing shape was detected between successfully vs unsuccessfully mating males in some, but not all trials; further research in this component is needed. We conclude that wing shape in *B. tryoni* is significantly affected by conditions experienced during larval development. This outcome has implications from research on population structure in the wild to pest management approaches such as the SIT where mating capability of mass-reared males is critical.

Inferring deep insect phylogenetic relationships using data from genomes and transcriptomes: research initiatives, methods, results, and prospects

Niehuis, O.

PLENARY SPEAKER

Centre for Molecular Biodiversity Research, Zoological Research Museum Alexander Koenig, Adenauerallee 160, 53113, Bonn, Germany, E-mail: o.niehuis@zfmk.de

The advent of next generation sequencing (NGS) techniques ushered a new era in phylogenetics. NGS not only simplified and accelerated nucleotide sequence data acquisition, but also allows researchers to compile datasets for studying novel, complex genomic meta-characters, such as gene structure and gene neighbourhoods. However, handling datasets in the gigabyte range not only proves to be challenging and – perhaps – intimidating, large datasets are also no guarantee of phylogenetic accuracy due to increased risk of systematic error.

In my talk, I will present methods and results from the international 1KITE project to illustrate the inference of a reliable insect backbone tree of life by analysing extensive NGS-derived transcriptomic data. I will emphasize the need for reliably assessing transcript orthology and present new software specifically developed for this purpose. In this context, I will highlight the importance of genomic data from non-model organisms, such as the ones currently being collected by the i5K initiative, for transcript orthology assessment. I will also present some of the methods employed by us to assess credibility of the newly inferred insect backbone tree of life.

Using the example of the enigmatic twisted-wing parasites, I will then exemplify how whole genome sequencing of non-model organisms gives access to novel, complex genomic meta-characters for phylogenetic inference. In this context, I will briefly outline goals of and opportunities provided by the i5K initiative. Last but not least, I will briefly exemplify how resources from the 1KITE project coupled with those from the i5K initiative will simplify molecular data acquisition in the near future by means of allowing target DNA enrichment and sequencing.

The beetle fauna of the Talbragar Fish Bed

Beattie, R.G.¹, Oberprieler, R.G.², Cai, C.³ and Slipinski, S.A.²

¹P.O. Box 320, Berry 2350, N.S.W., Australia; ²CSIRO Australian National Insect Collection, G.P.O. Box 1700, Canberra, A.C.T. 2601, Australia; ³State Key Laboratory of Palaeobiology and Stratigraphy, Nanjing Institute of Geology and Palaeontology, Chinese Academy of Sciences, 39 East Beijing Road, Nanjing 210008, China.

The Upper-Jurassic Talbragar Fish Bed in New South Wales, famous of its fish and conifer fossils, has yielded over 100 beetle fossils in recent years. The palaeo-environment of the site comprised a shallow lake environment fringed by a diverse woodland flora of conifers and other plants, allowing the fossilisation of both aquatic and terrestrial insects. After Hemiptera, the beetles are the largest of the nine insect orders found at the site thus far. A number of the beetle taxa have recently been described, but a variety of further specimens remains to be studied in detail. Many specimens are well preserved, whereas others are difficult to identify and assign to families with confidence. The main families recognisable are Cupedidae, Carabidae, Hydrophilidae, Elateridae, Derodontidae, Staphylinidae and Nemonychidae, spanning the feeding guilds of carnivory, fungivory, detritivory and herbivory. We present an overview of their diversity and of the likely nature of the Talbragar beetle fauna in the late Jurassic.

Trichromatic vision in the Australian bull ant

Ogawa, Y.¹, Narendra, A.², Zeil, J.² and Hemmi, J.M.¹

¹School of Animal Biology & UWA Oceans Institute, The University of Western Australia; ²Australian Research Council Centre of Excellence in Vision Science, Research School of Biological Sciences, The Australian National University. Email: yuri.ogawa@uwa.edu.au.

For over 30 years it has been thought that ants are the only Hymenopterans to only have two spectral photoreceptor types and therefore dichromates. Many ants are highly visual animals, however. The Australian bull ants of the genus *Myrmecia*, for instance, rely solely on visual information when navigating during foraging excursions. Different *Myrmecia* species are active at different times of the day. *M. vindex* forage exclusively after sunset when light levels are very low, while *M. croslandi* is active during the day. We investigated the spectral and temporal sensitivity of the two species in order to assess how the differing light environments affect their compound eyes. Flicker electroretinography (ERG) with monochromatic adaptation lights and intracellular electrophysiology revealed that the existence of three types of photoreceptor in the retina of both species with peaks at 360 nm, 450 nm and 550 nm (n=5-24) in *M. vindex* and 370, 470 and 510 nm (n=7) in *M. croslandi*. This is the first clear evidence that ants are trichromats as the other hymenopterans. The UV sensitive in both species decreases with increasing stimulation frequency, suggesting that UV photoreceptors are slower than blue and green receptors. ERG recordings also show that the temporal sensitivity clearly differs between the two species. The night-active *M. vindex* has a slower critical flicker fusion frequency than the day active *M. croslandi* (130 Hz and 180 Hz, respectively) at high light intensities, but is faster at low light intensities.

IOBC Global and the Asia and Pacific Regional Section (APRS)

Barratt, B.I.P.¹ and Palmer, W.A.²

¹AgResearch Invermay, Private Bag 50034, Mosgiel, New Zealand; ²Biosecurity Queensland, Ecosciences Precinct, Level 3, 41 Boggo Road, Dutton Park, QLD, 4102

The International Organisation for Biological Control (IOBC) <http://www.iobc-global.org/index.html> was established in 1955 as a global organisation affiliated to the International Council of Scientific Unions (ICSU). It is a non-profit scientific body which promotes sustainable pest and disease management. IOBC provides a forum for biocontrol practitioners to network and contribute globally. The organisation promotes international cooperation, communication and advocacy for biocontrol, providing training, assistance to non-English speaking members, financial support to young scientists and professional independent advice to policy makers. IOBC actively seeks to raise public/stakeholder awareness of the importance and potential for biocontrol. Amongst other activities, IOBC coordinates global working groups, and commissions on specific biocontrol and IPM issues. For example, the Commission on Biological Control and Access and Benefit Sharing (part of the CBD) has been a focus of activity over the last few years with the aim of ensuring that exploration and exchange of biocontrol organisms can continue unencumbered by excessive bureaucracy. IOBC comprises six regional sections. The Asia and Pacific Regional Section is one of the largest and most geographically diverse and includes most Asian nations and Australasia. The new executive committee with members from Australia, New Zealand and China is working hard to recruit members and to facilitate interaction between biological control researchers, practitioners and industry in the region. Our new website is about to be launched and this will be a vehicle for members to find out what is happening in biocontrol in the region including conferences and other events, significant publications, job and scholarship opportunities, and awards for young members to attend and present their work at conferences.

The sexual exploitation of thynnine wasps by deceptive signals emitted from Australian orchids

Peakall, R.¹, Bohman, B.^{1,2} and Phillips, R.D.¹

¹Research of Biology, The Australian National University, Canberra, ACT 0200; ²Research School of Chemistry, The Australian National University, Canberra ACT 0200.

Within Australia, one group of Hymenoptera, the thynnine wasps, stand out for their endemism, sheer species diversity and their unique mating system. The wingless females use sex pheromones to attract the winged males, which carry the females *in copula* to a food source. This reproductive behaviour has been exploited by several hundred species of sexually deceptive orchids, which emit deceptive semiochemical signals to sexually lure male wasps as pollinators. We have taken advantage of this interaction to elucidate the sex pheromone chemistry of these wasps, where females are typically difficult to find. Our studies of these orchids revealed that one, two or three compounds from a pool of six related 2,5-dialkylcyclohexane-1,3-diones, called chiloglottones, are used to attract the wasps. These compounds represent a unique class of natural products with one compound being confirmed as the sex pheromone of *N. cryptoides*, the pollinator of *C. trapeziformis*. Phylogenetic analysis of both *Chiloglottis* orchids and pollinators shows that while many species share components of their pheromone blends, speciation is typically associated with changes in the semiochemicals involved. Our work on *Zaspilothynnus* pollinators of *Drakaea* orchids (sister to *Chiloglottis*) revealed entirely different sex pheromones. We discovered alkylpyrazines and novel hydroxymethyl pyrazines as components of the sex pheromones of *Z. trilobatus* males, which pollinate *D. glyptodon*. Pyrazines have rarely been implicated as insect sex pheromone components, with our discovery representing the first confirmed case of pyrazines as sex pheromones in insects. Evidence for several other chemical systems is emerging, hinting at extraordinary sex pheromone diversity within the thynnines. An overlay of orchid exploitation onto a phylogeny of the wasps further reveals that some groups are more readily exploited, a pattern we predict will be underpinned by sex pheromone chemistry.

Biological control past, present and future in the greenhouse industry?

Pilkington, L. J.

NSW Department of Primary Industries, Central Coast Primary Industries Centre, Locked Bag 26, Gosford,
NSW 2250

The evidence supporting the use of biological control in the greenhouse industry is wide and varied. In many parts of the world where the greenhouse industry has flourished, there is little doubt that these systems are highly successful. In Australia, the biological control industry does not enjoy the same abundant access to native biological control agents and the greenhouse industry is not as advanced as it is in other parts of the world. The use of biological control agents in Australia, however, is beginning to gain momentum in a variety of commodities and greenhouse systems. Current routine biological control use in greenhouse systems will be presented along with current limitations and scope to extend their use. Accessibility of commercially available biological control agents will be discussed. The overseas evidence will be presented and discussed with a view to extrapolate to a local perspective and where we need to go in Australia to enjoy the same successes as other parts of the world.

Comparing herbivore guilds: seed-feeding weevils from different continents

Pinzon Navarro, S.

Australian National Insect Collection, CSIRO, Black Mountain, Canberra, ACT 2617

The Australian genus *Melanterius* (*Coleoptera: Curculionoidea*) is a large group of seed-feeding weevils closely associated with Australian Acacias. *Melanterius* species are of economic importance given their use as biocontrol agent, nevertheless thorough studies have been lacking. For the past three years Acacias have been inspected yielding more than 3000 specimens, representing 42 genera. A subset of weevils has been sequenced for 3 mitochondrial and 3 nuclear genes to delimit species molecularly and study their host specificity. The phylogeny of the weevils will be analyzed with the *Acacia* phylogeny, available from collaborators, to determine the evolutionary patterns between these groups. Determining the host specificity of the weevils and their relationship to the acacias is crucial for the control of African weeds and insights into the diversity of Australian weevils. We further compare different attributes of *Acacia* species: distribution, morphology and life form to predict host occurrence by weevils and compare this to our observations. Previous studies of Neotropical seed feeding weevils show a higher degree of host specificity. We compare our previous studies to our new Australian data, as well as data from the Old Tropics and temperate forests. This shows an insight into highly complex patterns of specificity even in one of the most specific guilds within the herbivores.

Discovering the Australian weevil fauna

Pullen, K.R.¹, Jennings, D.² and Oberprieler, R.G.³

¹Agriculture, CSIRO, Clunies Ross Street, Acton, ACT 2601; ²Australian National Insect Collection, CSIRO, Clunies Ross Street, Acton, ACT 2601; ³Australian National Insect Collection, CSIRO, Clunies Ross Street, Acton, ACT 2601

The weevils (Coleoptera: Curculionoidea) globally comprise nearly 60,000 described species, of which over 80 per cent are assigned to the family Curculionidae. A total of 4110 species – seven per cent of the world fauna – is Australian, representing all seven known families, a feature shared only with the South American fauna. The Australian fauna is distinctive, with large imbalances in the representation of the constituent families and subfamilies compared to the described world fauna. Among the families, Belidae, Nemonychidae and particularly Caridae are well represented, while Anthribidae, Attelabidae and Brentidae are poorly represented. Within the Curculionidae, Cyclominae and a group of unplaced tribes are well represented; Brachycerinae, Conoderinae, Dryophthorinae, Platypodinae and Scolytinae are poorly represented. Two tribes are endemic to Australia: Rhinorhynchidiini (Brentidae: Apioninae) and Amycterini (Curculionidae: Cyclominae).

The history of discovery of the Australian weevil fauna largely follows that of its insect fauna in general. The first weevils were collected on Cook's British voyage of discovery in 1770, and described by Fabricius in Europe. Important early collections were made by naturalists attached to British and French expeditions. Pascoe, receiving material in England from a developing community of colonial collectors, was the most important author of Australian weevil names during the first 80 years of their taxonomic study. It was not until the second half of the 19th century, under the patronage of the Macleays, that Australian-based taxonomists such as W.J. Macleay and Blackburn began to have an impact. By far the most prolific author of Australian weevil names was Lea, whose death in 1932 marked a sudden drop in the rate of description of the fauna. More recent work by Zimmerman and others, together with renewed interest internationally in the higher classification of weevils, indicate a return to activity around documentation of the fauna.

The role of gall formers as biological control agents of the broad-leaved paperbark tree *Melaleuca quinquenervia* in Florida USA

Purcell, M.¹, Pratt, P.², Makinson, J.¹, Brown, B.¹, Davies, K.³, Taylor, G.⁴, Giblin-Davis, R.⁵ and Scheffer, S.⁶

¹USDA ARS Australian Biological Control Laboratory, CSIRO Biosecurity, GPO Box 2583, Brisbane, QLD 4001; ²USDA ARS Invasive Plant Research Laboratory, 3225 College Ave, Fort Lauderdale, FL 33314 USA; ³Australian Centre for Evolutionary Biology and Biodiversity, and School of Agriculture, Food and Wine, The University of Adelaide, Waite Campus, PMB 1, Glen Osmond, SA 5064; ⁴Australian Centre for Evolutionary Biology and Biodiversity, and School of Earth and Environmental Sciences, The University of Adelaide, North Terrace, Adelaide, SA 5005; ⁵Fort Lauderdale Research and Education Center, University of Florida, 3205 College Ave, Davie, FL 33314-7799; ⁶Systematic Entomology Lab, USDA-ARS, 10300 Baltimore Av., Beltsville, MD 20705 USA

The Australian broad-leaved paperbark tree, *Melaleuca quinquenervia*, is a serious weed in wetland systems of Florida USA. This tree was introduced in the late 1800's as an ornamental and greatly expanded its range causing significant environmental and economic damage. It also threatened environmentally sensitive areas such as the Florida Everglades whose habitat was highly favourable to the rapid growth of *M. quinquenervia*. In 1984 a classical biological control program commenced to find agents in the native range of this tree along the east coast of Australia. Among more than 450 insect species that were found to feed on *M. quinquenervia* and its close relatives, gall formers were discovered that damaged mature trees, saplings and seedlings. Cecidomyiidae and Fergusoninidae flies, gall-forming Eriococcidae scales and Eriophyiidae mites were all evaluated for their potential as biological control agents. The fly, *Fergusonina turneri* (Diptera Fergusoninidae), which forms galls in a mutualistic association with nematodes, was released in 2005 but failed to establish after multiple attempts. The stem-galling fly *Lophodiplosis indenata* (Diptera: Cecidomyiidae) was released in 2008 and rapidly established causing extensive damage, particularly to sapling and seedlings. This fly and two other biological control agents have contributed to the successful control of *M. quinquenervia* in Florida. Another three *Lophodiplosis* species are being evaluated in case further control measures are required.

A hidden world revealed: using MicroCT scanning to see inside a gall

Purcell, M.¹, Cooper, P.¹, Yeates, D.² and Rowell, D.¹

¹Research School of Biology, Australian National University, Canberra ACT 0200 Australia; ²CSIRO Ecosystem Sciences, Clunies Ross Street, Acton, ACT 2601, Australia

Members of the genus *Fergusonina* (Diptera: Fergusoninidae) are small (2-3 mm) flies that are almost entirely restricted to Australia. Their association with the nematode *Fergusobia* (Tylenchida: Neotylenchidae) is the only known mutualism between insects and nematodes. Together the flies and nematodes form galls in the bud tissue of myrtaceous plants. Their unique association is the only known mutualism between insects and nematodes, and *Fergusobia* is the only nematode with parthenogenetic and sexual plant-living generations followed by an insect-parasitic generation. While the biology of the *Fergusonina-Fergusobia* system was first described in the 1930's, many of the details of these organisms' behavior within the gall are poorly understood, as it has not been possible to observe them without dissecting the galls that contain them, which disrupts their natural behaviour. There are many questions about their interactions that dissection has not been able to answer, such as how the pre-parasitic nematodes enter the female fly larvae. By freezing the occupants of a gall and essentially obtaining a snapshot of their activity using MicroCT scanning, some outstanding questions concerning the biology of the system may finally be answered.

Lablab (*Lablab purpureus* (L.) Sweet) used for bio-control by native beneficial arthropods in Pumpkins in Queensland Australia

Qureshi, S.A., Angove, M., Wilkens, S. and Syeda, S.S.

School of Pharmacy & Applied Science, LaTrobe University,
Bendigo, Victoria 3550, Australia

Pumpkin crop hosts a wide range of serious sap-sucking insect pests, including silverleaf whitefly (SLW) and aphids. These represent considerable risk to the Australian horticulture industry. The control of insects is made difficult through insecticides use because of resistance, pollution and other side-effects. The aim of this study was to employ a biological control strategy by planting lablab in association with pumpkin crop in an attempt to attract predatory species that prey on problem insects. Over the trial 21-week period weekly sampling measured the population of beneficial (ladybird beetle, lacewing adults, lacewing larvae, European bees) and problem insects (SLW and aphids).

Pumpkin in the pumpkin/lablab treatment had significantly ($P < 0.05$) more ladybirds and lacewing larvae, and tended ($P = 0.12$) to have more lacewing adults and spiders per plant per sampling occasion than pumpkin in the pumpkin-only treatment. Pumpkin plants in the pumpkin/lablab treatment had similar numbers of harmful insects (pests) per plant per sampling occasion as pumpkin in the pumpkin-only treatment except for adult SLW where pumpkin plants in the pumpkin/lablab treatment had fewer ($P < 0.05$) adult SLW than pumpkin from the pumpkin-only treatment. The total weight (kg) and number of marketable pumpkin per hectare harvested between 10 November and 20 December 2008 was greater ($P < 0.05$) for the pumpkin/lablab treatment than the pumpkin-only treatment.

Lablab appears to be viable option to grow within cucurbits or as field boundary crops to attract and increase beneficial insects and spiders for the control of sap-sucking insect pests. Use of these bio-control strategies affords the opportunity to minimise pesticide usage and the risks associated with pollution and insect resistance.

Head roll stabilisation in bull ants *Myrmecia pyriformis* during twilight

Raderschall, C.A., Narendra, A. and Zeil, J.

Research School of Biology, The Australian National University, Canberra, 0200 ACT

As animals move, they generate image motion in their visual field. Image motion generated by translation contains information about the environment, while image motion generated by rotations does not and therefore needs to be minimised. Locomotion – be it flying or walking – induces rotations of the body and the head of an animal thereby degrading vision. To reduce these unintended locomotion-induced eye rotations, animals are known to perform compensatory head movements that help stabilise gaze.

To date, most studies investigating head stabilisation in insects have come from flying species. Yet, walking insects have a special problem in keeping their head stable because they are in direct contact with the substrate, which will induce complex and unpredictable body rotations as they walk.

Bull ants (*Myrmecia pyriformis*) are crepuscular animals that experience a wide range of light intensities during their foraging trips. These ants rely heavily on visual cues for navigation and for catching prey.

To measure their ability to control head orientation in the presence of substrate-induced body roll, we took advantage of the ants' motivation for walking along fallen sticks. We induced ants to walk along a twisted band that gradually induced body roll. Filming ants from the front allowed us to quantify head and body roll in a range of ambient light conditions in the ants' natural habitat, as well as in room light and complete darkness in the laboratory.

We find that (1) ants are able to keep their head horizontally aligned against body roll of up to 60 degrees; (2) head stabilisation is partly visually controlled, because there is a small degradation of the response as light levels drop; (3) however, the ants also compensate partially for body roll in complete darkness, suggesting non-visual information contributing to head stabilisation.

Miniaturisation in ants: size, number and distribution of antennal sensilla

Ramirez Esquivel, F., Zeil, J. and Narendra, A.

Research School of Biology, The Australian National University, Building 46, Biology Place, Canberra,
Australian Capital Territory 0200, Australia

Ants, like other insects, have at their disposal a battery of sensors, or sensilla, on their antennae which provide information about a range of environmental factors. Sensilla not only detect chemical and mechanical cues but also respond to changes in temperature, humidity and CO₂ levels. Information obtained from these sensors is used to carry out a range of tasks including nest maintenance, nestmate recognition, recruitment and brood care. However, the body size of different species of ants covers a wide range, which raises the question: how does the antennal array scale with decreasing body size?

To address this question we studied the antennal sensilla of the Australian bull ant *Myrmecia pyriformis* using Scanning Electron Microscope (SEM) images. The workers of *M. pyriformis* are highly polymorphic (body length: 12–26 mm), providing us with the opportunity to study the consequences of changing body size on sensilla type, number size and distribution within a single species. We identified eight types of sensilla and constructed maps of the location of each sensillum revealing distinct distribution patterns for different types of sensilla. In ants of all body sizes, all 8 types of sensilla are present with a fairly consistent distribution. In most cases, the number of sensilla increases with body size. Conversely, the size of the sensilla themselves did not appreciably increase with body size. We provide preliminary results for a larger comparative study that includes species of a range of body sizes (body length: 2–26 mm).

Molecular identification of immature parasitoids

*Reynolds, O.L.*¹, *Jenkins, C.*², *Smart, J.*¹ and *Fell, S.*²

¹Graham Centre for Agricultural Innovation (NSW Department of Primary Industries and Charles Sturt University), NSW Department of Primary Industries, Private Bag 4008, Narellan, NSW 2567, olivia.reynolds@dpi.nsw.gov.au; ²NSW Department of Primary Industries, Private Bag 4008, Narellan, NSW 2567, Australia.

Worldwide, fruit flies (Diptera: Tephritidae) of economic importance attack a wide range of commercial fruit and vegetable crops and pose a significant biosecurity threat to domestic and international trade. In several regions of the world, inundative and/or augmentative releases of parasitoid wasps (Hymenoptera: Braconidae) as part of an integrated pest management program have been successfully used for the control of pest fruit flies. However, most tephritid parasitoids have never been subjected to molecular characterisation, despite their use as biological control agents. In this study, genetic markers were sequenced from four parasitoid species of the Queensland fruit fly, *Bactrocera tryoni* (Froggatt) found in Australia and successfully used in control programs worldwide. These include the native larval parasitoids *Diachasmimorpha tryoni* (Cameron) and *D. kraussii* (Fullaway) and the introduced larval and egg-larval parasitoids respectively, *D. longicaudata* (Ashmead), and *Fopius arisanus* (Sonan). Sequence data from the COI and 28S D2 regions indicated that *Diachasmimorpha* spp. form a phylogenetically coherent group, consistent with current morphological taxonomy. The morphologically distinct *F. arisanus* clusters outside of this group. PCR-RFLP assays for the COI regions were successfully evaluated against DNA from all four adult parasitoids and *B. tryoni* larvae exposed to adult female *D. tryoni*. Verification of the COI PCR-RFLP assay indicated this was both specific and sensitive with a detection limit of 1.8 pg of *D. tryoni* DNA. Such an assay may be valuable in biological control programs that utilise *Diachasmimorpha* spp. or *F. arisanus*. Particularly where a rapid result may be required for within-host detection of immature parasitoids, thus avoiding the arduous and protracted rearing and dissection processes involved with morphological identification.

Effect of *Botrytis cinerea*-infected leaves and berries of *Vitis vinifera* on the ovipositional preference and larval performance of *Epiphyas postvittana*

Rizvi, S.Z.M.^{1,2}, Raman, A.^{1,2}, Wheatley, W.¹ and Cook, G.¹

¹Charles Sturt University, PO Box 883, Orange, NSW 2800, Australia; ²Charles Sturt University & E H Graham Centre for Agricultural Innovation, PO Box 883, Orange, NSW 2800, Australia

There is a growing body of knowledge on the ovipositional preference of phytophagous insects and its consequences on the life-history performance of the offspring. The extent to which ovipositional choices service the nutritional needs of her offspring remains an open debate. This paper reports a mismatch between the ovipositional preference and larval performance of *Epiphyas postvittana* in a tripartite system with its host *Vitis vinifera* and commonly co-occurring fungus *Botrytis cinerea*. Populations of *E. postvittana* and *B. cinerea* often exist concurrently on *V. vinifera* and their interaction and mutual influence are currently being explored. Host-seeking gravid female of *E. postvittana* assessed the infection status of the host plant using olfactory, visual, and tactile cues. In consequence, she laid significantly fewer eggs on *B. cinerea*-infected leaves and berries of *V. vinifera*. On the contrary, larvae of *E. postvittana* showed the best performance on *B. cinerea*-infected berries. The larvae fed on *B. cinerea*-infected berries of *V. vinifera* showing greater survival rate, shorter time to pupation, greater pupal mass, and on becoming adults they laid more numbers of eggs than the larvae that were enabled to feed on uninfected berries. External and internal examination of the larvae established that the larvae carry and transport viable conidia of *B. cinerea* on the body surface and within the gut.

Auditory information processing in insects under real world conditions

Römer, H.

Zoology, Karl-Franzens University, Graz, Austria

In the past, behavioral ecologists had a tendency to study communication systems by looking at signal design and signaling behavior, but ignoring the sensory and brain mechanisms that enable receivers to make sense of signals in a noisy world. They simply assumed that natural or sexual selection would have provided individuals with the sensory and neuronal machinery to perform a given task sufficiently well (i.e., to increase their fitness). However, a comprehensive understanding of communication systems and sexual selection by female choice greatly benefits from considering the cognitive mechanisms underlying decisions where signal processing is involved.

The information needed by an organism for shaping its behavior and for decision making is transmitted via afferent nerves and encoded in trains of action potentials. Sensory systems and the brain have to make adaptive assumptions about what had happened in the physical world, by decoding this information. In all sensory systems investigated, receptor cells or sensory interneurons always reveal short episodes of high-frequency firing of action potentials (bursts) in addition to single, spontaneous APs. These bursts convey information about important stimulus features.

In my contribution I take a strictly brain-based point of view and ask how crickets and katydids can communicate acoustically and listen to conspecifics or predators in a “cocktail party-like” situation. After describing the ecological and behavioral evidence for substantial masking in the airborne sound channel I present a method for recording action potential activity of identified, single neurons directly in the field, before presenting several solutions for this problem on the receiver side. These include evolutionary changes in frequency filters, spatial release from masking, and neuronal gain control mechanisms.

An innovative approach promoting entomology and molecular biology to the next generation of scientists

Rundle, B.J.

Faculty of Science, Trinity Grammar School, Kew, Victoria, Australia, 3101; Department of Zoology, Bio21 institute, The University of Melbourne, Parkville, Victoria, Australia, 3010

The future of our natural environment will become the responsibility of the next generation of scientists – these are the students who currently sit in secondary school science laboratories around the country. Therefore, part of the challenge for teachers is to deliver programs and curricula that foster student interest in the biological world and exposes them, through their own involvement, to the work and practices undertaken in current research. This presentation describes an approach taken by a secondary school that aims to raise the profile of entomology and molecular science at the secondary school level and facilitates the involvement of students in hands-on research projects, conducted at the school, in collaboration with a tertiary institution. This approach has resulted in the development of a self-sufficient research laboratory within the school, enabling students to work on projects both in and out of the classroom. One such project has seen students working on parasitoid wasps of the genus *Trichogramma*. In order to identify field caught strains they have been sequencing ITS2 regions and comparing their results to known sequences. This project has led to students discovering a strain with what appears to be a unique ITS2 sequence and as a consequence they are now planning what other regions of the *Trichogramma* genome to investigate. To my knowledge this is a unique innovation in a secondary school environment. Raising the profile of entomology and molecular science and introducing secondary students to current scientific practice will lead to a more informed awareness within the community of the contributions of this area of scientific endeavour. In addition, given that youth generally seek vocational pursuits as a consequence of their experiences I believe that an early introduction to entomology and molecular science is likely to encourage young people to follow a career in these fields.

Rising threats from *Arundo donax*: Australian contribution to a successful US project

*Sands, D.P.A.*¹, *Goolsby, J.A.*² and *Palmer, W.A.*³

¹Ecosciences Precinct, CSIRO, Brisbane; ²USDA-ARS, 22675 N. Moorefield Rd., Moore Airbase #6419, Edinburg, Texas 78541 ; ³Biosecurity Queensland, Ecosciences Precinct, Level 3, 41 Boggo Road, Dutton Park, QLD, 4102

Giant reed, *Arundo donax* (Poaceae), originally from the Mediterranean region, is a serious weed in south-western USA, particularly riparian zones edging the Rio Grande Valley. There, impenetrable thickets extend upstream for 1600 k, replacing native vegetation, reducing visibility for law enforcement on the international border, consuming valuable irrigation water, and enhancing the invasion and survival of the cattle fever tick from Mexico. Between 2005 and 2012, three potential biological control agents from the Mediterranean wetlands of France and Spain were shipped to Texas for further evaluation; a diaspid scale, *Rhizaspidotus donacis* (Hemiptera: Diaspidae), a parthenogenetic gall-forming wasp, *Tetramesa romana* (Hymenoptera: Eurytomidae) and a leaf-sheath miner, *Lasioptera donacis* (Diptera: Cecidomyiidae). Problems rearing the scale insect and gall-former were overcome in a collaborative project between USDA and an emeritus CSIRO scientist using information gained with similar insects in historical Australian biocontrol projects. The gall wasp was reared in “Sands” cages screening in black mesh, which allowed normal oviposition behaviour. Controlled high nitrogen fertilization and created soft, nutritious plant tissues which increased fecundity. Methods were developed for the bivoltine diaspid scale to stimulate reproduction. Live crawlers from individual, isolated females were held in gelatine capsules until crawlers or parasitoids emerged. Crawlers could be isolated in clean capsules for biosecurity inspection and use in rearing. Cultures on plants were then easily made by pinning opened capsules onto plants used for tests or culture. The leaf-sheath miner required a symbiotic saprophytic fungus for development of larvae. Both leaf miner and several accessions of the fungus (from North America and Europe) were successfully cultured. The wasp is now widely established in the Rio Grande Basin and is causing significant damage to stems and lateral shoots. The scale, although limited in distribution, is reducing recruitment of new stems. Large areas of giant reed along the Rio Grande River are now impacted, so that this project may be the first to demonstrate the successful biocontrol of a grass. Development of these successful methods provides other countries including Australia an opportunity to carry out necessary tests, with minimal adjustments, for two otherwise potentially difficult valuable agents for biocontrol of giant reed.

Effect of shade on the susceptibility of two varieties of *Canna edulis* Kerr to defoliators

Sasaerila, Y.¹, Tajuddin, T.² and Asri, S.¹

¹Biology Department Universitas Al Azhar Indonesia, Jl. Sisingamangaraja, Samping Kompleks Masjid Agung Al Azhar, Kebayoran Baru, Jakarta Selatan, Indonesia. ²Agency for Assessment and Application of Technology (BPPT), Center for Biotechnology Research, PUSPIPTEK, Serpong, Tangerang Selatan, Indonesia

Canna edulis is an agricultural crop species with many uses, including baby food, flour, animal feed, insecticide, treatment of rheumatic, fever, constipation, etc.

This species is relatively nutritious with considerably good level of carbohydrate, protein and elements such as K, P, Fe and vitamin B1, and is used for food in South America and Asia. As species that naturally grown under stories (Sasaerila, et.al., 2011) *C. edulis* grow best at low light environment. This finding has the implication that this plant could be cultivated under the tree canopy, such as under the oil palm or rubber plantation, or even under the canopy of tropical rain forest without damaging the environment. Mass plantation of *C. edulis*, however, will raise the possibility of pest infestations. This experiment explores species of defoliators attack two varieties of *C. edulis*, red and white, and the level of susceptibility of each variety to defoliators when grown under high and low light environments. Results indicate that insects that attacked *C. edulis* were *Valanga nigricornis* (Orthoptera: Acrididae), *Systoloderus* sp. (Orthoptera: Tetrigiidae), Lepidoptera: Nymphalidae, Pyralidae and Psychidae. Both varieties are significantly more susceptible to defoliators when grown under high light environment, compare to those grown under low light environment: about 25% and 17% of leaf damage in high light grown *C. edulis* of red and white variety, respectively, compared to 0.53% and 1.02% of leaf damage of shaded grown red and white *C. edulis*.

Wild pollinator communities in almond plantations and mallee woodlands

Saunders, M.E.

Institute for Land Water and Society, Charles Sturt University, Albury NSW 2640

Almond plantations have expanded rapidly across northwest Victoria's mallee regions, with more than half of Australia's plantings now located in the area. Almonds are 100% reliant on insect pollinators to set fruit, yet limited information exists on insect pollinators in Victoria's mallee regions. In addition, no prior research has examined how insect pollinator communities may be influenced by homogeneous tree plantations that encroach upon dynamic mallee woodlands. In 2010 and 2011, almond plantations and mallee woodlands were sampled in northwest Victoria during the late winter almond flowering period. The goal of this research was to identify how management practices in plantations influenced wild pollinator community composition in plantations and adjacent mallee vegetation. Abundance of native bees was higher at sites with intermediate levels of ground cover vegetation and was positively associated with plant richness on the orchard floor. There was no evidence of an edge effect on native bee abundance and richness at the ecotone between plantations and woodlands, but overall vegetation structure and changes in heterogeneity along the ecotone were likely influencing native bee communities. In addition, potential wasp and fly pollinators were abundant in woodlands, but mostly absent from monoculture plantations. These findings provide valuable ecological information for almond growers, as diverse insect pollinator communities can provide pollination services to pollen-limited almond. The study has also contributed to knowledge of insect pollinator fauna in Victoria's unique mallee regions, which are being increasingly impacted by agricultural land use change.

Arthropods in agricultural landscapes: challenging and supporting food and fibre production

Schellhorn, N.A.

CSIRO, Brisbane Australia

Demands for food, fiber, and bioenergy are projected to escalate in the coming decades. Arthropods challenge production by damaging crops pre- and post-harvest. However, arthropods support production directly and indirectly by water and nutrient facilitation, pollination and pest control. These ecosystem services offer us opportunities to meet the demands of impending resource constraints and to close the yield gap. Nancy will discuss the unique challenges and opportunities arthropods pose in Australian agricultural systems, in the context of global research trends in arthropod-based ecosystem services. Using empirical and theoretical examples, Nancy will show that fundamental to capturing these services is identifying the interaction between species movement traits, disturbance, and the landscape context. Yet, more has to be done to demonstrate impact in order to integrate these services into Australian agricultural systems.

Searching behaviour in insects

Schultheiss, P.¹ and Cheng, K.²

¹Research School of Biology, Australian National University, Canberra, ACT 0200; ²Department of Biological Sciences, Macquarie University, Sydney, NSW 2109.

Insects often face the task of having to find a precise location in space, such as a food source or the nest/hive entrance. Ants and bees in particular use a range of navigational mechanisms, such as path integration or visual navigation by terrestrial visual landmarks, to travel to the correct area. Should they fail to find the exact target, they engage in systematic searching behaviour. Such a search path consists of loops of increasing size, which are centred on the starting point. The structure, especially the size of this searching behaviour is highly flexible. It tracks the animal's level of navigational accuracy, with a tight search indicating very precise navigation, and a larger search showing less accurate navigation.

Australian desert ants (Formicidae) adapt their systematic search to the errors of path integration, which increase with the distance that is integrated. Their search paths also reveal that the accuracy of visual navigation depends on the amount of information contained in the visual panorama. A comparison of two species of *Melophorus* ants from very different visual environments (cluttered and featureless) shows that each species relies mostly on the navigational strategy that works best in these respective environments. *Melophorus bagoti* in its cluttered scrub-desert environment relies strongly on visual navigation by terrestrial landmarks, while (the as yet undescribed) *Melophorus* sp. in its featureless salt-pan environment relies more strongly on path integration. Thus, by investigating searching behaviour in detail we can gain insight into how these animals process navigational information.

Requiem for a fruit fly: the end of the road for *Bactrocera papayae* Drew & Hancock and *Bactrocera invadens* Drew, Tsuruta, & White (Diptera: Tephritidae). But what does it mean for Australia?

*Schutze, M.K.*¹ and *Clarke, A.R.*^{1,2}

¹School of Earth, Environmental and Biological Sciences, Queensland University of Technology, G.P.O. Box 2434, Brisbane, Queensland 4001; ²Plant Biosecurity Cooperative Research Centre, L.P.O Box 5012, Bruce, ACT 2617.

Bactrocera dorsalis (Oriental fruit fly), *B. papayae* (Asian papaya fruit fly), and *B. invadens* (Invasive fruit fly) are major pests in Asia, the Pacific, and Africa; however, none occurs on the Australian mainland. Consistent characters separating these taxa have proven elusive due to their high degree of morphological similarity; this has confounded management, quarantine, and research. While the latter species are well-known to Australian entomologists, *B. invadens* is less familiar as it occurs beyond our region. Since detection in Kenya in 2003, *B. invadens* has displaced other fruit fly pests as it spread across sub-Saharan Africa, including South Africa.

We report findings of a major international collaborative effort using multidisciplinary approaches to resolve cryptic tephritid species complexes. It builds on 20 years of research on *B. papayae* and *B. dorsalis* (among other *dorsalis*-complex taxa), and 10 years of research on *B. invadens*. Integrated behavioural, genetic, cytogenetic, morphological, and chemoeological data present a compelling case that *B. papayae*, *B. invadens*, and *B. dorsalis* are the same biological species.

Redefining these taxa as one species poses significant quarantine and regulatory implications for Australia. *Bactrocera papayae* is a major plant biosecurity threat to the north because of multiple entry pathways from Indonesia and PNG; yet, its potential invasive range is likely to be restricted to the Australian tropics based on its current tropical SE Asian distribution. However, nearly all of cropping Australia becomes climatically suitable following recognition it is the same species as the more widely distributed, and highly invasive, *B. dorsalis*. Given this, a continental-scale incursion, with probable displacement of both Qfly and Medfly, becomes a likely scenario given successful establishment. The biosecurity implications of this remain to be fully appreciated, particularly as *B. dorsalis* is recognised as Australia's #1 biosecurity threat with a potential invasion cost of \$1 billion.

DNA barcoding reveals hidden diversity among Australia's Trichoptera (Caddisflies)

Shackleton, M.

Murray-Darling Freshwater Research Centre, La Trobe University, University Drive, Wodonga, VIC 3691.

DNA barcoding is increasingly being recognised as a useful tool for species identification. Over the past four years a number of projects have aimed at compiling DNA barcode databases for freshwater macroinvertebrates. In particular, during 2013 and 2014 the Murray Darling Basin Authority funded the collection, identification, and sequencing of freshwater macroinvertebrates from the Murray-Darling Basin. The database that has resulted from this funding currently contains over 700 sequences from 160 species across 11 orders. The database was made publically available through the Barcode Of Life Database (BOLD) in the hope that it would aid future researchers working on Australian aquatic fauna and encourage others to add to the database.

Further to this, a project aimed at sequencing the Trichoptera (Caddisflies) of Australia has been progressing over the past four years. To date the Trichoptera database contains nearly 1000 sequences from 237 species. While these data are currently stored in a private project within BOLD, the researchers involved are working towards making them publically accessible.

The barcode data on Trichoptera have revealed some taxonomic and interpretative issues that have implications for our current understanding of the taxonomy of Trichoptera and the usefulness of DNA barcoding as a tool for identifying Trichoptera species. For example, *Tamasia variegata* exhibit relatively large genetic variation compared to other Trichoptera species. Despite this, the data support the status of this species as a single taxonomic unit, suggesting that the simple delineation of species based on a percent divergence value may not be widely applicable for all trichopteran species. In contrast, data on *Antipodoecia*, currently recognised as being monotypic, indicate that this genus contains a number of sympatric cryptic species separated by very large genetic divergences. These and other findings from the Trichoptera DNA barcode data are discussed.

100 years of continually successful weed biological control in Australia

Sheppard, A.¹, Cullen, J.¹ and Palmer, W.²

¹ CSIRO Biosecurity Flagship GPO Box 1700 Canberra ACT 2601

² Biosecurity Queensland, Department of Agriculture, Forestry & Fisheries, Ecosciences Precinct, GPO Box 267, Brisbane, Qld 4001

Biological control of weeds started in Australia in 1903 when the Queensland Department of Agriculture and Stock imported *Dactylopius ceylonicus* cochineal (ex Brazil via India/Sri Lanka) to work on as a potential biological control agent for *Opuntia vulgaris* (Barbary fig) but the culture died out before any releases were made. Then in 1913-1914 Department of Agriculture and Stock imported three more *Dactylopius* spp., *Cactoblastis cactorum* and a disease of *Opuntia*. In 1914 *D. ceylonicus* was released in Queensland and quickly led to the successful control of *O. vulgaris*. In the same year the moth *Epinotia lantana* and the fly *Agromyza lantanae* were released on lantana (ex Mexico via Hawaii) but did not achieve any control. From 1921 to 1940, 19 other insect agents were released against seven *Opuntia* spp. and 12 of these agents established. The major success of the *Cactoblastis* moth complemented by *Dactylopius opuntiae* led to the world renowned successful control of *Opuntia stricta* (prickly pear) over 25M ha of Queensland and NSW. Since then Australia has run 73 weed biological control programs (69 on weeds exotic to Australia) against weeds of agriculture, the environment, recreation, amenity and health. Of these 58 were fully developed programs. In summary 14 have been very successful, 11 seasonally or regionally successful, 11 programs were unsuccessful and 22 programs are still ongoing and too early to assess. That is a confirmed success rate of 69% programs and included targets like salvinia, rubber vine, bridal creeper and Paterson's curse. A 2006 independent evaluation also showed that for an annual investment of \$4M a year since 1903 weed biological control has returned, not including environmental benefits, an annual benefit of \$95M to the \$4.4 Billion a year financial problem weeds cause to Australian agriculture. The 1970s through to the 1990s saw the most weed biological control programs in Australia. Since then activity and capability have gone into serious decline. This paper will tell the story of 110 years of weed biological control, a century on from the first effective release, and look to the future around opportunities and capacity to deliver.

Putting Australian Flower Flies (Diptera: Syrphidae) into a world phylogenetic context

Skevington, J.H.^{1,2}, *Young, A.D.*^{1,2}, *Mengual, X.*³, *van Steenis, W.*⁴, *van Zuijen, M.*⁵,
*Ståhls, G.*⁶, *Hauser, M.*⁷, *Kelso, S.*¹ and *Thompson, F.C.*⁸

¹Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, K1A0C6, Canada; ²Carleton University, Biology Department, 207 Nesbitt Biology Building, 1125 Colonel By Drive, Ottawa, Ontario, K1S5B6, Canada; ³Zoologisches Forschungsmuseum Alexander Koenig, Leibniz Institute for Animal Biodiversity, Adenauerallee 160, Bonn D-53113, Germany; ⁴Zoological Museum Amsterdam, part of Naturalis Biodiversity Center, Darwinweg 2, 2333 CR Leiden, The Netherlands; ⁵Wageningen, The Netherlands; ⁶Finnish Museum of Natural History, Entomology Dept., P.O.Box 17 FIN-00014, University of Helsinki, Helsinki, Finland; ⁷California Department of Food & Agriculture, 3294 Meadowview Road, Sacramento, California, 95832-1448, USA; ⁸Department of Systematic Biology – Entomology, NHB MRC 169, PO Box 37012, Washington DC 20013-7012, USA.

Flower flies are increasingly being used as models and study organisms in ecological research. The demand for predictive phylogenies at both generic and species levels have thus increased substantially. We are coordinating a global effort involving 28 scientists from 13 countries to assemble these phylogenies. Six genes are being used to form the backbone of the effort (all of COI, 28S D2-3, 18S, 2 regions of CAD, AATS and Period, for a total of ~ 6kB of data). We are also using anchored phylogenetic techniques on a subsample of syrphids to build a strong phylogenetic hypothesis for higher-level relationships. At this point we have 513 species of 144 genera included in the six gene project (over 42% of the world's syrphid genera) and 30 species of 29 genera sampled using a 500 probe dataset (>200,000 kB of data). Additionally, we are building a large dataset of 5' COI obtained from pinned museum specimens for use in supplementing phylogenetic hypotheses and for help with taxonomy and association of life stages and sexes (12,817 specimens of 1,499 species). The Australasian fauna is the least studied and least understood of the syrphid world fauna, and the lack of any modern revision makes Australia a focal point to fill in the last big gap for a world phylogeny. It is the last real "white spot" on the world map of syrphids and a phylogeny must include as many taxa from every part of the earth, so Australia is the crucial last missing piece in the puzzle. With this in mind, Skevington and Young are working to obtain fresh material of as many of the Australian syrphids as possible to fit into this phylogenetic framework. Preliminary phylogenetic results and an overview of the project will be provided during the talk.

Phylogeny and classification of the beetle families classified in the Cerylonid Series (Coleoptera: Polyphaga: Cucujoidea)

Robertson, J.A.^{1,2}, Ślipiński, A.³ and McHugh, J.V.²

¹Department of Entomology, 410 Forbes Building, University of Arizona, Tucson, AZ 85721-0036, USA; ²Department of Entomology, 413 Biological Sciences Building, University of Georgia, Athens, GA 30602-2603, USA; ³Australian National Insect Collection, CSIRO, GPO Box 1700, Canberra, ACT 2601, Australia

The Cerylonid Series (=CS) is a cluster of presumably highly derived beetle families within superfamily Cucujoidea comprising Alexiidae, Bothrideridae, Cerylonidae, Coccinellidae, Corylophidae, Discolomatidae, Endomychidae, Latridiidae and Akalyptoischiidae. Together, the CS families comprise 32 subfamilies, 645 genera and nearly 10,000 species. Phylogeny of Cucujoidea, with focus on the taxa classified in Cerylonid Series, was investigated using eight genes: nuclear 18S rRNA (18S), 28S rRNA (28S), histone subunit 3 (H3) and carbamoyl-phosphate synthetase (CPS locus of CAD), and mitochondrial 12S rRNA (12S), 16S rRNA (16S), cytochrome-c oxidase subunit I (COI) and cytochrome-c oxidase subunit II (COII). The taxon sampling included 384 taxa representing all 6 superfamilies of Cucujiformia, 35 of the 37 families of Cucujoidea (including all 9 CS families), 26 of the 32 CS subfamilies. Maximum likelihood and mixed-model Bayesian analyses were performed. The CS was recovered as a major Cucujiform clade, sister group to the remaining superfamilies of Cucujiformia. Of the major CS families only Discolomatidae, Corylophidae, and Coccinellidae were recovered as monophyletic. Endomychidae, Bothrideridae and Cerylonidae were recovered as paraphyletic and would need to be divided into monophyletic family level taxa.

Settling down to dine on a dioecious Gondwanan relict: why are psyllid nymphs more abundant at the base of branchlets?

Steinbauer, M.J.¹, Lubanga, U.K.¹ and Taylor, G.S.²

¹Department of Zoology, La Trobe University, Melbourne, Vic. 3086; ²Australian Centre for Evolutionary Biology & Biodiversity, The University of Adelaide, Adelaide, S.A. 5005.

The trioqid psyllid *Aacanthocnema dobsoni* (Froggatt) is host specific for drooping sheoak, *Allocasuarina verticillata* (Lam.) L. Johnson (Casuarinaceae), a 4-10 m tall, dioecious, wind-pollinated tree common to parts of south-eastern Australia. The morphology of this host is uniquely adapted to tolerating drought, e.g. the true leaves are greatly reduced and lack chlorophyll (photosynthesis is conducted by green branchlets) and stomata are encrypted within the furrows of the sclerophyllous branchlets. The nymphs of *A. dobsoni* are unique in appearance; they are heavily sclerotized, elongate, scale-like and virtually sessile – adaptations to tolerating aridity (Taylor *et al.* 2011, *Zootaxa* 3009: 1-45).

Females preferentially oviposit between scale leaves on the tops of ridges rather than into the furrows between them. In oviposition bioassays with branchlet halves, females oviposited around most whorls of scale leaves, not just the basal whorls. In a survey of six trees (3 ♀ & 3 ♂), nymphs of *A. dobsoni* were significantly more abundant on 2/3 female trees and significantly more abundant at the base of branchlets on all trees. Hence, oviposition site selection may not explain the distribution of nymphs; first instar nymphs probably migrate from oviposition sites to settle more basally on branchlets. Perhaps more importantly, it is suspected that in the wild, adults shelter at the base of branchlets where they mate and oviposit.

Branchlets of female and male trees differed in their morphology and had comparable concentrations of free amino acids; concentrations were higher in the apical halves (growing tip) of branchlets. Branchlets of female trees had lower chlorophyll concentrations than those of male trees, reflecting the chlorosis caused by feeding nymphs. Branchlets of female trees were higher in total phenolics than those of male trees. We discuss the significance of primary and secondary metabolites and female behaviour on host selection/assessment and nymphal distribution/development of *A. dobsoni*.

Dispersal and inbreeding in a fig-pollinating wasp and its parasitoid

Sutton, T.L., DeGabriel, J.L., Riegler, M. and Cook, J.M.

Hawkesbury Institute for the Environment, University of Western Sydney, Locked Bag 1797, Penrith NSW

Figs (*Ficus* spp.) and their pollinators (Hymenoptera: Agaonidae) are a classic example of obligate symbiosis. Their symbiosis is exploited by parasitoid wasps, which kill pollinator offspring and can thus reduce fig pollen transfer. Interactions between fig, pollinator and parasites play an important role in both the ecology and the coevolution of this system. Pollinator dispersal mediates fig gene flow, while attack by parasitoids may help stabilise the mutualism by moderating seed predation by pollinators. Differential dispersal between pollinator and parasitoid may affect fig – pollinator dynamics, particularly in isolated fig populations. Here, we present the first comparative population genetic analysis, using microsatellites, of a fig-pollinator and its parasitoid.

We co-sampled *Pleistodontes imperialis* sp. 1 and *Sycoscapter* sp. A at a series of sites in eastern Australia, and genotyped all wasps at six microsatellite loci. Results indicate that *P. imperialis* sp. 1 comprises two distinct populations, corresponding to a northern (Atherton Tablelands) and southern (Byron Bay to Sydney) populations. Combining these results with data from other markers and other species within the *P. imperialis* complex suggests that incipient speciation may be occurring. In contrast, *Sycoscapter* sp. A comprises a single population that displays weak isolation by distance throughout its ~3000 km range. Inbreeding measures were higher in the pollinator, consistent with our prediction that fewer pollinator than parasitoid females contribute eggs to each fig, making sib-mating more likely in the next generation.

Our study shows that fig wasp populations are large and geographically expansive. Fig, pollinator and parasitoid gene flow thus occur over large distances and may prevent the evolution of local genetic adaptation between sites with, for example, differing climates. However, where populations are disjunct, as with the pollinator in our study, it may facilitate the evolution of new pollinator species, without linked speciation of the fig or its parasitoid. The existence of this symbiotic system over a wide geographic and climatic range provides an excellent opportunity to study the “geographic mosaic of coevolution”.

Vulnerability of a fig – pollinator system to climate change

Sutton, T.L., DeGabriel, J.L., Riegle, M. and Cook, J.M.

Hawkesbury Institute for the Environment, University of Western Sydney, Locked Bag 1797, Penrith NSW 2751, Australia

Interactions between species are crucial to ecosystem functioning and may be disrupted by global change. Mutualisms are expected to be particularly sensitive to climate change as shifts in the phenology of interdependent species are likely to desynchronise their life histories. Figs (*Ficus*, Moraceae) and their pollinating wasps (Hymenoptera: Agaonidae) share an obligate reproductive mutualism. The Port Jackson fig (*Ficus rubiginosa*) is found along most of Australia's east coast, from the tropics to the temperate zone, and is pollinated by wasps of the *Pleistodontes imperialis* species complex. Environmental niche modelling indicates that each species may be restricted to a relatively narrow climate zone, and may be sensitive to shifts in temperature or humidity. *Pleistodontes imperialis* sp. 1 pollinates *F. rubiginosa* in south-eastern Australia, from Brisbane in the north to Eden in the south. It experiences a broad range of climatic conditions, and is likely to be affected by the increase in extreme heat events that is forecast to accompany climate warming trends

We measured the longevity of *P. imperialis* sp. 1 wasps experimentally exposed to a range of temperatures from 25 to 40°C, coupled with high or low humidity (30 or 70% RH). Experiments were performed on wasps from two sites; a cooler, wetter coastal site and a hotter, drier inland site. Lifespan was reduced at higher temperatures and was shorter across all temperature for the low humidity treatment. Coastal wasps performed better under most temperature/humidity treatments, except at 39°C where almost no wasps survived past 3 hours.

The treatments applied here represent realistic heat wave conditions that are commonly experienced during Sydney summers, and the frequency of these events is predicted to increase throughout temperate regions worldwide. This could have profound impacts on temperate fig – pollinator mutualisms around the world, and serious consequences for the rich vertebrate assemblages they support.

The costs of pheromone signalling in female moths

Symonds, M.R.E.¹, Barling, A.¹, Buttemer, W.A.², Cheah, C.¹, Kokko, H.³ and Umbers, K.D.M.^{3,4}

¹Centre for Integrative Ecology, Deakin University, Burwood, VIC 3125; ²Centre for Integrative Ecology, Deakin University, Waurn Ponds, VIC ; ³Research School of Biology, Australian National University, Canberra, ACT; ⁴School of Biological Sciences, University of Wollongong, Wollongong, NSW

Moths are well known for their remarkable mate signalling system where females produce tiny quantities of pheromone, which the male responds to over long, sometimes prodigious, distances. In many mating systems the cost of advertising for mates (e.g. through elaborate displays) is known to be high. However, in moths, it is usually assumed that, because nanograms or picograms of pheromone are released, there must be almost no physical cost to this behaviour. We demonstrate from theoretical models and empirical analysis of patterns of mate signalling behaviour across 44 moth species, that females increase their pheromone signalling effort as they age, in response to lack of mating. Such a pattern is indicative of a cost to pheromone signalling since otherwise females should signal maximally at all times. We therefore investigated physical costs to the behaviour, through analysis of signalling behaviour in female silk moths (*Bombyx mori*). Flow-through respirometry analysis shows that calling behaviour is associated with higher metabolic output than other behaviours. Furthermore, females that call more tend to have reduced lifespans. However, when mated, they lay a greater number of viable eggs. This suggests that higher quality females may be able to expend greater effort into signalling for a mate, again consistent with the idea of a cost to this behaviour.

The impact of the non-native superb lyrebird on Tasmanian invertebrate assemblages

Tassell, S., Wapstra, E., Richardson, A.M.M. and Barmuta, L.

School of Biological Sciences, University of Tasmania, TAS 7001

Some 900 species of bird have been introduced throughout the world but the research effort regarding their ecological impact on native invertebrates has been minimal. We addressed this knowledge gap by investigating the effect of the non-native superb lyrebird (*Menura novaehollandiae*) on native soil- and leaf litter-dwelling forest invertebrates within the wet eucalypt forests of Tasmania. Superb lyrebirds were introduced to Tasmania in the 1930s and are predators of invertebrates and ecosystem engineers capable of turning over hundreds of tonnes of soil and leaf litter per hectare every year. The absence of any native equivalent-sized predator of invertebrates or native species capable of such large-scale habitat modification within Tasmanian wet forest means that superb lyrebirds have the potential to have significant negative effect on invertebrates. We used an integrative approach combining surveys and field based experimental manipulations to assess the nature, magnitude and pattern of lyrebird impact on meso- and macroinvertebrates at a range of spatial and temporal scales. Superb lyrebirds had a profound effect on the structure and composition of invertebrate assemblages at small spatial scales and short timeframes. However, these effects were weaker over longer timeframes and at intermediate and landscape scales. Impact on invertebrate taxa appeared to be influenced by their habitat preferences and their size. In general, leaf-litter dwelling macroinvertebrates showed a stronger response to the presence of lyrebirds than did mesoinvertebrates or soil dwelling macroinvertebrates. We use these findings to discuss the potential impacts of lyrebirds across their introduced range in Tasmania.

Selection of non-target species for risk assessment of biological control agents: testing a decision-support system

Todd, J.H.^{1,3}, Barratt, B.I.P.^{2,3}, Tooman, L.K.¹ and Malone, L.A.¹

¹The New Zealand Institute for Plant & Food Research Limited, Private Bag 92 169, Auckland, New Zealand 1142; ²AgResearch Limited, Invermay Agricultural Centre, Private Bag 50034, Mosgiel, New Zealand 9053; ³Better Border Biosecurity (www.b3nz.org), New Zealand.

The release of entomophagous biocontrol agents into a new country can pose risks to the existing insects in the release area. Risk assessment of these biocontrol agents can be difficult and costly and usually only a few of the at-risk non-target species can be selected to undergo biosafety testing. To provide some decision-support around this selection process in New Zealand, the PRONTI (priority ranking of non-target invertebrates) species selection method has been developed. This system uses a database of taxonomic, biological and ecological information on New Zealand invertebrates, and a model that systematically assesses each species in the database to produce a ranked list of at-risk species for each proposed agent. This resulting list can be used to guide and support decisions on which species to select for tests with each agent. The system is being tested with three different biological control agents: (1) the Asian paper wasp, *Polistes chinensis antennalis* Pérez (a generalist predator that could hypothetically be used to control lepidopteran pests), (2) the hymenopteran parasitoid *Cotesia urabae* Austin & Allen (introduced to New Zealand in 2011 to control the gum leaf skeletonizer *Uraba lugens* Walker), and (3) the braconid parasitoid *Microctonus aethiopoides* Loan (introduced to New Zealand to control the pest weevil *Sitona discoideus* Gyllenhal in 1982). In the first of these tests, the PRONTI list was compared with the diet of *P. chinensis* to validate the risk predictions made by the model. The second two tests will compare the PRONTI lists with those that were produced for each agent prior to its release. These tests will help us to assess the usefulness of this method for risk assessments with biological control agents in terms of its ability to identify the most appropriate species for non-target testing with each agent.

Climate change and the spread of vector-borne diseases: insight into BYDV and the aphid pathosystem

Trebicki, P.¹, Nancarrow, N.², Freeman, A.¹, Bosque-Perez, N.⁴, Yen, A.² and Fitzgerald, G.¹

¹Department of Environment and Primary Industries (DEPI), 110 Natimuk Rd, Horsham, VIC, 3400; ²DEPI, AgriBio, 5 Ring Road, Bundoora, Vic 3083; ³University of Idaho, Moscow, ID, USA.

With the continued use of fossil fuels to support our ever increasing energy consumption, levels of atmospheric carbon are projected to increase by over 40% in the next few decades. Our population also continues to grow and is estimated to increase to over 9 billion by 2050. In order to feed this increasing population, understanding how increasing levels of CO₂ will affect agriculture is essential if we hope to increase our current food crop production.

Insect pests and diseases are one of the major factors shaping agricultural production. Over 700 of the known plant pathogens have a wide range of hosts and cause serious damage to the plants they infect. For example, Barley and cereal yellow dwarf virus (B/CYDV), transmitted by the bird cherry-oat aphid (*Rhopalosiphum padi*) can infect over 150 species in the Poaceae family including important food crops such as wheat, barley, oats and corn. During outbreaks of this virus, B/CYDV infection can account for over 50% infection in Australian crops depending on the year.

In this study, we investigate the impact of aphid transmitted plant disease on wheat under current and future climate conditions. We quantify the BYDV titre in plants from two CO₂ levels and changes to wheat physiology, mediated by elevated CO₂ (eCO₂). BYDV titre increased in wheat plants grown under eCO₂ while aphid biology and feeding behaviour was also altered under eCO₂ conditions. The results from this study show that there are major implications for the spread and severity of BYDV as well as changes in aphid biology under future climate conditions.

Olfactory detection and discrimination: engineering lessons from an insect

Nowotny, T.¹, de Bruyne, M.², Berna, A.Z.³, Warr, C.G.² and Trowell, S.C.³

¹Centre for Computational Neuroscience and Robotics, School of Engineering and Informatics, University of Sussex, Brighton, UK; ²School of Biological Sciences, Monash University, Clayton, VIC, Australia; ³CSIRO Food and Nutrition Flagship, Black Mountain Laboratories, Canberra, ACT, Australia.

One aim of research into machine olfaction is to replace the use of animal olfaction, for some routine sniffing tasks, with instruments called electronic noses (e-Noses). However, despite three decades of development, e-Noses have not been able to match the discriminating power of the biological original. Our approach to this problem has been twofold. Firstly, we compared the fundamental properties of arrays of electronic nose sensors with the characteristics of insect olfactory receptors. By doing this we aimed to understand how engineered chemical sensor arrays depart from the naturally evolved, presumed ideal, version. Our second approach was to investigate the performance of a virtual array of insect olfactory receptors in an artificial discrimination task. By doing this, we sought to understand how well an array of evolved sensors might perform when challenged with a discrimination task of industrial, agricultural or medical interest. We used the well-characterised olfactory system of the fruit fly, *Drosophila melanogaster* (Diptera: Drosophilidae), as our biological model. We compared this with a set of metal oxide (MOx) sensors, the type most commonly used in e-Noses. The chemicals we used for these comparisons included "Hallem's set" of 110 volatile odorants and a subset of 20 of these chemicals. For the discrimination task we used 36 chemicals related to wine and 35 chemicals of security or safety concern. The following results were obtained. Compared with a fly's odorant receptors, MOx sensors from an electronic nose are on average more narrowly tuned and more highly correlated with each other. Despite lower average response levels, *Drosophila* receptors appear highly capable of distinguishing chemicals that they had not evolved to discriminate. In contrast to previous work with metal oxide sensors, *Drosophila* receptors achieved their best recognition accuracy if the outputs of all available receptor types were used.

Soil management and ecosystem services in grapes

van Helden, M.^{1,2} and Keller, M.¹

¹Adelaide University, School for Agriculture Food and Wine, SA 5005; ²Bordeaux University, Bordeaux Sciences Agro, 1 cours de Gen. De Gaulle, 33175 Gradignan CEDEX, France.

Soil management in viticulture has a strong impact on primary production parameters, but it also influences many soil related processes. During 2014/2015, different soil management techniques (herbicide, tillage, mowing, sowing of green manure) will be compared in a manipulative experiment in existing Shiraz vineyard blocks in the McLaren Vale region, for their effects on soil chemistry, physical and biological properties and the influence of soil micro- and meso-fauna on these parameters. Arthropods will be observed using simple Berlese (Tullgren) extractions, and different sentinel systems will be used to measure soil organic matter degradation (Tea-Bag index, Biolog ecoplates), insect mortality (exposure on and in the soil) and seed predation (seed-cards). A similar three year European project (PromESSinG) will include wine growing regions in Germany, Austria, Switzerland and Rumania? The outcomes of these experiments should allow optimizing soil functioning for a more sustainable production of high quality wine grapes. We are interested in collaboration with other wine growing areas in order to establish a long term intercontinental project on this subject.

Insect sleep and attention

van Swinderen, B.

Queensland Brain Institute, The University of Queensland, St Lucia QLD, Australia

The need to sleep seems to have co-evolved with the capacity to pay attention. Although it remains unclear whether sleep and attention are present in some invertebrates such as nematodes and jellyfish, both phenomena have now been well documented in insects. Here, I will outline how sleep and visual attention can be studied in insects such as honeybees and fruit flies, and I will propose a hypothesis for a function of sleep that is relevant to maintaining an optimal level of selective attention.

Bee colour vision in relation to flowers colours

Vorobyev, M.¹ and Hempel de Ibarra, N.²

¹University of Auckland, Department of Optometry and Vision Science, Auckland, New Zealand; ²University of Exeter, Psychology, Centre for Research in Animal Behaviour, Exeter, UK

The relationship between flower colours and pollinator colour vision has been established for many groups of pollinators. For example, birds are sensitive to red light and they usually pollinate red flowers. A glaphyridae beetle has a red sensitive photoreceptor and it pollinates red poppies, which, in turn, largely depend on glaphyridae beetle for reproduction (Martinez-Harms et al., 2012, *J. Comp Physiol*, 198:451-463). Bees do not have red sensitive receptor and the colours of flowers that they pollinate are usually blue, yellow or white. Bees with long proboscis, such as bumble bees, often pollinate blue flowers, while bees with short proboscis usually pollinate yellow and white flowers. However, all bees have very similar colour vision systems - they are trichromatic with UV receptor peaking at around 350 nm, blue receptor peaking around 440 nm and green receptor peaking at around 540 nm (Peitsch et al., 1992, *J. Comp Physiol*, 170:23-40). The set of photoreceptors found in bees appears to be optimal for discrimination of flower colours in general. Also, the same arrangement of photoreceptors is optimal for discriminating colours of all theoretically possible colours. Therefore the spectral positions of photoreceptors of bees could have evolved in common ancestor of bees before flowers evolved, as a general adaptation for colour discrimination. Hence, flower colours could have evolved as an adaptation to pre-existing colour vision system of bees. Since bees have similar sets of photoreceptors the differences in colours of flowers preferred by different groups of bees cannot be explained by spectral positions of photoreceptors. It is likely that bees with long proboscis tend to pollinate blue flowers because blue flowers often offer large amount of nectar and this nectar can be accessed with long proboscis only.

History, accomplishments and challenges of forensic entomology in Australia

Wallman, J. F.

School of Biological Sciences, University of Wollongong, NSW 2522

The use of insects in legal matters in Australia dates back to the early 20th century when carrion-breeding flies were first used to assist the police in interpreting the circumstances of a murder. Since then, many hundreds of civil and criminal cases throughout the continent have featured insects as part of their investigations. The advancement of applied entomology as a branch of forensic science has been based on research in taxonomy and systematics (what species infest corpses and how do we identify them?), ecology (what is the distribution and abundance of such species?) and behaviour and physiology (what governs the interactions among and development of such species?). A main aim has been to improve the precision and accuracy of estimates of the minimum time since death of victims of misadventure. There is also an overarching and compelling need for scientific rigour, ethical standards, and appropriately qualified conclusions whenever insect evidence is applied in a legal context.

This talk summarises, with the help of an historical perspective, the main innovations in forensic entomology in Australia and where the future priorities lie.

The effects of temperature on the development and mortality of *Eretmocerus warrae* (Nauman & Schmidt)

Wang, T., Hogendoorn, K. and Keller, M.A.

School of Agriculture, Food & Wine, University of Adelaide, Adelaide, SA 5064

Greenhouse whitefly, *Trialeurodes vaporariorum*, is a cosmopolitan pest in greenhouses. *Eretmocerus warrae* is a biological control agent of the greenhouse whitefly. It was found in a commercial greenhouse during hot summer temperatures by Biological Services (Loxton, South Australia) and is suspected to be a better biological control agent at high temperatures than another wasp, *Encarsia formosa*, which is widely sold for control of *T. vaporariorum*. Experiments had been conducted to investigate how temperature affects the development and behaviour of *E. warrae*.

Development and behaviour were recorded at 15, 20, 25, 30, and 33°C. The results showed that the optimum temperature for the development rate of *E. warrae* is approximately 31.5°C. It takes around 15 days for the wasps grow from egg to adult at this temperature. The optimum temperature for searching activity is approximately 30.5°C. One female can deposit nearly 37 eggs in three hours at this temperature.

The development of *E. warrae* was compared to that of *En. formosa* at 30, 33, 34.5, 36 and 37.5°C. The development rate of *E. warrae* declined at 34.5°C and no wasps emerged at 36 or 37.5°C. The developmental rate of *En. formosa* is lower at 33 °C than at 30°C and no wasps completed development at 34.5, 36 or 37.5°C.

The mortality of adults of the two wasp species at high temperatures of 36 and 37.5°C were observed. The data shows that the survival rate of *E. warrae* was markedly higher than that of *En. formosa* after 15 hours.

The experiments showed that *E. warrae* is better adapted to high temperatures than *En. Formosa*, and suggest that it should be a better biological control agent during the summer months.

A computational model of the insect mushroom body can account for ant route memory in complex environments

Webb, B.¹, Ardin, P.¹, Peng, F.², Mangan, M.¹ and Lagogiannis, K.

¹School of Informatics, University of Edinburgh, 10 Crichton St, Edinburgh EH8 9AB, UK; ²Biological and Experimental Psychology, School of Biological and Chemical Sciences, Queen Mary University of London, Mile End Road, London E1 4NS, UK.

Many insects, including ants, exhibit excellent memory for visual routes, but the neural mechanisms underlying their abilities in this complex task are unknown. For the simpler task of olfactory conditioning the mushroom body neuropils have been strongly implicated as a site of memory. It has recently been suggested that ants store a high density of images seen along a route, and can then follow the route by comparing all stored images with their current view to decide which direction appears most familiar. We show that this apparently computationally costly method can be implemented in a spiking neural model of insect mushroom body memory circuits. The key insight is that the MB, considered as a sparse associative net, allows many complex and arbitrary input patterns to be stored as direct synaptic mappings to a small set of outputs required to drive behaviour. In the real ant, these patterns might combine olfactory, visual and other sensory inputs into a multimodal ‘gestalt’ of the current location. Although this function could be interpreted as labelling or classification (familiar vs. unfamiliar), and thus could potentially be performed by a variety of alternative network architectures, our model produces successful performance with a very simple and fast learning mechanism; there is no need for neural implementation of a more complex classification algorithm. The model supports successful behaviour when tested in a realistic simulation based on the recorded routes of real ants, *Cataglyphus velox*, in their natural environment of scrubby desert in southern Spain.

Exploiting behaviour to create novel deterrents for the Queensland Fruit Fly (*Bactrocera tryoni*)

Webb, O.¹, Cunningham, P.¹, Clarke, A.¹ and Furlong, M.²

¹Queensland University of Technology; ⁴University of Queensland

Fruit odours are complex structures, made up of multiple volatiles, which are necessary for host detection and orientation in herbivorous insects. While different host fruits produce distinctive odours, these odours are not fixed and their composition at any time is determined by a combination of factors such as ripeness and damage. Therefore the structure of fruit odours not only indicates host presence but also host suitability.

By exploiting the innate decision making process of insect host choice within the Queensland Fruit Fly my research aims to identify naturally occurring chemical compounds that act as strong oviposition deterrents. These deterrents could then be deployed alongside attractants in push-pull management strategies in order to prevent crop damage.

Focusing on volatiles produced by microorganisms during fungal decay and bacterial fermentation of host fruit, I have shown that the presence of fungal growth or bacterial infestation deters oviposition. I have carried out analysis of the volatiles produced by these microorganisms and have identified candidate deterrent volatiles. Here I will present the results of experiments aiming to deter oviposition through the addition of these single volatiles to ripe fruit odours.

Exploring phenotypic variation in populations of the funnel-web spider *Atrax sutherlandi*

Wong, M.¹, Woodman, J.D.² and Rowell, D.M.¹

¹The Australian National University, Canberra, ACT 0200; ²Australian Plague Locust Commission, Unit 7, 50 Collie St, Fyshwick ACT 2609

Previous research on the funnel-web spider *Atrax sutherlandi* has uncovered high levels of genetic differentiation among geographically distinct populations within Tallaganda forest in south-eastern New South Wales. Such fine-scale geographic variation has also been documented for a variety of other invertebrates in Tallaganda, and is believed to be associated with the dynamic shifting of regional forest tree lines during Pleistocene climatic cycles. In this short talk I shall discuss my Honours research project, which examines phenotypic variation amongst *A. Sutherlandi* populations at Tallaganda, and the congruence between phenotypic variation and the established patterns of genetic divergence within this species.

Mathematically consistent DNA models for time-inhomogeneous mutation

Woodhams, M.¹, Sumner, J.¹ and Fernández-Sánchez, J.²

¹School of Mathematics and Physics, University of Tasmania, Private Bag 37, Hobart, TAS 7001;

²Departament de Matemàtica Aplicada I, Universitat Politècnica de Catalunya, Barcelona, Spain

If you evolve a DNA sequence under a GTR model, then evolve it further under a different GTR model, the combined process cannot in general be described by a single GTR model. As a consequence, if we model a time inhomogeneous GTR model over a tree, pruning the tree changes the distributions at the remaining taxa. The Lie Markov models were designed to avoid this problem. I describe a hierarchy of 37 Lie Markov models and perform likelihood testing on real world data sets.

Effects evaluation of entomopathogenic fungus *Beauveria bassiana* on predatory mite and biological control of their shared pest *Frankliniella occidentalis*

Wu, S., Gao, Y. and Lei, Z.

State Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing 100193, P.R. China

In order to improve biocontrol effect on single target pest and minimize economic losses, multiple natural enemies to be integrated has been put forward in the IPM strategy. The entomopathogenic fungus *Beauveria bassiana* and predatory mite *Neoseiulus barkeri* are both potential biocontrol agents against their shared pest west flower thrips, *Frankliniella occidentalis*. Our study was conducted in laboratory and greenhouse to evaluate the compatibility between *B. bassiana* and *N. barkeri* and the potential use of *B. bassiana* in combination with *N. barkeri* for the control of *F. occidentalis*.

From laboratory bioassay and scanning electron microscopic observation, *B. bassiana* has no negative effect to *N. barkeri*. *Neoseiulus barkeri* displayed effective defense against *B. bassiana*. When inoculated by *B. bassiana* suspension, *N. barkeri* can carry a large number of conidia within a short time, the conidia can be dispersed and infected adults *F. occidentalis*, and these synergistic effects were rapidly weakened by the self-grooming behavior of *N. barkeri*. Furthermore, conidia could be fed by *N. barkeri*, which probably reduce the infection of *B. bassiana*. We also found that *N. barkeri* prefer to prey the infected larvae of *F. occidentalis*, and the life table parameters of *N. barkeri* were strongly affected when fed on infected *F. occidentalis*.

When combined application of *B. bassiana* and *N. barkeri* for controlling *F. occidentalis* in cucumber greenhouse experiments, there were obvious interactions between *B. bassiana* and *N. barkeri* with little synergistic effects for *F. occidentalis* biological control when combined both simultaneously, so the application of *B. bassiana* in combination with *N. barkeri* at certain intervals was suggested.

Inferring the relationships of early Dipteran lineages using transcriptomic data

Yeates, D.K. and Meusemann, K.

The Australian National Insect Collection, CSIRO National Research Collections Australia, Canberra ACT 2601. David.yeates@csiro.au, karen.meusemann@csiro.au

While the Diptera and Brachycera are undoubtedly monophyletic, the relationships between the earliest evolving lineages of this megaradiation are not resolved. A recent molecular analysis offered a monophyletic clade of Lower Brachycera excluding the Empidoidea (Wiegmann et al. 2011), but previous analyses using molecular or morphologic data have inferred the group to be a paraphyletic grade, with the Asiloidea being more closely related to the Eremoneura than the other main lineages of Lower Brachycera. Recent published analyses have also disagreed on the monophyly and position of the Nemestrinoidea (nemestrinidae and Acroceridae). Previous studies have been based on a relatively small number of genes (thousands of base pairs) and have been hampered by short branch lengths and low support levels at critical nodes. By including much larger samples of the genome (millions of base pairs), phylogenetic approaches may address these challenges. We present the results of our analyses using ~2,000 orthologous single copy genes for phylogenetic inference derived from transcriptome data from the 1KITE project, published resources and collaborating laboratories.

A revision of the Australian Flower Flies (Diptera: Syrphidae)

Young, A.D.^{1,2}, Skevington, J.H.^{1,2}, Thompson, F.C.T.³, van Steenis, W.⁴ and van Zuijen, M.⁵

¹Canadian National Collection of Insects, Arachnids and Nematodes, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada; ²Carleton University, 1125 Colonel By Dr, Ottawa, ON K1S 5B6, Canada; ³National Museum of Natural History, Smithsonian Institution, Washington, D.C. 20013-7012, United States of America; ⁴ Breukelen, The Netherlands; ⁵Wageningen, The Netherlands

Flower Flies, or Syrphidae, are a large, relatively well-known family of Diptera. Most species are beneficial insects of considerable economic importance, as adults are known to be important pollinators in both wild and agricultural settings, while the larvae of the subfamily Syrphinae are important natural control agents of aphids, scales, and their relatives. However, some groups within the subfamily Eristalinae, such as *Eumerus*, are plant feeders as larvae and may be significant pests. Syrphids also attract considerable attention from ecologists for studies of mimicry, evolution of feeding specialization, etc., and from naturalists, because they are often large, conspicuous, and brightly coloured. Despite all of this, there are still several genera in Australia that have yet to be formally described, and others in dire need of revision. In addition, existing species keys are poor to non-existent. The main goals of this project will be to review and revise the taxonomy of the 54 genera of syrphids present in Australia, and to provide photographic, species level keys to all taxa. This will be accomplished through separate publications for each major generic revision, as well as producing a photographic atlas to the Australian Syrphidae that will include colour photos, species keys, range maps, and known life history of all Australian species.

From natural history to continental scale perspectives: contributions of Australian Entomologists to Ecology - a play in three acts

Zalucki, M.

The University of Queensland, Brisbane, 4072

Act 1 - Prequel: From the foundation of the colony to the formation of the Australian entomological society, much of Australian entomology was driven by the need to come to grips with and manage a raft of indigenous pests and invasive pest species. This very applied imperative influenced how folk approached ecology, which tended to be very much autecological: species focused questions addressing the distribution and abundance of the organism. Not surprisingly that applied focus continued after the formation of the Society in Act 2: The last 50 years. The dramatis personae and events (what they published and did) are “real”. I take responsibility for the interpretation and opinions expressed about the influence of those that have passed on or have been retired for a long time. I express no opinion of those that are currently active in research except to cite their papers.

I use some of the key native and imported pests; Locusts, Helicoverpa, Queensland Fruit flies, Sugar cane feeding scarabs, Diamondback moth; to illustrate how ecological thinking and in fact research groups developed, often like the colony, fractured in part down State lines or, in some cases, a State versus Federal fracas. I focus in part on what has been published on ecology in our flagship Journal for the last 50 years and analyse the trends that are evident: who, what, citations and fields. There were some giants in the field, and their public disagreements continue to reverberate. But there have been many notable contributions by lesser mortals, if only students and their mentors would read and cite appropriately!

One can only allude to the encore of Act 3: the sequel or the next 25 to 50 years. The thinking of Australian entomologists continues to be at the forefront of spatial ecology. Perhaps reflecting the scale at which fieldwork is undertaken in Australia. Other younger members of the Society will no doubt write the epitaph, obituary of the current crops of researchers and judge their contributions.

Visual homing

Zeil, J.

Research School of Biology, Bldg 46, Biology Place, The Australian National University, Canberra ACT 0200, Australia. Email: Jochen.zeil@anu.edu.au

Many insects, in particular ants, bees and wasps, are competent navigators and are known to rely heavily on vision to memorize places and routes. The landmark panorama, the sun, the pattern of polarized skylight and even the Milky Way provide them with an external compass reference. For visual homing, insects acquire scene memories at their nest or at newly discovered feeding sites during highly structured learning flights or learning walks.

Given the importance of navigational competence for all aspects of animal life, it is of great interest to understand the rules governing the active acquisition of visual representations and the algorithms insects employ during homing. Visual homing is a challenge for both biological and technical systems and insects are as good at it as any animal. They are quite unique, however, because they allow us to analyse in detail how visual place memories are actively acquired and subsequently used for homing.

It is an exciting time to study visual homing: Novel tracking and reconstruction techniques now allow us to quantify the navigational information content of different habitats, comparative analysis shows how the blend of navigational mechanisms depends on habitat structure and there are solid advances in theory and neuro-ethological simulation.

In search of hexapod origins: capturing phylogenetic signal from serine with 21-amino-acid models

Zwick, A.

Australian National Insect Collection, CSIRO, GPO Box 1700, Canberra, ACT 2601.

The evolutionary relationships of arthropods have been studied extensively during the past century, with the origin of Hexapoda being of particular interest, but consensus on the higher relationships has remained elusive. Despite the publication of several very large molecular data sets, the number of truly independent data sets is more limited than it might seem. One of these data sets is based on 62 nuclear, protein-coding genes from representatives of all pancrustacean classes, including Hexapoda (Regier et al. 2010. *Nature* 463:1079-1083). It provides a robustly supported topology for most Arthropoda, placing Hexapoda as sister to Xenocarida (Remipedia + Cephalocarida).

Xenocarida and four other higher pancrustacean taxa of particular interest have been disputed, because support values for amino acid model analyses are significantly lower than for nucleotide and codon model analyses. In-depth analyses reveal that the strong support in nucleotide and codon model analyses is largely contributed by serine, while support is reduced in standard 20-amino-acid analyses due to a lack of distinction between two disjunct clusters of serine codons (TCN / ATY). This is directly evidenced by 21-amino-acid models that do distinguish between these two clusters, yielding high support values for the nodes of interest (Zwick et al. 2012. *PLoS ONE* 7(11):e47450).

The average substitution rate between the two clusters of serine codons is intermediate between non-synonymous and synonymous substitution rates of other codons. In phylogenetic analyses, this unique characteristic of serine might be particularly informative for clades of a certain age, while it might be uninformative or even misleading through codon usage bias for very old clades. In the present case of Pancrustacea, the strong signal of serine is A) not linked to a serine codon usage bias that could drive the analyses, and B) congruent with the signal of other amino acids.

POSTER PRESENTATIONS

The role of abiotic factors for the fluctuation of Jassid (*Amrasca biguttula biguttula* (Ishida) population on Aubergine (*Solanum melongena* L)

Ali, M.¹, Ashfaq, M.², Ashfaq, M.¹, Rana, N.³, Khalid, S.⁴ and Ali, A.¹

¹Institute of Agricultural sciences, University of the Punjab, Lahore Pakistan; ²Department of Agricultural Entomology, University of Agriculture, Faisalabad, Pakistan; ³Department of Zoology and Fisheries, University of Agriculture, Faisalabad, Pakistan; ⁴Environmental Sciences Department, Fatima Jinnah Women University Rawalpindi, Pakistan; Email: ali.klasra@gmail.com

The data about the jassid population from the different dates were recorded which were correlated with the weather factors so that to find out the effects of maximum temperature, minimum temperature, average temperature, relative humidity and rainfall. The Experiment was laid out in 2009. The coefficient of determination values were observed to find the role of weather effects on population fluctuation of jassid, *Amrasca biguttula biguttula* (Ishida) on Aubergine. The data were recorded from the adjoining meteorological observatory of Physiology Section, Ayub Agricultural Research Institute, Faisalabad. The recorded data were transformed to square root transformation and processed for the Simple Correlation and Multiple Linear Regression analysis for study to check the role of weather factors in the fluctuation of pest population. To see the results that maximum temperature played the vital role for the fluctuation of jassid population i.e 37.4% followed by the minimum temperature, average temperature, and rain fall with 20%, 5.6% and 3% respectively. While the relative humidity showed the negligible contribution 0.1%.

Atlas Moth Conservation Network: a new community group to recover a threatened species in the Northern Territory

Braby, M.F.

Department of Land Resource Management, Darwin NT 0831, Australia; and
School of Biological Sciences, The Australian National University, Canberra ACT 0200,
Australia

There are few community-based recovery teams for threatened invertebrates in Australia: perhaps the two largest and best known are those for the Richmond Birdwing and Eltham Copper butterflies. The Atlas Moth (*Attacus wardi*), Australia's second largest moth, is endemic to NW Australia (Kimberley, Top End) where it is restricted to the higher rainfall areas which support large patches of coastal semi-deciduous monsoon vine-thicket. The species is currently listed as Vulnerable under the *Territory Parks and Wildlife Conservation Act* because of its limited spatial distribution (Area of Occupancy <640 km²), extent of habitat fragmentation and limited number of populations (6), and inferred decline from analysis of its critical habitat and threatening processes (inappropriate fire regime, invasion of grassy weeds, habitat loss). A number of community-based landcare groups facilitated through Conservation Volunteers Australia have recently commenced restoration of the moth's habitat in the Darwin area, including establishment of its rainforest larval food plants (*Croton habrophyllus*, *Litsea glutinosa*). In response to this community interest, a public forum was held in February 2014 to disseminate information and establish the 'Atlas Moth Recovery Network'. The forum, which brought together for the first time a wide range of stakeholders (scientists, naturalists, environmental consultants, CVA, Greening Australia, landcare groups etc), included a series of formal presentations and field trips. Subsequently, a steering committee was established to develop the aims, constitution and membership structure of the Network. One of the long-term goals of the Network is to reintroduce Atlas Moth back into Darwin where it is now locally extinct through research, habitat restoration, captive breeding, translocation, monitoring, education and community engagement.

The effect of temperature on *Aphidius gifuens* (Hymenoptera: Aphidiidae) and *Diaeretiella rapae* (Hymenoptera: Aphidiidae)

Chen, W.

Institute of Entomology, Guizhou University, Guiyang, Guizhou, 550025, P. R. China

Myzus persicae (Sulzer) was a main pest of many vegetables and tobacco, and cause serious damage. Both *Aphidius gifuens* (Ashmaed) and *Diaeretiella rapae* (M'Intosh) are parasitic natural enemy agents of *M. Persicae*, and play important roles in biological controlling *M. persica*. The comparative studies of their biological characteristics were rare. The effects of temperatures on the development and fecundity of two parasitic wasps were compared. The results showed that the development of different stages of *A. gifuens* and *D. rapae* decreased with the increase of temperature, but development period prolonged if the temperature was above 28°C. The development period of *D. rapae* was shorter than that of *A. gifuens* from egg to adult. The highest emergence rate of *A. gifuens* was at 22°C, while *D. rapae* was at 28°C. The emergence rate of both wasp dropped to 48% and 52% respectively when the temperature reached to 31°C. The average longevities of both wasp were longest at 19°C, and they decreased with the increase of temperature, the longevities as shorter than 3 days at 31°C. The adult longevity of *A. gifuens* was longer than that of *D. rapae* under any temperature. The fecundities of *A. gifuens* and *D. rapae* decreased with the increase of temperature. The eggs laid by *A. gifuens* were 136.83, 117.67, 105.33, 92.50 and 23.00 respectively at 19, 22, 25, 28 and 31°C, While *D. rapae* were 80.33, 56.83, 44.67, 36.00, 23.33 respectively. The fecundities of *A. gifuens* were higher than that of *D. rapae* at all 5 temperatures.

Studying *Myzus persicae* performance and feeding behaviour, and associated plant viruses under increasing CO₂

Dader, B.¹, Fereres, A.¹ and Trebicki, P.²

¹Instituto de Ciencias Agrarias-Consejo Superior de Investigaciones Científicas (ICA-CSIC), Calle Serrano 115 dpdo., 28006 Madrid, Spain; ²Department of Environment and Primary Industries, Grains Innovation Park, 110 Natimuk Road, Horsham, Victoria, 3400, Australia.

Ambient carbon dioxide concentration has reached an average of 385 ppm and future estimations predict an increase up to 550 ppm within this century. Among the observed effects on plants, increasing concentrations stimulate plant growth, reduction in stomatal conductance and transpiration, improved water-use efficiency and higher rates of photosynthesis. At the same time, these changes have an indirect impact on pest biology and behavior, e.g. altering their population growth or feeding habits, as well as on the symptomatology and incidence of associated pathogens such as plant viruses.

Therefore, the first aim of our work will be to study the effect of ambient and elevated CO₂ on the performance and feeding behaviour of the green peach aphid, *Myzus persicae* Sulzer (Hemiptera: Aphididae). Pepper plants (*Capsicum annuum* L.) will be grown from seeds under ambient and elevated CO₂. Wingless nymphs will be caged on each pepper plant and monitored until adulthood stage. Its offspring will be counted for an equal number of days to the pre-reproductive period. The parameters pre-reproductive period, effective fecundity, intrinsic rate of natural increase, mean relative growth rate and mean generation time will be then calculated. Aphid feeding behaviour will be studied using the Electrical Penetration Graph (EPG) technique, which provides a live visualization and recording of plant penetration by aphid mouthparts.

Secondly, we will determine the response of secondary metabolites and plant chemistry to ambient and elevated CO₂ concentrations. Height and leaf area will be measured and pepper plants harvested to analyse secondary metabolites, dry weight, carbon and nitrogen content, among others.

Lastly, we will study the acquisition and inoculation of *Cucumber mosaic virus* (CMV, *Bromoviridae*, *Cucumovirus*) by *M. persicae* on pepper plants exposed to ambient and elevated CO₂, as well as symptom development and severity of infection using TBAI and PCR methods.

Phylogeny of subfamilies Macropsinae and Megophthalminae (Hemiptera: Cicadellidae) from China based on partial DNA data

Dai, R., Li, H. and Li, Z.

Institute of Entomology, Guizhou University, Guiyang, Guizhou, 550025, P. R. China

The phylogeny was analyzed based on data of CO I, 28S rDNA and ITS2 from 40 species of 5 genera in Macropsinae and 10 species of 6 genera in Megophthalminae. One species of Idiocerinae was included as outgroup. Parsimonian, distance and likelihood methods were used to estimate the phylogenetic relationships. 15 phylogenetic trees were generated and different trees was quite similar. Phylogenetic trees support Megophthalminae as monophyletic group in this study, its genera and species always could cluster together to a separated branch in all trees, indicating Megophthalminae phylogeny was a natural classification group, supporting the current classification system. The study support Macropsinae at subfamily level was monophyletic, most Macropsinae species could be separated from Megophthalminae in all trees, especially based on 28S rDNA. The research partially resolved the relationships about the subfamilies and among genera of the Macropsinae and Megophthalminae. But the results resolved poorly the taxonomic status of *Pediopsoides*.

Eucalypt-feeding psyllids use colour to locate the choicest leaves: what looks good must also taste good

Farnier, K.¹, Dyer, A.G.², Peters, R.A.¹ and Steinbauer, M.J.¹

¹Department of Zoology, La Trobe University, Kingsbury Drive, Melbourne, VIC. 3086, ²School of Media and Communication, RMIT University, Melbourne, VIC. 3001, Australia.

Whilst many economically important host-specific herbivorous insects use olfaction to find their hosts, psyllids may be more reliant on visual cues. Most herbivores possess three types of photoreceptors (sensitive in the UV, blue and green regions of the light spectrum), which allow them to perceive the most prominent wavelengths of electromagnetic radiation in their environment.

Early studies of closely related Hemiptera such as aphids and whiteflies have revealed that this ancestral visual system leads insects to preferentially orient to yellow and green reflecting objects. Most plant pigments reflect in the “green” region, which renders plants conspicuous to herbivores but rarely provides sufficiently specific cues to permit them to discriminate between host and non-host plants. Nevertheless, herbivore preferences for specific colours have frequently been suggested to assist insects to orient to leaves of specific physiology or stage of ontogeny.

We investigated the colour preferences of four species of psyllid and the relationship between leaf reflectance and foliar nutritional quality. We found that (1) some species of psyllid exhibit colour preferences that match the foliar pigments associated with specific host leaf ontogenies, (2) psyllid orientation is influenced by their visual acuity and exposure to different host leaf types (expanding, fully expanded or senescing) and (3) visual cues potentially attract psyllids to leaves providing them with essential amino acids.

Our findings support the hypothesis that psyllids exploit plant pigments to locate their preferred foliage and provides demonstratable evidence that leaf reflectance properties are likely linked to the incidence and abundance of this important taxon of eucalypt herbivore.

A review of necrophagous insects colonising human remains in south-east Queensland

*Farrell, J.F.*¹, *Whittington, A.E.*² and *Zalucki, M.P.*¹

¹The University of Queensland, Brisbane, Qld 4072; ²The University of Florida, Gainesville FL32610, USA.

A review of insects collected from decomposing human remains in south-east Queensland yielded 32 species in three orders (Diptera, Coleoptera, Hymenoptera) and 11 families (Calliphoridae, Sarcophagidae, Muscidae, Phoridae, Sepsidae, Chironomidae, Dermestidae, Cleridae, Histeridae, Staphylinidae, Encyrtidae). There were 15 cases where remains were located indoors and five cases where remains were outdoors, in both terrestrial and aquatic environments. Coleoptera were strongly associated with outdoors remains, while dipteran species composition was similar in both indoor and outdoor habitats. Some Diptera were only associated with indoors remains, while others were similarly restricted to remains recovered outdoors. Hymenopteran parasitoids were active in both habitats.

The predominance of Calliphoridae (*Chrysomya rufifacies*, *Ch. megacephala*, *Ch. saffrana*, and *Ch. nigripes*), which were present in 15 of the 20 cases, reflects its close association with human and other vertebrate remains, justifying the ongoing use of blowflies in forensic investigations. Sarcophagidae species were collected from 9 of the 20 mortuary cases, and in three of these cases, were the only larvae present, indicating a potential for *Sarcophaga crassipalpis* and *S. impatiens* to behave as primary invaders. They appeared to behave as secondary invaders in other cases where much more developmentally advanced calliphorid larvae were present.

Comparative collections were made from other vertebrate remains, including road-kill and farmed animals throughout south-east Queensland and northern New South Wales during the same period. Similar succession patterns and dominant species were observed over a range of vertebrate remains in south-east Queensland.

From death to dust – using insects to determine post mortem intervals in Queensland

Farrell, J.F.¹, Zalucki, M.P.¹ and Whittington, A.E.²

¹The University of Queensland, Brisbane, Qld 4072; ²The University of Florida, Gainesville FL32610, USA.

Forensic entomology and necrophagous insect succession have been extensively studied in southern Australia, however long-term data describing insect taxa associated with decomposition are scarce in northern and sub-tropical Australia. A succession study of the invertebrates associated with carrion in south-east Queensland was conducted over two years to investigate seasonal and annual variation. Colonisation, successional patterns, species diversity, relative abundance of sarcosaprophagous insects, and their potential as forensic indicators were investigated. Data were collected from 64 pig carcasses (*Sus scrofa* Linnaeus) decomposing in open grassland and timbered peri-urban habitats at a field site on the western Darling Downs.

Caloglyphus berlesei (Acari) outnumbered all other necrophagous invertebrates, however the Calliphoridae and Sarcophagidae (Diptera) are the most useful forensic indicators in terms of specimens observed, collected and reared from the carcasses. The primary colonisers of the carcasses varied seasonally, and seven calliphorid (blow fly) and four sarcophagid (flesh fly) species were identified as forensically significant for the region. The most important calliphorids and sarcophagids from a forensic viewpoint were *Calliphora augur*, *C. stygia*, *Chrysomya megacephala*, *Sarcophaga impatiens*, *S. aurifrons*, *S. froggatti* and *S. praedatrix* because they indicated clear seasonal preferences and bred in the pig carrion. The suites of species occurring as primary and secondary invaders in Queensland are quite different to those recorded in southern and Western Australia. The implication is that succession data generated elsewhere in Australia could not be accurately used for post mortem interval estimations in Queensland.

Comparative data were also collected on an opportunistic basis from road-kill, farmed livestock carcasses in the region, and from human remains in the Queensland Health Forensic and Scientific Services mortuary in Brisbane. Results indicate similar succession patterns and dominant species over a range of vertebrate remains in south-east Queensland.

Studies of the susceptibility of *Aedes aegypti* from Timor-Leste to synthetic pyrethroids

*Frances, S.P.*¹, *Morton, C.J.*² and *Pettit, W.*³

¹Australian Army Malaria Institute, Gallipoli Barracks, Enoggera, Qld 4052, ²RAAF Base Amberley, Qld, 4306, (3) Northern Territory Department of Health, Darwin, NT.

Aedes aegypti (L.) is the principal mosquito vector of dengue in South east Asia, and also occurs in far northern Queensland, where cases of dengue occur annually. *Aedes aegypti* from a colony established from Townville and Dili, Timor-Leste were exposed in bottle bioassays to determine their susceptibility to 3 synthetic pyrethroids, malathion and 2 commercial insecticides. *Aedes aegypti* from Dili, Timor-Leste were resistant to permethrin, lambda-cyhalothrin and resmethrin, but were susceptible to malathion and commercial insecticides containing pyrethroids and piperonyl butoxide. Biochemical microplate assays were used to measure activity levels of 3 enzymes (Oxidase, Esterase and Glutathione-S-transferase) and showed no increase in enzyme activity in *Ae. aegypti* from Timor-Leste.

The study showed that *Ae. aegypti* from Timor-Leste are more tolerant of pyrethroid insecticides used in Australia and monitoring of insecticide susceptibility in *Ae. aegypti* entering Australia needs to be maintained to ensure adequate control of dengue vectors is achieved.

Contrasting success of two introduced *Microctonus* spp (Hymenoptera: Braconidae) biocontrol agents in Waikato pastures

Gerard, P.J. and Wilson, D.J.

AgResearch, Ruakura Research Centre, PB 3123, Hamilton 3240, New Zealand.

Two parthogenetic *Microctonus* spp (Hymenoptera: Braconidae) parasitoids with almost identical life cycles have been introduced into New Zealand for the biocontrol of two major weevil pasture pests: *M. hyperodae* Loan in the early 1990s against Argentine stem weevil *Listronotus bonariensis* (Kuschel) and the Irish wasp *M. aethiopoides* Loan against clover root weevil *Sitona obsoletus* (Gmelin) (formerly *S. lepidus*) in 2006. However, while both introductions were highly successful with up to 90% parasitism within three years of release, unexpectedly low *M. hyperodae* parasitism levels were found in overwintering *L. bonariensis* collected during pre- and post-release sampling for *M. aethiopoides*. In order to investigate this further, *S. obsoletus* and *L. bonariensis* adult populations were sampled monthly at the two Waikato sites and parasitism by their respective parasitoids assessed from September 2011–June 2014.

In three consecutive years, *M. hyperodae* parasitism levels in early summer were between 20–60% while *M. aethiopoides* parasitism was barely detectable. *M. aethiopoides* parasitism levels increased through summer and autumn to 70–100% parasitism in winter, while *M. hyperodae* parasitism levels declined to around 10% over the same period. As a consequence, *M. aethiopoides* is highly effective at reducing the damaging winter *S. obsoletus* larval populations whereas *M. hyperodae* has little impact on *L. bonariensis* populations.

While further population studies are required to identify the causes of this apparent failure of *M. hyperodae*, our data indicates that late summer/early autumn is the pivotal time to investigate. Factors that have changed since the *M. hyperodae* releases in the early 1990s are climate (a strong El Niño event from 1991 to 1995 meant initial establishment was during a period of below average temperatures), agricultural intensification and the release of novel ryegrass endophytes. Other possibilities include the development of host resistance and natural enemies of indigenous *Microctonus* spp affecting introduced parasitoids.

The biology of *Dicrodiplosis manihoti* (Dip.: Cecidomyiidae) and its interactions with *Nipaecoccus viridis* (Hem.: Pseudococcidae)

Gheibi, M.¹, Hesami, Sh.¹ and Jahromi, S.²

¹Department of Entomology, College of Agriculture, Shiraz Branch, Islamic Azad University, Shiraz, Iran;

²Department of Entomology, College of Agriculture, Shahid Chamran University, Ahvaz, Iran

One species of *Dicrodiplosis* were collected in mealybugs colonies (*N. viridis*) on citrus trees in different parts of Fars Province, during 2011-2013. Since the most common fly species was *D. manihoti*. The biology and some predator - prey Interactions of this species were studied on *N. viridis* as prey in the laboratory conditions. The mean developmental times of *D. manihoti* from egg to adult at 15, 20, 27 and 30 °C were 23.78, 14.5, 13.14 and 12.71 days, respectively. By increasing temperature from 15 to 37 °C, the daily mean feeding rate of larvae increased. The fly larvae consumed maximum number of prey at 37 °C (4.5 ± 1.49 preys per day). The life table constructed for the midges fly at $26 \pm 1^\circ\text{C}$ showed that the female's longevity from emerging until death time was about 56 days and the probability of death increased during last 10 days of the adult's life expectancy. The life table revealed that each female produced 21.76 offspring during all over life time. The net reproductive rate (R_0), intrinsic rate of increase (r_m) and innate rate of increase (λ) were, 18.5, 0.109 and 1.11, respectively.

Bush Blitz in Tasmania, summer 2014

Grove, S.J.¹ and Byrne, C.²

¹Tasmanian Museum and Art Gallery, GPO Box 1164, Hobart, Tasmania 7001; ²Tasmanian Museum and Art Gallery, GPO Box 1164, Hobart, Tasmania 7001.

In February and March 2014, the Bush Blitz species-discovery program explored protected areas on Tasmania's Central Plateau and Flinders Island, providing an opportunity for TMAG's zoologists to contribute to the program while procuring valuable specimens for the Museum's collections. This poster summarises what was found, and showcases some of the more photogenic species.

Spatial variation in the parasitoid assemblage of a Wattle gall wasp

Henriksen, M.V., Chapple, D., Chown, S. and McGeoch, M.A.

School of Biological Sciences, Monash University, Clayton, VIC 3800, Australia.

The spread of a number of *Acacia* species in Australia beyond their native range is a potential threat to native plant communities. *Trichilogaster acaciaelongifolia* (Pteromalidae) is a gall forming herbivore of several *Acacia* species and inhibits tree growth and seed production by inducing gall development in flower buds. However, its potential contribution as a biocontrol agent is likely to be negatively affected by a range of parasitoids associated with the wasp. The abundance and composition of this parasitoid assemblage could vary spatially due to environmental variation and stochastic events, and parasitoid traits such as the ability to utilize alternative hosts can affect the structure and stability of the food web associated with the *Trichilogaster* galls. This could cause local variation in the stability of the *Acacia-Trichilogaster* interaction. To quantify spatial variation in parasitoid species composition, galls formed by *T. acaciaelongifoliae* were collected from two of its host plants (*Acacia floribunda* (Gossamer Wattle) and *Acacia longifolia* subsp *longifolia* (Sallow Wattle)) at 10 sites in the eastern suburbs of Melbourne. The maximum distance between sites was 32 km. The collected galls were reared and a rich assemblage of parasitoids emerged, including species of Torymidae, Eurytomidae and Ichneumonidae. Parasitoid species beta-diversity between sites was calculated and shown to decrease with increasing geographical distance between sites. The presence of distance decay over relatively short distances suggests that the parasitoid impact on *T. acaciaelongifoliae* will vary locally which could affect the stability of local biocontrol potential. Spatial variation in parasitoid presences and abundances should be considered when introducing or augmenting gall wasp populations to control invasive *Acacias*.

Flying doctors - bees deliver biological control - a new technique for Australian horticulture

Hogendoorn, K. and Scott, E.S.

The University of Adelaide, School of Agriculture, Food and Wine, Adelaide SA 5005;

This poster demonstrates the entomovectoring technique. Using bees as vectors for the delivery of biological control agents is an economic and sustainable method, as it results in targeted delivery while using minimal inputs. It is particularly suitable for the control of diseases caused by latent infections of *Botrytis cinerea* or *Monilinia* species, which enter fruit during flowering.

In Europe, entomovectoring is increasingly used in the strawberry industry for the control of grey mould. We are currently introducing this technique in Australia for the control of brown rot in cherries and *Botrytis* bunch rot in grapes.

With the development of new biological control agents, the technique can be used to control similar diseases in a wide range of crops, including almonds, apples, stone fruit and summer berries.

Native and invasive springtail interactions in a novel ecosystem

Lythe, M.J., Chown, S.L. and McGeoch, M.A.

School of Biological Sciences, Monash University, Clayton, VIC 3800

Invasive species can alter native species diversity and ecosystem processes and are a worldwide conservation concern. Plant invasion is often associated with changes in leaf litter type, chemistry and quantity, which can affect the springtail (Collembola) community. Many species of invasive springtails exist in Australia, likely introduced with agricultural crops and often associated with invasive plants. Long-term, multi-species plant invasion into the Mt Pilot National Park in northern Victoria has created a novel ecosystem where native and invasive springtails and plants interact in complex ways that alter community dynamics. This research investigates these interactions and the effects of climate and fire disturbance on springtail community composition. The strength of the combined impact of invasive springtails and plants on native springtails is also examined. We hypothesised that invasive springtail abundance would increase with invasive plant cover, and that the impact on native springtails would be functionally, rather than numerically, mediated. Soil and leaf litter samples were taken at each of 10 sites within the national park, and springtails were extracted, identified to species, and counted. Sites were chosen from across a gradient of plant invasion ranging from ~ 17 – 65% invasive plant richness, and a range of fire history from 3 – 60+ years. This paper presents a description of the system and the distribution of springtail species within the park, as well as discussion of the impact of invasive springtails and plants on native springtail abundance.

Coexistence of minicircular and a highly rearranged mtDNA molecule suggests that recombination shapes mitochondrial genome organization

Mao, M.¹, Austin, A.D.², Johnson, N.F.³ and Dowton, M.¹

¹Centre for Medical Bioscience, School of Biological Sciences, University of Wollongong, Wollongong, NSW, 2522, Australia; ²Center for Evolutionary Biology and Biodiversity, School of Earth and Environmental Sciences, University of Adelaide, S.A. 5005, Australia; ³Department of Evolution, Ecology and Organismal Biology, The Ohio State University, 1315 Kinnear Road, Columbus, OH 43212, USA.

Recombination has been proposed as a possible mechanism to explain mitochondrial (mt) gene rearrangements, although the issue of whether mtDNA recombination occurs in animals has been controversial. In this study, we sequenced the entire mt genome of the megaspilid wasp *Conostigmus* sp., which possessed a highly rearranged mt genome. The sequence of the A+T-rich region contained a number of different types of repeats, similar to those reported previously in the nematode *Meloidogyne javanica*, in which recombination was discovered. In *Conostigmus*, we detected the end-products of recombination: a range of minicircles. However, using isolated (cloned) fragments of the A+T-rich region, we established that some of these minicircles were found to be PCR artifacts. It appears that regions with repeats are prone to PCR template switching, or PCR jumping. Nevertheless, there is strong evidence that one minicircle is real, as amplification primers that straddle the putative breakpoint junction produce a single strong amplicon from genomic DNA, but not from the cloned A+T-rich region. The results provide support for the direct link between recombination and mt gene rearrangement. Furthermore, we developed a model of recombination which is important for our understanding of mtDNA evolution.

From plantings to the paddock: are ground-dwelling beetles and beneficial arthropods moving through fragmented agricultural landscapes?

Ng, K.¹, Driscoll, D.A.¹, Lindenmayer, D.B.¹, Macfadyen, S.², Lewis, M.³ and Arnott, A.³

¹Fenner School of Environment and Society, ARC Centre of Excellence for Environmental Decisions and National Environment Research Program, The Australian National University, Canberra, ACT 0200; ²CSIRO Ecosystem Sciences, Black Mountain, GPO Box 1700, Canberra, ACT 2601; ³NSW Central Tablelands Local Land Services, PO Box 510, Cowra NSW 2794.

Sustainable intensification of agriculture requires land management practices that improve production but reverse global declines in biodiversity. Plantings aim to restore fragmented habitats by improving connectivity and providing habitat and resources. However, little is known on the movement ecology of many invertebrate taxa, including predators of pest crops. We will examine movement through plantings and surrounding paddocks characterized by temporally and spatially diverse management regimes.

We hypothesize that the extent of movement from remnant woodland patches into the surrounding matrix will depend on the degree of contrast between the two habitats in terms of vegetation composition and structure, microclimate and management intensity. To test this, we have selected study sites across fragmented temperate woodlands in mixed-cropping areas of the Lachlan River Catchment (NSW, Australia). The composition, abundance, species richness and life-history traits of ground-dwelling Coleopteran and common beneficial and pest species will be compared between three paddock types adjacent to remnant woodland: plantings, cropping, and paddocks grazed during fallow. Sampling will be conducted along transects that extend from remnant woodland into these contrasting paddocks, three times in a year, during periods of low, mid and high crop growth. Experimental releases and observations of individual movement paths of Coleoptera will be documented using fluorescent powder. Animals will be released at the remnant-paddock boundary to quantify movement behaviour and microhabitat choices at contrasting edges.

Our findings will advance understanding on the role of restoration plantings and conservation strategies in influencing invertebrate movement and biodiversity. Project outcomes include increased use of ecosystem services, such as pest regulation, to enable improved integration of agriculture with conservation through targeted incentive payments within land stewardship schemes.

Cooled propylene glycol preserves DNA of remote field collected insects for next generation sequencing analysis

Patrick, H. and Armstrong, K.

Bio-Protection Research Centre, Lincoln University, Canterbury, New Zealand

Next generation sequencing (NGS) based methods can now be applied to large population scale studies. This often requires very high quality DNA which is relatively straight forward when material is already in the laboratory. However, for specimens collected from remote field locations DNA degradation is a problem that can only be overcome by logistically complex preservation techniques. Simpler preservation techniques are therefore required.

Laboratory trials were conducted to determine the DNA quality of the fly species *Fannia canicularis* stored at 4°C in a number of readily available preservatives. One of these, chilled propylene glycol, was subsequently used for the storage and carriage of field-collected *Bactrocera* fruit fly specimens from Australia to New Zealand for DNA extraction.

Fannia canicularis held in various buffers and proprietary preservatives for up to 15 days produced degraded DNA unsuitable for the NGS method of genotyping by sequencing (GBS). However, specimens similarly maintained at ~4 °C in either propylene glycol, Qiagen's Buffer AL, Qiagen buffer ATL, RNAlater® Soln. (Ambion) and RNA lysis buffer (Promega) did produce sufficiently high quality DNA. When the use of chilled propylene glycol was validated with *Bactrocera* species field-caught in Australia and processed up to 20 days later in New Zealand, DNA fragments of ~10-20 kb were obtained and successfully analysed by GBS.

Therefore, packing in thermo-protected ice, together with propylene glycol as a non-toxic, non-flammable preservative, offers a logistically simple and safe approach to long distance transportation of field-collected samples for NGS population genomic studies.

Can pre-release supplementation increase the success of Sterile Insect Technique programs for the Queensland fruit fly, *Bactrocera tryoni* (Froggatt)?

*Reynolds, O.L.*¹, *Orchard, B.*², *Collins, S.*³ and *Taylor, P.W.*³

¹Graham Centre for Agricultural Innovation (NSW Department of Primary Industries and Charles Sturt University), NSW Department of Primary Industries, Private Bag 4008, Narellan, NSW 2567, olivia.reynolds@dpi.nsw.gov.au; ²NSW Department of Primary Industries, Private Mail Bag, Wagga Wagga, NSW 2350; ³Department of Biological Sciences, Macquarie University, North Ryde, NSW, 2109.

The sterile insect technique has been used against the Queensland fruit fly, *Bactrocera tryoni* (Froggatt) (Diptera: Tephritidae). Mass rearing procedures lead to a reduction in the fitness of the released sterile males. We examined i) the effects of yeast hydrolysate (YH) supplementation prior to release on longevity of sterile *B. tryoni* under low and high environmental stress and when food becomes scarce, ii) the effects of pre-release YH supplements on the persistence and abundance of sexually mature sterile male *B. tryoni* under field conditions and iii) the separate and combined effects of YH and methoprene treatment on sexual maturation of sterile *B. tryoni*. In a low-stress cage study, there was no effect of diet (sugar only, sugar plus YH, or sugar plus YH for 48 h and sugar only thereafter), although overall females lived longer than males. In a high stress cage study that compared *B. tryoni* fed white sugar only, brown sugar only, white sugar plus YH or brown sugar plus YH, mortality was lower for YH-fed flies than YH-deprived flies and females lived longer than males. Under a food scarcity scenario, male and female *B. tryoni* provided with YH during the first two days of adult life have significantly shorter survival when subsequently deprived of food compared with flies that received only sucrose. In the field, 1.2 YH-supplemented *B. tryoni* were trapped for every YH-deprived fly trapped. Access to YH increased maturation of both male and female *B. tryoni* with maturation further augmented by methoprene treatment by approximately two days; similar effects were evident for males and females and for two application methods (topical and dipping). Under natural conditions, YH supplementation can increase the maturation rate and longevity of sterile male *B. tryoni* and may improve success of the SIT for *B. tryoni*. The release of YH-supplemented *B. tryoni* is advocated for SIT programs.

Responses of pest and non-pest fruit flies (Tephritidae: Dacinae: Dacini) to new lures in northern Australia

Royer, J.

Department of Agriculture Fisheries and Forestry, Ecosciences Precinct, GPO Box 267, Brisbane, QLD 4001.

The male lures cue-lure and methyl eugenol (ME) attract more than half of the known Dacini (*Bactrocera* and *Dacus*) fruit fly species and have been used successfully in fruit fly monitoring and control over the last 50 years. However, among the species non-responsive to these lures are several pests and without a lure their management is difficult. In this study several novel male lures and zingerone, a new male lure attractive to a minor pest *B. jarvisi*, were field tested widely in north Queensland. Raspberry ketone formate (RKF), an improved male attractant for melon fly (*B. cucurbitae*), was compared in the field to cue-lure. Cucumber volatile blend lure, a female-biased attractant developed for melon fly (*B. cucurbitae*), was tested for attractancy to cucumber fly, *B. cucumis* in comparison to orange ammonia, Cera Trap® and a control. The findings were that cucumber volatile lure more consistently trapped *B. cucumis*, was more attractive in low population densities and trapped this species earlier on average than the other lures/traps. RKF was significantly more attractive than cue-lure to three species of some economic importance: Queensland fruit fly (*B. tryoni*), the mango fly (*B. frauenfeldi*) and *B. bryoniae*, as well as several non-pest species. However cue-lure was significantly more attractive than RKF to lesser Queensland fruit fly (*B. neohumeralis*) and other non-pest species. An improved male lure was potentially identified for *B. kraussi*, a minor cue-responsive pest species in north Queensland. Three non-responsive (non-pest) *Bactrocera* species responded to the novel male lures and a new species of *Dacus* was trapped regularly at zingerone on Cape York Peninsula. Three other species with a known response to cue-lure or ME were more attracted to the novel male lures or zingerone. Twenty five species responded to more than one male lure with varying degrees of attraction.

Delicious honey, sticky propolis, productive pollen: antimicrobial products of the stingless bee nest

Shanks, J.¹, Haigh, A.¹, Riegler, M.² and Spooner-Hart, R.¹

¹School of Science and Health, University of Western Sydney, Locked Bag 1797, Penrith NSW 2751 Australia;

²Hawkesbury Institute for the Environment, University of Western Sydney, Locked Bag 1797, Penrith NSW 2751 Australia

Hive products of honey bee, *Apis mellifera* L. (Apidae: Apini), such as honey and propolis (mixture of plant resins and worker gland secretions) have been reported to possess human medicinal benefits (particularly as antimicrobials); their potential has also been reported as an inhibitor of the significant honey bee disease American foulbrood *Paenibacillus larvae* (White). Several studies have reported the chemical composition and antimicrobial activity of stingless bee propolis and honey; however, few have investigated their potential as inhibitors of specific bee pathogens. The Australian stingless bee, *Tetragonula carbonaria* (Smith) (Apidae: Meliponinae), has no recorded pathogens. We have previously observed effective hygienic behaviour in this species as one mechanism for reduced brood pathogens. Subsequently, we investigated the antimicrobial activity of honey, pollen and propolis as contributors to pathogen suppression. Disc-diffusion and microtiter plate assays were used to test the inhibitory activity of *T. carbonaria* and *A. mellifera* hive products on the growth and development of *P. larvae* and chalkbrood, *Ascosphaera apis* (Massen ex Claussen). Propolis of *T. carbonaria* had the greatest inhibitory effects on *P. larvae* development and mycelial growth of *A. apis*. Honey of *T. carbonaria* and *A. mellifera* had slightly better inhibition than the two pollen extracts, whereas pollen extracts were the least inhibitory. Chemical profiles of propolis, pollen, and callow brood comb were determined by LC-MS. Brood comb of *A. mellifera* was the least complex hive product, followed by the two pollen extracts. There were significant differences in the propolis profiles. Propolis of *A. mellifera* contained flavonoids, whereas *T. carbonaria* propolis also contained sesquiterpenoids and triterpenoids at higher concentrations. These latter plant compounds are known for their antimicrobial activities. It is hypothesised that when collected plant resins are incorporated into *T. carbonaria* hive materials, they provide an environment capable of suppressing pathogen establishment and spread within colonies.

Morphological comparison of Lord Howe Island Stick Insects originating from the Ball's Pyramid population and the extinct Lord Howe Island population

*Silcocks, S.*¹ and *Magrath, M.J.L.*²

¹Invertebrate Department, Melbourne Zoo, Zoos Victoria, P.O. Box 74, Parkville, Victoria, 3052; ²Wildlife Conservation and Science, Zoos Victoria, P.O.Box 74, Parkville, Victoria, 3052

The Lord Howe Island Stick Insect (*Dryococelus australis*) (LHISI) was first described by Montrouzier in 1855. By the 1930's, the species was determined to be locally extinct on Lord Howe Island. Dead specimens were located on Balls Pyramid (a volcanic spire, 20km south east of LHI) in the 1960's. In 2001, a remnant population of LHISI was found surviving on Balls Pyramid. In 2003, four animals were removed from Ball's Pyramid to establish a captive breeding program and a population has been maintained at Melbourne Zoo since then.

We located over 200 specimens of *Dryococelus australis* in Australian museums, collected from LHI between 1853 and 1915. The morphology of the specimens collected on LHI was found to differ from that of the captive bred specimens in terms of overall size, degree of sexual size dimorphism and size of male hind femora. A range of factors may contribute to these differences including collection bias, population divergence, selection in captivity and nutritional differences. Captive bred males are significantly smaller than museum specimens of the LHI animals and currently do not express the enlarged hind femora.

We have started investigating potential environmental effects on LHISI morphology by manipulating factors such as diet, stocking density and sex ratio. We also plan to determine the extent of genetic differentiation between the LHI and Ball's pyramid populations.

Molecular phylogeny of the Australian jumping plant lice and lerp insects (Hemiptera: Psylloidea) reveals host specificity

Taylor, G.¹, Fagan-Jeffries, E.¹, Steinbauer, M.² and Austin, A.¹

¹Australian Centre for Evolutionary Biology & Biodiversity, University of Adelaide, South Australia 5005;

²Department of Zoology, La Trobe University, Bundoora, Victoria 3086.

Jumping plant-bugs or ‘psyllids’ (Hemiptera: Psylloidea) show a high level of host specificity, where psyllid families are often associated with certain plant families, often with congruence at the generic level, and many species are associated with single, or few closely related plant species. Whether they have co-evolved with their hosts, or have undergone periodic host switches and subsequent radiations on ‘novel’ hosts, or a combination of both, has been little investigated.

In this study, comprising the first comprehensive molecular research on the Australian Psylloidea on a sclerophyllous flora characterised by its evolution in an aridifying environment, phylogenetic analysis of 140 isolates using combined COI (441 bp) and 18S (813 bp) sequences data depicted a basal monophyletic clade for the Australian spondyliaspidine Aphalaridae, host specific to the Myrtaceae. This clade comprised *Cardiaspina*+*Blepharocosta*, *Glycaspis*, *Creiis* (all lerp-formers); *Anoeconeossa*, *Platyobria*, *Eucalyptolyma* and *Blastopsylla* (all free-living on flush, meristematic foliage). A second clade contained *Phellopsylla*+*Phyllolyma* (stem and bark-inhabitants) + *Ctenarytaina* (free-living, flush foliage feeders). Another major lineage comprised *Calophya* (Calophyidae) nested within a clade of *Acizzia* (Psyllidae) (from multiple hosts including, Loranthaceae, Mimosaceae, Proteaceae and Sapindaceae) which together were within a diverse assemblage of Triozidae. This latter family depicted a high degree of structure associated with their host taxa, including *Acanthocasuarina* and *Aacanthocnema* on *Allocasuarina* and *Casuarinicola* on *Casuarina* (both Casuarinaceae), *Trioza* on *Eremophila* and *Myoporum* (both Scrophulariaceae) and *Schedotrioza* on *Eucalyptus* (Myrtaceae).

Ongoing studies aim to further resolve the apparent co-phylogeny of the Australian psyllid fauna and their hosts.

Biodiversity and ecosystem services for sustainability

Todd, J.H., Burgess, E.P.J., Barraclough, E.I., Poulton, J., Rheinlander, P., Sorce, M. and Malone, L.A.

The New Zealand Institute for Plant & Food Research Limited, Private Bag 92 169, Auckland, New Zealand
1142

The international push for ‘green growth’ continues to demand evidence-based measures of sustainability. Biodiversity, and the ecosystem services it can provide, is increasingly recognised as an important part of sustainable food production, however reliable and meaningful methods for measuring these services in agro-ecosystems are lacking. Consequently, we are working with the pipfruit, kiwifruit and winegrape industries in New Zealand to (1) obtain quantitative evidence for links between on-farm invertebrate and microbial biodiversity and the provision of ecosystem services, such as biological control, decomposition and nutrient cycling in orchards and vineyards, (2) investigate how different management practices affect biodiversity-related ecosystem services, and (3) identify cost-effective ways to enhance the right kind of biodiversity for growers. Initial results include

- Identification of 14 predator and five parasitoid species attacking pest leafrollers in kiwifruit orchards
- Detection of differences in invertebrate biodiversity in apple orchards managed using three different pest management systems
- Assessment of movement of orchard-dwelling invertebrates to nearby native restoration areas using community survey and mark-recapture techniques
- Preliminary evidence of macro-detritivores increasing the speed of decomposition in apple orchards and speed of decomposition varying between management systems
- Assessment of the species richness of microbial fungi in organic and conventionally managed vineyards, with higher diversity detected in organic vineyards
- Identification of the management practices in kiwifruit orchards affecting ground-active invertebrate functional group diversity.

Further work on all these areas will be conducted over the next two years with the aim of providing scientific support for sustainability claims for New Zealand’s export fruits and wine.

Long-term monitoring of in-crop aphid populations in south eastern Australia, as a component of a model to predict incidence of *Beet western yellows virus* in field crops.

Aftab, M.¹, Trebicki, P.¹, Salam, M.U.² and Freeman, A.¹

¹Department of Environment and Primary Industries, Private bag 260 Horsham, VIC 3400; ²Department of Agriculture and Food Western Australia, Locked bag 4, South Perth, WA 6983.

Beet western yellows virus (BWYV) has emerged as a serious problem in pulse and canola crops in south eastern Australia over the last eight years. This year the disease has a devastating impact on canola crops in South Australia and the incidence was as high as 100% in some crops. Previously in Victoria up to 20% BWYV incidence was recorded in chickpea crops in 2009. This virus is only transmitted by aphids and the most efficient vector is the green peach aphid (*Myzus persicae*). For the management of this virus, modellers of the Department of Agriculture and Food Western Australia (DAFWA) are constructing a forecasting model which will help in judicious decision making. The key drivers of this model are the factors that directly affect the aphid population during the growing season i.e. the in-season rainfall, temperature and frost. This model differs from WA models which are based on summer and autumn rainfall for aphid population and the presence of virus green bridge. In the last five years, data has been collected from canola and pulse field plot trials including (i) weekly monitoring of aphids on yellow sticky traps (ii) monitoring of live aphid numbers and species on the plants and (iii) virus incidence in the field plots. This field trial data will be associated with the climatic variables to construct the forecasting model for the management of BWYV. The main aphid species found in weekly yellow sticky traps include: green peach aphid (*Myzus persicae*), cabbage aphid (*Brevicoryne brassicae*), turnip aphid (*Lipaphis pseudobrassicae*), potato aphid (*Macrosiphum euphorbiae*), cowpea aphid (*Aphis craccivora*), alfalfa aphid (*Acyrtosiphon kondoi*), corn aphid (*Rhopalosiphum maidis*), spotted alfalfa aphid (*Therioaphis trifolii*) and oat aphid (*Rhopalosiphum padi*). All these species are reported to be vectors of BWYV except the cowpea aphid. The number of aphids trapped varied, reaching up to 2400 per trap, depending on adverse or favourable conditions during the season. The live colonies of dominating aphids, green peach aphid, cabbage aphid and turnip aphid, were observed on canola and cowpea aphid on faba bean and lentil.

The control efficiency of *Orius similis* (Heteroptera: Anthocoridae) to *Frankliniella occidentalis* (Thysanoptera: Thripidae)

Zhi, J., Mo, L. and Zhang, J.

Institute of Entomology, Guizhou University, Guiyang, Guizhou, 550025, P. R. China

Members of the genus *Orius* are general predators of many insects including mites, thrips, aphids, eggs and small larvae of moths and other small, soft-bodied insects. They are important biological control agents for many pests. Research on the effect of different preys on the predation and prey preference of *Orius* spp. can lead to more effective use the agent and strengthen the control over the prey species. *Orius similis* is the dominant species in southern China. Western flower thrips, *Frankliniella occidentalis* (Pergande), invaded China in 2003, is now distributed to many provinces and areas, and has caused serious damage to horticulture and vegetable production. In order to assess the effectiveness of *O. similis* in controlling *F. occidentalis* populations, the control abilities of *O. similis* influenced by biotic and abiotic factors were studied. The functional responses of 4th instar nymphs, 5th instar nymphs and adult females of *O. similis* to *F. occidentalis* were fitted by Holling II's equations, but the coefficients varied with the life stage and the temperatures. The preying capacity was higher from 22-28°C, and was lower at 19°C or 31°C. The predation efficiency of 4th instar, 5th instar, and adult female of *O. similis* on *F. occidentalis* increased with increasing temperature from 19°C to 25°C, and reached the maximum at 25°C. The predation rates of *O. similis* on *F. occidentalis* were higher on common bean and pepper, and lowest on cucumber and tomato. Spatial heterogeneity significantly affected the functional response of *O. similis* which hunted *F. occidentalis* more efficiently when space was small and spatial heterogeneity was low. The most suitable enemy: pest ratio was 9: 120, which may result in better biological control at a relatively low cost.

INDEX OF AUTHORS

Adcock, M.	63	Chown, S.L.	149, 150
Aftab, M.	160	Clarke, A.R.	5, 12, 31, 85, 108, 127
Ali, A.	136	Collins, S.	154
Ali, M.	136	Cook, G.	100
Anderson, S.	63	Cook, J.M.	43, 44, 114, 115
Ang, G.C.K.	1, 2	Cook, L.G.	82
Angove, M.	96	Cooper, P.D.	20, 95
Ardin, P.	126	Cranston, P.S.	21, 59
Armstrong, K.	153	Cribb, B.	72
Arnott, A.	152	Cullen, J.	110, 127
Ashfaq, M.	136	Cunningham, P.	127
Asri, S.	104	Cunningham, S.	23
Austin, A.D.	3, 45, 151, 158	Dader, B.	24, 139
Baird, D.	62	Dai, R.	140
Baker, G.	4, 26	Dang, K.	25, 69
Balagawi, S.	5	Davies, K.	94
Barling, A.	116	de Bruyne, M.	120
Barmuta, L.	117	DeGabriel, J.L.	114, 115
Barnes, J.	81	Del Socorro, A.	26
Barraclough, E.I.	159	Delamoir, S.	84
Barratt, B.I.P.	6, 41, 78, 89, 118	Dennis, A.B.	14
Barron, A.B.	7	Dickinson, M.	27
Barry, K.	47	Doggett, S.L.	25, 28, 29, 55, 69
Barton, P.S.	8	Dominiak, D.	30
Batley, M.	23	Downes, S.J.	72
Beattie, R.G.	87	Downton, M.	67, 75, 151
Beekman, M.	9	Drew, R.A.I.	5
Berenbaum, M.R.	10	Driscoll, D.A.	152
Berna, A.Z.	120	Dunning, L.T.	14
Binns, M.	26	Dyer, A.G.	141
Blacket, M.J.	11	Ekanayake, E.W.M.T.D.	32
Bohman, B.	90	Eow, L.X.	32
Boontop, Y.	12	Escalona, H.E.	33
Bosque-Perez, N.	119	Fabricant, S.	47
Bouwer, M.C.	64	Fagan-Jeffries, E.	158
Braby, M.F.	137	Fanson, B.	30
Brodeur, J.	6	Farnier, K.	34, 71, 81, 141
Brown, B.	94	Farrell, J.F.	35, 142, 143
Brown, S.D.J.	13	Fell, S.	99
Bryant, L.M.	60	Feng, Y.	36
Bu, W.	25	Fereres, A.	24, 139
Buckley, T.R.,	14	Ferguson, C.	78
Burgess, E.P.J.	159	Fernández-Sánchez, J.	129
Buttner, W.A.	116	Fisher, N.	61
Byrne, C.	15, 147	Fitzgerald, G.	119
Cai, C.	87	Fletcher, M.J.	37
Cameron, S.L.	12, 16, 17, 32	Flynn A.R.	38, 42
Campos, M.P.	20	Forbes, R.J.	30, 61
Car, C.A.	18	Fountain-Jones, N.	40
Castalanelli, M.A.	48	Frances, S.P.	144
Chapple, D.	148	Freeman, A.	119, 160
Cheah, C.	116	Furlong, M.J.	1, 2, 127
Chen, W.	138	Gao, Y.	130
Cheng, K.	19, 107	Gerard, P.J.	78, 145

Gheibi, M.	146	Lei, Z.	130
Giblin-Davis, R.	94	Leijs, R.	50
Gibson, T.	75	Leschen, R.A.B.	65, 66
Gimmel, M.L.	66	Lessard, B.D.	67, 68
Glatz, R.	51	Lewis, M.	152
Goldson, S.L.	41, 78	Li, H.	140
Goolsby, J.A.	103	Li, Z.	140
Grant, N.	81	Lilly, D.G.	25, 69
Gregg, P.	26	Lindenmayer, D.B.	152
Grove, S.J.	147	Lo, N.	70
Gulliver, S.	26	Lovell, D.	63
Gunawardana, D.N.	42	Lubanga, U.K.	71, 113
Gunter, N.L.	17	Luong, T.T.A.	72
Haigh, A.	156	Lythe, M.J.	150
Hall, A.	43, 44	Macfadyen, S.	73, 152
Hardwick, S.	78	Magrath, M.J.L.	157
Harrison, S.E.	45	Majer, J.	48
Hauser, M.	111	Makinson, J.	94
Hayes, R.A.	46	Maleszka, R.	74
Hemmi, J.M.	88	Malipatil, M.B.	11
Hempel de Ibarra, N.	123	Malone, L.A.	118, 159
Henriksen, M.V.	148	Mangan, M.	126
Herberstein, M.E.	47, 57, 83	Mantle, B.	62, 63
Hesami, Sh.	146	Mao, M.	75, 151
Heterick, B.	48	Marris, J.W.M.	76
Hoddle, M.S.	49	Matthews, E.G.	77
Hogan, B.	84	McGeoch, M.A.	149, 150
Hogendoorn, K.	50, 125, 149	McHugh, J.V.	112
Hossain, Z.	84	McNeill, M.R.	78
Hunter, D.M.	51	Mengual, X.	111
Il'ichev, A.L.	52	Mesibov, R.	18, 79
Jahromi, S.	146	Meusemann, K.	80, 131
Jenkins, C.	99	Mikac, K.,	54
Jennings, D.	93	Miller, R.	81
Jermiin, L.	53	Mills, P.J.	82
Johnson, A.P.	54	Misof, B.	80
Johnson, N.F.	151	Mo, L.	161
Johnson, S.	43, 44	Moore, C.M.	64
Johnston, E.	55	Moreno, A.	24
Kainer, D.	56	Morton, C.J.	144
Keller, M.A.	36, 121, 125	Mound, L.A.	32
Kelso, S.	111	Muschett, G.	83
Kemp, D.J.	57	Nahrung, H.F.	46
Khalid, S.	136	Nancarrow, N.	119
Klopfstein, S.	58	Narendra, A.	88, 97, 98
Kokko, H.	116	Naumann, I.D.	84
Kravchuk, O.	36	Neave, M.J.	23
Krosch, M.N.	12, 21	Newman, J.D.	85
Krosch, M.N.	59, 60	Ng, K.	152
Kwak, M.L.	61	Niehuis, O.	86
La Salle, J.	61, 62	Niko, P.	2
Lagogiannis, K.	126	Nowotny, T.	120
Lanfear, R.	56	O'Connor, E.	61
Lawrence, J.F.	33, 77	Oberprieler, R.G.	87, 93
Lawson, S.A.	64	Ogawa, Y.	88
Lee, W.	84	Orchard, B.	154
Legge, E.L.G.	19	Palmer, W.A.	89, 103, 110

Parry, H.	4, 73	Sinclair, B.J.	14
Patrick, H.	153	Skevington, J.H.	111, 132
Peacock, M.	51	Ślipiński, A.	17, 33, 76, 87, 112
Peakall, R.	90	Smart, J.	99
Pearson, H.G.	42	Smith, T.E.	46
Peng, F.	126	Sopow, S.	42
Perkins, L.E.	72	Sorce, M.	159
Perry, C.J.	7	Spetch, M.L.	19
Peters, R.A.	141	Spooner-Hart, R.	156
Pettit, W.	144	Ståhls, G.	111
Phillips, C.	78	Steinbauer, M.J.	34, 39, 44, 61, 71, 81, 113, 158
Phillips, R.D.	90	Sumner, J.	129
Piggott, A.M.	46	Sutton, T.L.	114, 115
Pilkington, L. J.	91	Syeda, S.S.	96
Pinzon Navarro, S.	92	Symonds, M.R.E.	116
Poulton, J.	159	Tajuddin, T.	104
Pratt, P.	94	Tan, C.	4
Pullen, K.R.	93	Tassell, S.	117
Purcell, M.	94, 95	Taylor, G.S.	44, 94, 113, 158
Qureshi, S.A.	96	Taylor, P.W.	154
Raderschall, C.A.	97	Thompson, F.C.T.	111, 132
Raman, A.	100	Throssell, A.	15
Ramirez Esquivel, F.	98	Todd, J.H.	118, 159
Rana, N.	136	Toi, C.S.	25, 55
Rathnayake, D.	47	Tomasetto, F.	41
Reynolds, O.L.	99, 154	Tooman, L.K.	118
Rheinlander, P.	159	Trebicki, P.	119, 139, 160
Rice, A.D.	11	Trowell, S.C.	120
Richardson, A.M.M.	117	Twort, V.	14
Riegler, M.	43, 44, 114, 115, 156	Ueese, A.	2
Rix, M.G.	45	Umbers, K.D.L.	83
Rizvi, S.Z.M.	100	Umbers, K.D.M.	116
Robertson, J.A.	112	van Helden, M.	121
Robinson, S.	81	van Steenis, W.	111, 132
Römer, H.	101	van Swinderen, B.	122
Ronquist, F.	58	van Zuijen, M.	111, 132
Rowell, D.M.	95, 128	Vilhelmsen, L.	58
Royer, J.	155	Vorobyev, M.	123
Rundle, B.J.	102	Wallman, J.F.	54, 67, 124
Salam, M.U.	160	Wanat, M.	33
Sandhu, H.,	36	Wang, T.	125
Sands, D.P.A.	103	Wapstra, E.	117
Sandwith, R.	61	Warr, C.G.	120
Sasaerila, Y.	104	Webb, B.	126
Saunders, M.E.	105	Webb, C.E.	69
Scheffer, S.	94	Webb, O.	127
Schellhorn, N.A.	73, 106	Weinstein, P.	55
Schultheiss, P.	107	Weir, T.	17
Schutze, M.K.	12, 31, 85, 108	Wheatley, W.	100
Scott, E.S.	149	White, T.	47
Seijdhour, F.P.	71	Whiting, M.J.	57
Semeraro, L.	11	Whittington, A.E.	35, 142, 143
Shackleton, M.	109	Wighton, S.	54
Shanks, J.	156	Wilkens, S.	96
Shattuck, S.	48	Williams, C.	55
Sheppard, A.	110	Wilson, D.	78
Silcocks, S.	157		

Wilson, D.J.	145	Zeil, J.	88, 97, 98, 134
Wong, M.	128	Zhang, J.	161
Woodhams, M.	129	Zhi, J.	161
Woodman, J.D.	128	Zwick, A.	135
Woolston, M.	62		
Wratten, S.D.	36		
Wu, S.	130		
Wystrach, A.	19		
Yazdani, M.	36		
Yeates, D.K.	68, 80, 95, 131		
Yen, A.	119		
Young, A.D.	111, 132		
Zalucki, M.P.	2, 35, 72, 133, 142, 143		
Zborowski, P.	29		