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AÇOREANA Revista de Estudos Açoreanos

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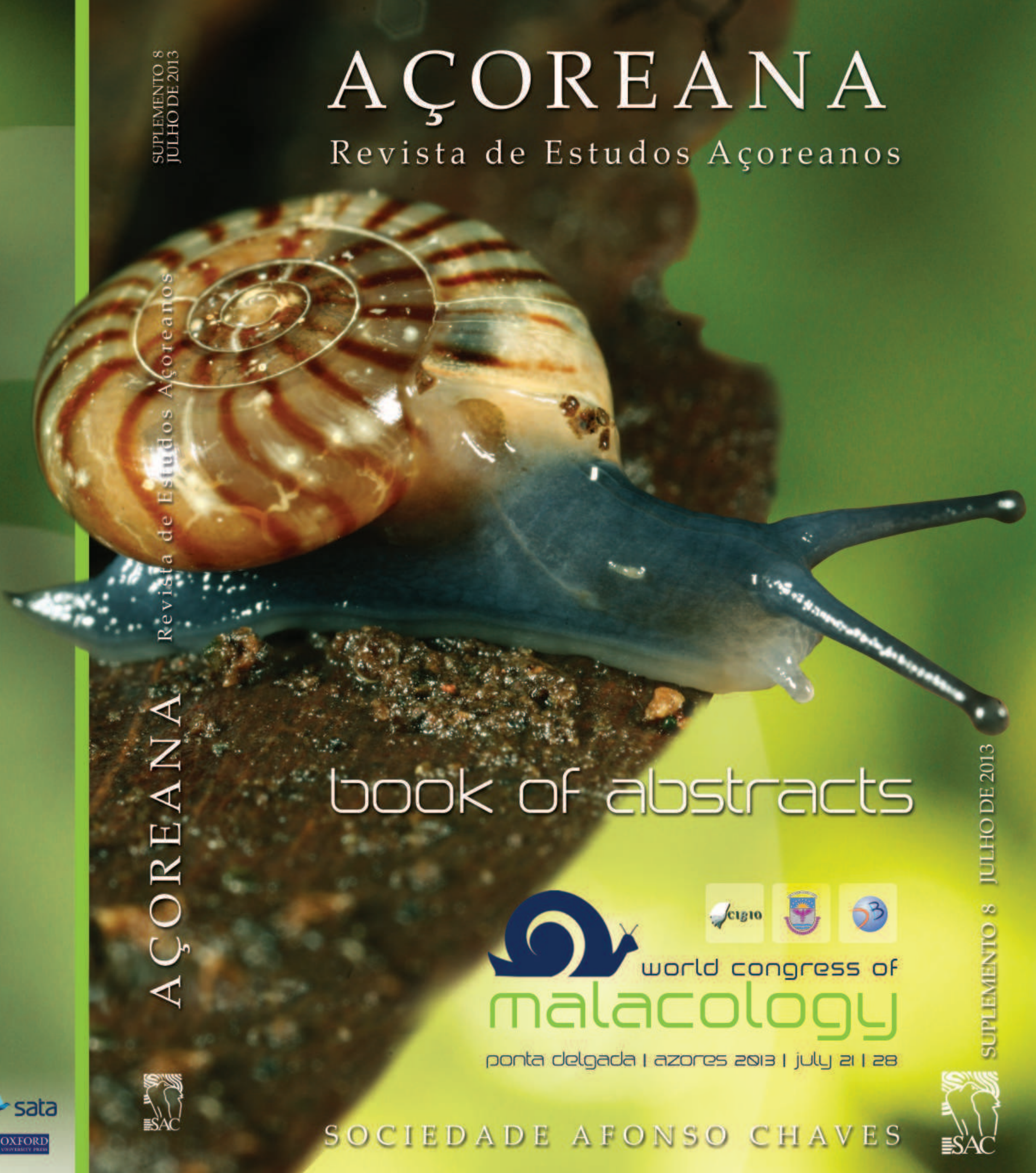

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Revista de Estudos Açoreanos

PROPRIEDADE da
Sociedade Afonso Chaves
Associação de Estudos Açoreanos
Sede: Observatório Afonso Chaves – Relvão

PRESIDENTE e EDITOR
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Edição deste Suplemento
António M. de Frias Martins
Ana Cristina Costa
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PAGINAÇÃO
EMANUEL CORDEIRO
Soluções Informáticas e Design

IMPRESSÃO E ACABAMENTO
EGA - Empresa Gráfica Açoreana, Lda

Julho de 2013

TIRAGEM
750 exemplares

DEPÓSITO LEGAL
113 234 / 98

ISSN
0874 - 0380

Capa
DDDD, Lda

Esta edição é totalmente impressa (à excepção da capa) em papel ecológico, sem cloro, ácidos ou branqueamentos ópticos


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AÇOREANA

Revista de Estudos Açoreanos

SUPLEMENTO 8 **JULHO DE 2013**

WORLD CONFRESS OF MALACOLOGY 2013

Book of Abstracts

Ponta Delgada, São Miguel, Açores
July 22-28, 2013

Organized by

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Edited by
António M. de Frias Martins
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Ponta Delgada

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Doutor António M. Gomes de Menezes
Fundação para a Ciência e a Tecnologia, Lisboa

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Oxford University Press
The Malacological Society of London
American Malacological Society
Instituto Português de Malacologia
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and the media of São Miguel, who kindly conveyed to the population the scope of this meeting and the enthusiasm of its organizers

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… and many, who helped in various ways in the preparation and during the event to assure that the congress would run smoothly

WELCOME

From the middle of nowhere, at the ultra-periphery of Europe, we greet you. We are small and few and wanting experience, but we overflow with enthusiasm and eagerness to make it right. It was a heroic act (a foolish act, some would say) when we accepted the mandate of Unitas Malacologica to host its 18th Congress in this faraway land. All this is utterly irrelevant, for it is you, over four hundred participants from 50 countries, and the over one thousand authors who signed the works, that really make the congress. Your presence puts the Archipelago at the centre of Malacology; your interest brings to these islands, to this town, to our university the attention of the scientific community.

The physical and political ultra-peripheral location of the Azores betrays its geographic centrality. In fact, the archipelago is at the hinge of the Eurasian, African and American tectonic plates, at the crossroads of winds and sea-currents, at the interface of the temperate and subtropical realms. The tectonic conjunction is responsible for our volcanic activity and has stirred peoples' imagination with rumours of Atlantis; the meteorological framing spreads the misconception that the Azores should have as bad a reputation as its anticyclone; the biogeography provides you with a mixed biota characteristic of a mild environment where, sometimes unfortunately, any newcomer thrives well and successfully.

We welcome you to this land of many contrasts and yet calm in its living and smooth in its feeling. Our fearsome volcanism bathes us warmly, feeds us exotically and provides renewable energy; we hope you will have a chance to dive in it and to taste it, in spite of how outrageous our wish may seem. Our infamous anticyclone, in spite of onsets of moody weather, gives us mild temperatures responsible for our evergreen, restful landscapes; we hope you will experience the soothing, cool touch of its breeze. Our biogeographical location has not only recorded the comings and goings of species, associated with the seesaw of the glaciations, but has preserved alive remnants of what has vanished elsewhere in Europe; they are here for you to study and, were you to stumble over one of these many novelties, please be sure to share your findings with us, for we live here and may be our endemic knowledge can be of use to you. For volcanoes and land, ocean and isolation have turned the Azores into a living natural laboratory, and this is our best invitation to scientists like yourselves.

You are warmly welcomed.

António M. de Frias Martins
President, Unitas Malacologica

Sunday 21				
16:00-17:30	Registration (Amphitheater complex, University Campus)			
18:00	Ice-Breaker (Centro Cultural de Ponta Delgada)			
Monday 22				
08:00-09:00	Registration (Amphitheater complex, University Campus)			
09:00-10:20	Opening Session: Welcome – Keynote Lecture (V. Tunnicliffe) (K1)			
	Aula Magna	**Amphitheatre North**	**Amphitheatre South**	**Amphitheatre IV**
10:50-12:30	Tempo and Mode (T2.O1-O5)	Mudflat Molluscs (T9.O1-O5)	Freshwater Bivalves (T8.O1-O5)	Reproduction (T15.O1-O5)
14:00-15:40	Tempo and Mode (T2.O6-O10)	Mudflat/Invasive (T9.O6-O7)/(T11.O1-O3)	Freshwater Bivalves (T8.O6-O.10)	Living in the Extreme (T1.O1-O4)
16:10-17:50	Tempo and Mode (T2.O11-O16)	Invasive Molluscs (T11.O4-O11	Freshwater Bivalves (T8.O11-O16)	Living in the Extreme (T1.O5-O8)
17:50-18:30	Meeting Bivalvia Treatise working group			
Tuesday 23				
08:40-10:20	Tempo and Mode (T2.O17-O21)	Climate Change (T10.O1-O4)	Aculifera (T5.O1-O5)	(Palaeo)biogeography (T6.O1-O4)
10:50-12:30	Tempo and Mode (T2.O22-O26)	Climate Change (T10.O5-O9	Aculifera (T5.O6-O10)	(Palaeo)biogeography (T6.O5-O7)
14:00-15:40	Biodiversity Pulmonata (T4.O1-O5)	Climate Change (T10.O10-O14)	Aculifera (T5.O11-O16)	Bivalves (T16.O1-O5)
16:00-18:30	Poster Session			

	Aula Magna	Amphitheatre North	Amphitheatre South	Amphitheatre IV	Amphitheatre III
Thursday 25					
08:40-10:20	Biodiversity Pulmonata (T4.O6-O10)	Cephalopods (T13.O1-O5)	Freshwater Molluscs (T14.O1-O5)	Structure (T17.O1-O5)	
10:50-12:30	Biodiversity Pulmonata (T4.O11-O16)	Cephalopods (T13.O6-O10)	Freshwater Molluscs (T14.O6-O10)	Structure (T17.O6-O10)	
14:00-15:40	Biodiversity Pulmonata (T4.O17-O21)	Cephalopods (T13.O11-O15)	Freshwater Molluscs (T14.O11-O15)	Biodiversity (T18.O1-O5)	Environmental effects (T19.O1-O5)
16:10-18:10	Opisthobranchs (T7.O1-O6)	Cephalopods (T13. panel)	Molecular Phylogenetics (T3.O1-O4)	Biodiversity (T18.O6-O10)	Ecology issues (T20.O1-O6)
18:10-xxyy	AMS auction				
Friday 26					
08:40-10:20	Opisthobranchs (T7.O7-O11)	Cephalopods (T13.O16-O20)	Molecular Phylogenetics (T3.O5-O9)	Metabolism (T21.O1-O4)	
10:50-12:30	Opisthobranchs (T7.O12-O17)	Cephalopods (T13.O21-O25)	Molecular Phylogenetics (T3.O10-O14)	Colour in Molluscs (T12.O1-O5)	
13:15-13:55	AMS Business Meeting				
14:00-15:40	Opisthobranchs (T7.O18-O22)	Cephalopods (T13. panel)	Molecular Phylogenetics (T3.O15-O18)	Population issues (T22.O1-O5)	
16:00-17:00	Closing Session – Keynote Lecture (R. Cameron) (K2)				
17:00-18:30	UM General Assembly				
20:00-23:30	Congress Dinner (Coliseu Micaelense)				
Saturday 27	Sectorial Activities				

WCM2013

Symposia

- T1 | Living in the extreme: molluscan communities of chemosynthetic habitats
- T2 | Tempo and mode in land snail evolution: the origins and limits of diversity
- T3 | Molecular phylogenetics and paleontology
- T4 | Biodiversity and evolution of pulmonate taxa
- T5 | Who are the ‘Aculifera’?
- T6 | How did they get here?: (Palaeo)Biogeography of Terrestrial and marine molluscs
- T7 | There’s something about Opisthobranchia
- T8 | Gains and Losses of Freshwater Bivalves and their consequences for ecosystems
- T9 | Mudflat molluscs
- T10 | Climate Change and Molluscan Ecophysiology
- T11 | Invasive molluscs
- T12 | Colour in Molluscs
- T13 | The role of cephalopods in marine ecosystems
- T14 | Taxonomy and ecology of freshwater molluscs in the molecular age

General themes

- T15 | reproduction
- T16 | Bivalves
- T17 | Structure
- T18 | Biodiversity
- T19 | Environmental effects
- T20 | Ecology issues
- T21 | Metabolism
- T22 | Population Issues

PROGRAMME

SUNDAY, 21

16:00-17:30	REGISTRATION (AMPHITHEATER COMPLEX, UNIVERSITY CAMPUS)
18:00-19:30	ICE-BREAKER (CENTRO CULTURAL DE PONTA DELGADA)

MONDAY, 22

AULA MAGNA

08:00-09:00	REGISTRATION (AMPHITHEATER COMPLEX, UNIVERSITY CAMPUS)
09:00-10:20	OPENING SESSION: WELCOME – KEYNOTE LECTURE (V. TUNNICLIFFE)
10:20-10:50	**COFFEE BREAK**
	CHAIR: Beata Pokryszko
10:50-11:10	**T2.O1** – DIVERGENT MITOCHONDRIAL CLADES OF SNAILS WITH A *TROCHULUS HISPIDUS* PHENOTYPE. HOW TO CONFINE A SNAIL SPECIES? **Luise Kruckenhauser**, Michael Duda, Daniela Bartel, Josef Harl, Helmut Sattmann, Elisabeth Haring
11:10-11:30	**T2.O2** – ENVIRONMENTAL CHANGES IN THE COURSE OF TIME: CONSTRAINTS ON ECOLOGICAL SPECIATION IN *MURELLA MURALIS* **V. Fiorentino,** G. Manganelli, F. Giusti, V. Ketmaier
11:30-11:50	**T2.O3** – PHYLOGEOGRAPHY OF *CIRCASSINA FRUTIS* (GASTROPODA: HELICOIDEA: HYGROMIIDAE) IN THE CAUCASUS REGION **Marco T. Neiber,** Bernhard Hausdorf
11:50-12:10	**T2.O4** – SPECIES DIVERSIFICATION IN THE SOUTH ASIAN LAND-SNAIL GENUS *CORILLA* (PLECTOPYLOIDEA: CORILLIDAE) **Dinarzarde C. Raheem**, Fred Naggs, Chris Wade, Thierry Backeljau
12:10-12:30	**T2.O5** – GETTING THE PHYLOGENY OF *THEBA* STRAIGHT AND CAN FOSSILS MEANINGFULLY BE INTEGRATED IN ORDER TO DATE INTERNAL NODES? **Martin Haase**, Carola Greve, Rainer Hutterer, Bernhard Misof
12:30-14:00	**LUNCH**

Chair: Martin Haase

14:00-14:20 **T2.O6** – A SHORT HISTORY OF THE GENUS *LEIOSTYLA*

Beata M. Pokryszko, Andrzej Falniowski, Robert A. D. Cameron

14:20-14:40 **T2.O7** – EVOLUTIONARY HISTORY OF A VANISHING RADIATION: THE PACIFIC ISLAND TREE SNAIL FAMILY PARTULIDAE

Diarmaid Ó Foighil, Taehwan Lee, Jingchun Li, Celia Churchill

14:40-15:00 **T2.O8** – TRUNCATELLOIDEAN GASTROPODS INFORMING GEOLOGY: CONTINUOUS EMERGENCE OF ISLANDS OF VANUATU ALREADY SINCE THE MID PLIOCENE

Susan Zielske, Martin Haase

15:00-15:20 **T2.O9** – AN OUTSTANDING RADIATION OF HELICINIDS ON THE GAMBIER ISLANDS, FRENCH POLYNESIA: EXTINCT BEFORE ITS DISCOVERY

Ira Richling, Philippe Bouchet

15:20-15:40 **T2.O10** – PATTERNS OF GENETIC RELATEDNESS AMONG POPULATIONS OF THE GENUS *CERION* (CERIONIDAE: GASTROPODA: MOLLUSCA) IN THE FLORIDA KEYS

M. G. Harasewych, Yesha Shrestha

15:40-16:10 **COFFEE BREAK**

Chair: Robert Cowie

16:10-16:30 **T2.O11** – ADAPTATION IN LAND SNAIL SHELL SHAPE—30 YEARS SINCE GOODFRIEND

Menno Schilthuizen, Satoshi Chiba

16:30-16:50 **T2.O12** – LAND SNAIL RICHNESS AND ABUNDANCE ALONG A SHARP ECOLOGICAL GRADIENT AT TWO SAMPLING SCALES: DISENTANGLING RELATIONSHIPS

Michal Horsák

16:50-17:10 **T2.O13** – DISCOVERING FACTORS RESPONSIBLE FOR THE EXISTENCE OF TERRESTRIAL MOLLUSCAN ASSOCIATIONS AND ROLE OF SOME OF THOSE FACTORS IN SPECIATION

Igor V. Muratov

17:10-17:30 **T2.O14** – SYMPATRY WITHOUT CO-OCCURRENCE: EXPLORING THE PATTERN OF THE DISTRIBUTION OF TWO *HELIX* SPECIES IN GEORGIA USING ECOLOGICAL NICHE MODELING APPROACH

Levan Mumladze

17:30-17:50 **T2.O15** – PREDATION ON GREEK *ALBINARIA* (PULMONATA: CLAUSILIIDAE) AS A POSSIBLE DRIVER OF SPECIATION

Renate A. Helwerda, Els Baalbergen, Rense Schelfhorst, Sinos Giokas, Menno Schilthuizen

17:50- 18:10	**T2.O16** – REFUGIAL POPULATIONS OF GLACIAL RELICT *VERTIGO* SPECIES IN CENTRAL EUROPE **Veronika Schenková,**-Michal Horsák
	AMPHITHEATRE NORTH
	Chair: Peter G. Beninger
10:50- 11:10	**T9.O1** – IMPACT OF REPEATING MASSIVE EARTHQUAKES ON INTERTIDAL MOLLUSCAN COMMUNITY IN JAPAN **Kenji Okoshi**
11:10- 11:30	**T9.O2** – ALLOMETRIC MODELLING IN THE MUDFLAT SPECIES *TAPES PHILIPPINARUM* AND *CERASTODERMA EDULE* USING THE COPULA APPROACH **Inna Boldina**, Peter Beninger
11:30- 11:50	**T9.O3** – POPULATION DYNAMICS AND LIFE-TABLES CONSTRUCTION OF THE SOFTSHELL CLAMS *MYA ARENARIA* L. ON AN INTERTIDAL SILTY-SAND FLAT IN THE WHITE SEA **Alexandra V. Gerasimova**-, Nikolay V. Maximovich
11:50- 12:10	**T9.O4** – THE EFFECT OF MACROFAUNA ON THE SUCCESS OF COCKLE (*CERASTODERMA EDULE*) POST-LARVAL COLONISATION **Timothy Whitton**, Chris Richardson, Jan Hiddink, Stuart Jenkins, Bryan Jones
12:10- 12:30	**T9.O5** – DESCRIBING MORPHOLOGICAL FEATURES OF OOCYTES: AN ATTEMPT TO UNRAVEL REPRODUCTIVE ASPECTS OF TELLINIDAE AND PSAMMOBIIDAE SPECIES (BIVALVIA: TELLINOIDEA) **Gisele Orlandi Introíni**, Lenita de Freitas Tallarico, Ariane Campos, Fabrízio Marcondes Machado, Marilda da Cruz Fernandes, Teresinha Stein, Flávio Dias Passos, Shirlei Maria Recco-Pimentel
12:30- 14:00	**LUNCH**
	Chair: Peter G. Beninger
14:00- 14:20	**T9.O6** – ULTRA-STRUCTURAL SPERM FEATURES AND MOLECULAR DATA OF *CARYOCORBULA CARIBAEA* (D'ORBIGNY, 1853), A SPECIES WITH EXTRAORDINARY CONCHOLOGICAL PLASTICITY **Lenita de Freitas Tallarico**, Gisele Orlandi Introíni, Amanda Bonini, Flávio Dias Passos, Fabrizio Marcondes Machado, Eliane Pintor de Arruda, Shirlei Maria Recco-Pimentel
14:20- 14:40	**T9.O7** – *CREPIDULA*'S ARROWS: STRUCTURE AND UNUSUAL TRANSMISSION MODE OF SLIPPER SHELL SPERMATOZOA **Peter G. Beninger**, Alexandra Valdizan

14:40-15:00 **T11.O1** – THE SLUGS OF BRITAIN AND IRELAND: UNDETECTED AND CRYPTIC SPECIES INCREASE A WELL-STUDIED, ECONOMICALLY IMPORTANT FAUNA BY UP TO 29%

Ben Rowson, Roy Anderson, James A. Turner, William O. C. Symondson

15:00-15:20 **T11.O2** – THE *ARION* SLUG INVASION

Miriam Zemanova, Eva Knop, Gerald Heckel

15:20-15:40 **T11.O3** – INTERACTION BETWEEN AN INVASIVE SLUG *ARION LUSITANICUS* AND AN AGGRESIVE WEED *TARAXACUM OFFICINALE*

Alois Honek, Zdenka Martinkova

15:40-16:10 **COFFEE BREAK**

Chair: Peter G. Beninger

16:10-16:30 **T11.O4** – INDIGENOUS AND INTRODUCED GASTROPODS, AND THEIR TREMATODES: IMPLICATIONS FOR BIODIVERSITY

Frida Ben-Ami

16:30-16:50 **T11.O5** – HABITAT QUALITY INFLUENCES THE TOLERANCE OF THE ASIAN GREEN MUSSEL *PERNA VIRIDIS* TOWARDS HYPOXIA

Mareike Huhn, Mark Lenz, Karen von Juerzenka, Martin Wahl

16:50-17:10 **T11.O6** – THE INVASIVE *CORBICULA FLUMINEA* POPULATIONS IN PORTUGAL

Cidália Gomes, Ronaldo Sousa, Pedro Vilares, Vitor Vasconcelos, Lúcia Guilhermino, Agostinho Antunes

17:10-17:30 **T11.O7** – THE MOST AGGRESSIVE FRESHWATER INVADERS: PARALLELS, CONTRASTS, SPREAD AND ECOSYSTEM IMPACTOR OF ZEBRA AND QUAGGA MUSSELS

Alexander Y. Karatayev, Lyubov E. Burlakova, Dianna K. Padilla

AMPHITHEATRE SOUTH

Chair: Jürgen Geist

10:50-11:10 **T8.O1** – CONSERVATION STATUS OF FRESHWATER MUSSELS IN EUROPE: STATE OF THE ART, PERSPECTIVES AND FUTURE CHALLENGES

Manuel Lopes-Lima, David C. Aldridge, Rafael Araujo, Jakob Bergengren, Yulia Bespalaja, Erika Bódis, Lyubov Burlakova, Karel Douda, Juergen Geist, Albertas Gurskas, Ian Killeen, Jasna Lajtner, Rosaria Lauceri, Bjørn Larsen, Sabela Lois, Stefan Lundberg, Evelyn Moorkens, Gregory Motte, Karl-Otto Nagel, Momir Paunovic, Ondina Paz, Vincent Prié, Ted von Proschwitz, Nicoletta Riccardi, Maris Rudzitis, Mudite Rudzite, Mary Seddon, Svetlana Sokolova, Ronaldo Sousa, Katharina Stoeckl, Tõnu Talvi, Frankie Thielen, Dirk Van Damme, Simone Varandas, Heinrich Vicentini, Katarzyna Zajac, Tadeusz Zajac

11:10-11:30	**T8.O2** – CONSERVATION OF THE ENDANGERED FRESHWATER HABITATS UNDER HIGH ANTHROPOGENIC PRESSURE AROUND SAINT-PETERSBURG **Igor Popov**
11:30-11:50	**T8.O3** – ECOLOGY AND CURRENT STATUS OF THE FRESHWATER PEARL MUSSELS *MARGARITIFERA DAHURICA* (MIDDENDORFF, 1850) AND *MARGARITIFERA LAEVIS* (HAAS, 1910) (BIVALVIA: UNIONOIDEA) IN THE FAR EAST OF RUSSIA **Julia Bespalaya**, Ivan Bolotov, Ilja Vikhrev, Aleksander Kondakov, Mikhail Gofarov, Irina Voroshilova, Inga Paltser, Artem Frolov
11:50-12:10	**T8.O4** – UNIONID ASSEMBLAGE RESPONSE TO A TAR SANDS OIL SPILL IN THE KALAMAZOO RIVER, MICHIGAN USA **Daelyn A. Woolnough**, Samantha S. Parker
12:10-12:30	**T8.O5** – SUITABILITY OF DIFFERENT MARGARITIFERA STOCKS FOR BIOINDICATION STUDIES **M. Denic**, J. Geist
12:30-14:00	**LUNCH**
	Chair: Rafael Araujo
14:00-14:20	**T8.O6** – *DREISSENA* IMPACTS ON UNIONIDAE: A SYNTHESIS OF TRENDS IN NORTH AMERICA AND EUROPE AND RECENT FINDINGS FROM THE LOWER GREAT LAKES **Lyubov E. Burlakova**, Alexander Y. Karatayev, Brianne L. Tulumello, David T. Zanatta, Frances E. Lucy, Sergey E. Mastitsky
14:20-14:40	**T8.O7** – IMPACTS OF *DREISSENA* FOULING ON THE PHYSIOLOGICAL CONDITION OF NATIVE AND NON-NATIVE BIVALVES: INTERSPECIFIC AND TEMPORAL VARIATIONS **E. Bódis**, B. Tóth, R. Sousa
14:40-15:00	**T8.O8** – *CORBICULA FLUMINEA* IMPACT IN LAKE MAGGIORE (ITALY): FEEDING PLASTICITY AND DIETARY OVERLAP WITH NATIVE MUSSELS Irene Guarneri, Alice Cardeccia, Rosaria Lauceri, Lyudmila Kamburska, Anna Visconti, Marina Manca, **Nicoletta Riccardi**
15:00-15:20	**T8.O9** – INFLUENCE OF WATER TEMPERATURE AND TURBIDITY ON SPAWNING OF THE THREATENED FRESHWATER PEARL MUSSEL *MARGARITIFERA MARGARITIFERA* **Martin E. Österling**
15:20-15:40	**T8.O10** – INTERACTIONS BETWEEN FRESHWATER MUSSELS AND THEIR HOST FISHES: IMPLICATIONS FOR CONSERVATION **Juergen Geist**, Jens-Eike Taeubert
15:40-16:10	**COFFEE BREAK**

Chair: Arthur Bogan

16:10-16:30 **T8.O11** – THE EFFECTS OF FRESHWATER MUSSEL GLOCHIDIA ON FISH HOST BEHAVIOUR: CONSEQUENCES FOR UPSTREAM PHORESIS

Pavel Horký, **Karel Douda**, Matúš Maciak, Libor Závorka, Ondřej Slavík

16:30-16:50 **T8.O12** – RESCUING FRESHWATER PEARL MUSSELS (*MARGARITIFERA MARGARITIFERA*) FROM EXTINCTION - A RACE AGAINST TIME: A CASE STUDY FROM NORTHERN IRELAND

Mark Horton, Alan Keys, Francis Denis Mitchell, Rebecca Kyle, **Dai Roberts**

16:50-17:10 **T8.O13** – SUCCESSFUL CAPTIVE REARING OF *MARGARITIFERA MARGARITIFERA*: DO WE KNOW ENOUGH?

Joaquim Reis, Sandra Vieira, Alexandrina Pipa

17:10-17:30 **T8.O14** – SALMONID FISH HATCHERIES OF THE WHITE SEA AS FRESHWATER PEARL MUSSEL (*MARGARITIFERA MARGARITIFERA*(L., 1758)) BREEDING STATIONS

Ilya Vikhrev, Ivan Bolotov, Yulia Bespalaya, Aleksandr Kondakov, Artyom Frolov, Inga Paltser

17:30-17:50 **T8.O15** – CONSERVATION OF TWO EUROPEAN ENDANGERED FRESHWATER MUSSELS. A THREE YEARS BREEDING EXPERIMENT

R. Araujo, M. Campos, C. Feo, Q. Pou

17:50-18:10 **T8.O16** – HOW TO ESTABLISH A NEW POPULATION OF *UNIO CRASSUS*? A CASE STUDY IN THE BIAŁA RIVER

Katarzyna Zając, **Tadeusz Zając**, Paweł Adamski, Wojciech Bielański, Adam Ćmiel, Anna Lipińska

AMPHITHEATRE IV

Chair: Heather Ylitalo

10:50-11:10 **T15.O1** – MATING BEHAVIOR IN *OCTOPUS OLIVERI*, A HAWAIIAN INTERTIDAL OCTOPUS

Heather Ylitalo

11:10-11:30 **T15.O2** – REPRODUCTIVE CYCLE AND FEMALE GONAD STRUCTURE OF THE SOUTHERN CARIBBEAN ENDEMIC GASTROPOD *VOLUTA MUSICA* (CAENOGASTROPODA: VOLUTIDAE)

A. C. Peralta, P. Miloslavich, G. Bigatti, C. Ituarte

11:30-11:50 **T15.O3** – SPERM PRECEDENCE IN THE HERMAPHRODITIC FRESHWATER SNAIL, *HELISOMA TRIVOLVIS*

Cynthia G. Norton, Morgan K. Wright

11:50-12:10 **T15.O4** – IMPACT OF GLOBAL WARMING ON THE SPAWNING SUCCESS AND EMBRYOGENESIS OF A SPECIALIZED SOFT CORAL-FEEDING NUDIBRANCH, *ARMINA MACULATA*

Vanessa L. Pires, Marta S. Pimentel, Miguel Baptista, Filipa Faleiro, Vanessa M. Lopes, Ana Rita Lopes, Luís Narciso, Rui Rosa

12:30-14:00	**LUNCH**
	Chair: Anders Warèn
14:00-14:20	**T1.O1** – A CONCEPTUAL MODEL OF CHEMOSYMBIOSIS EVOLUTION IN THE THYASIRIDAE **Suzanne C. Dufour**, Rebecca T. Batstone, Heather Zanzerl
14:20-14:40	**T1.O2** – POPULATION STRUCTURE IN THREE POPULATIONS OF THE 'SCALY-FOOT GASTROPOD' INDICATE LACK OF CONNECTIVITY BETWEEN HYDROTHERMAL VENTS OF CENTRAL INDIAN RIDGE AND SOUTH WEST INDIAN RIDGE **Chong Chen**, Jonathan T. Copley, Alex D. Rogers
14:40-15:00	**T1.O3** – A MORPHOLOGICAL APPROACH TO THE EVOLUTIONARY HISTORY OF BASAL HETEROBRANCH FAMILIES (GASTROPODA: ECTOBRANCHIA) **Andreas Hawe,** Gerhard Haszprunar
15:00-15:20	**T1.O4** – SEASONAL VARIABILITY IN A DYNAMIC SYMBIOTIC RELATIONSHIP: *THYASIRA AFF. GOULDI* AND ITS CHEMOSYNTHETIC BACTERIAL SYMBIONTS. **Jason Robert Laurich**, Suzanne C. Dufour
15:40-16:10	**COFFEE BREAK**
	Chair: Verena Tunnicliffe
16:10-16:30	**T1.O5** – TAXONOMIC REVIEW OF *TURBONILLA* (GASTROPODA: PYRAMIDELLIDAE) COLLECTED THROUGH THE MD55 EXPEDITION, OFF SE COAST OF BRAZIL. **Rachel Turba de Paula,** Alexandre Dias Pimenta
16:30-16:50	**T1.O6** – ENVIRONMENTAL IMPACTS ON THE EVOLUTION OF METHANE SEEP MOLLUSKS **Steffen Kiel**
16:50-17:10	**T1.O7** – ARE EVOLUTIONARY STRATEGIES FOR A LIFE ON SUNKEN WOOD COMMON OR DISTINCT IN DEEP-SEA LIMPETS? **Jenna Judge**
17:10-17:30	**T1.O8** – EVOLUTION AND RADIATION OF NEOMPHALINE GASTROPODS: TRUE ANTIQUITY AT HYDROTHERMAL VENTS? **Yasunori Kano**, Anders Warén
17:50-18:30	**MEETING BIVALVIA: TREATISE WORKING GROUP** **Chair: Joseph Carter**

TUESDAY, 23

AULA MAGNA

CHAIR: Menno Schilthuizen

08:40-09:00 **T2.O17** –*CEPAEA* – CHANGES IN SPECIES DISTRIBUTIONS AND MORPH FREQUENCIES ON THE MARLBOROUGH DOWNS

Robert H. Cowie, J. S. Jones, A. Mark Beaumont

09:00-09:20 **T2.O18** – RAPID EVOLUTION IN LAND SNAILS

Malgorzata Ozgo

09:20-09:40 **T2.O19** – UPSTREAM OR DOWNSTREAM? LAND SNAIL, *VENTRIDENS LIGERA* (SAY, 1821) POPULATION STRUCTURE IN THE POTOMAC RIVER WATERSHED

Colleen M. Winters

09:40-10:00 **T2.O20** – INVENTORYING THE LAND MOLLUSCAN FAUNA OF NIGERIA RAINFOREST: THE STORY SO FAR

Chris Oke, Rosemary Egonmwan

10:00-10:20 **T2.O21** – USING PREDICTIVE MODELS OF SPECIES DISTRIBUTION AS A TOOL FOR ECOLOGY AND CONSERVATION OF MADEIRAN LAND SNAILS

Dinarte Teixeira, Pedro Cardoso, Cátia Gouveia

10:20-10:50 **COFFEE BREAK**

CHAIR: Robert Cameron

10:50-11:10 **T2.O22** – BIOGEOGRAPHICAL PATTERNS IN THE LAND SNAIL FAUNA OF THE CAUCASUS REGION

Frank Walther, Marco T. Neiber, Bernhard Hausdorf

11:10-11:30 **T2.O23** – PALAEOBIODIVERSITY AND PALAEOBIOGEOGRAPHY OF EUROPEAN SNAILS: A PLEISTOCENE PERSPECTIVE

Nicole Limondin-Louzouet

11:30-11:50 **T2.O24** – DEVELOPMENT AND LOSS OF LAND SNAIL DIVERSITY DURING THE LATEGLACIAL AND HOLOCENE: A PERSPECTIVE ON THE MODERN FAUNA OF NW EUROPE

Richard Preece

11:50-12:10 **T2.O25** – PUNCTUATED EQUILIBRIUM ALIVE OR PLAIN ISLAND SPECIATION?

António M. de Frias Martins, Ana F. Ferreira, David James Harris, Armindo Rodrigues, Regina Cunha, Robert A. D. Cameron, Thierry Backeljau

12:10-12:30 **T2.O26** – THE PUNCTUATED EQUILIBRIUM THEORY: EVIDENCE FROM GASTROPODS REVIEWED

Michael W. Rasser, Christian Albrecht, Mathias Harzhauser, Rainer Schoch, Bert Van Bocxlaer

12:30-14:00 **LUNCH**

Chair: Benoît Dayrat

14:00-14:20 **T4.O1** – USING ‘NEXT GENERATION’ SEQUENCING TO RESOLVE DEEP PHYLOGENETIC RELATIONSHIPS IN THE LAND MOLLUSCS (EUPULMONATA)

Luisa-Teasdale, Andrew Hugall, Tim O’Hara, Frank Kohler, Adnan Moussalli

14:20-14:40 **T4.O2** – SYSTEMATICS AND BIOGEOGRAPHY OF SOUTHERN AFRICA’S DWARF CANNIBAL SNAILS (PULMONATA: RHYTIDIDAE)

D.G. Herbert, A. Moussalli

14:40-15:00 **T4.O3** – A BIODIVERSITY HOTSPOT HOT FOR LAND SNAILS TOO: THE CASE OF MAPUTALAND-PONDOLAND-ALBANY

Sandun J. Perera, David G. Herbert, Şerban Procheş

15:00-15:20 **T4.O4** – TOWARDS A REVISION OF A TAXONOMICALLY DIFFICULT SNAIL FAMILY: PROBLEMS WITH DEFINING NEW SPECIES OF GLESSULIDAE IN NEPAL (GASTROPODA: PULMONATA: STYLOMMATOPHORA)

Prem B. Budha, Fred Naggs, Thierry Backeljau

15:20-15:40 **T4.O5** – DIFFERENTIAL SURVIVAL AMONG TAHITIAN TREE SNAILS DURING A MASS EXTINCTION EVENT: PERSISTENCE OF THE RARE AND FECUND

Cindy S. Bick, Diarmaid Ó Foighil, Trevor Coote

Amphitheatre North

Chair: Peter Marko

08:40-09:20 **T10.O1** – WARMING FORE-REEF SLOPES AND ITS EFFECT ON THE BIOLOGY AND DISTRIBUTION OF *NAUTILUS:* REPLAY OF ANCIENT GREENHOUSE MASS EXTINCTION HISTORY?

Peter Ward

09:20-09:40 **T10.O2** – VERTICAL MIGRATION ACROSS ENVIRONMENTAL GRADIENTS OF TEMPERATURE, OXYGEN AND CARBON DIOXIDE IN THE JUMBO SQUID, *DOSIDICUS GIGAS*, IMPLICATIONS FOR CHANGING CLIMATE

Brad A. Seibel

09:40-10:00 **T10.O3** – LOWER HYPOXIA THRESHOLDS OF MOLLUSK EARLY LIFE STAGES LIVING IN A WARM ACIDIFIED OCEAN

Rui Rosa, Katja Trübenbach, Tiago Repolho, Marta Pimentel, Filipa Faleiro, Joana Boavida-Portugal, Miguel Baptista, Gisela Dionísio, Miguel Costa Leal, Ricardo Calado, Hans O. Pörtner

10:00-10:20	**T10.O4** – CAN COASTAL CALCIFIERS ADAPT TO A FUTURE, MORE ACIDIC OCEAN? **Frank Melzner**, Meike Stumpp, Jörn Thomsen, Isabel Casties, Marian Y. Hu, Magdalena A. Gutowska
10:20-10:50	**COFFEE BREAK**
	Chair: Brad A. Seibel
10:50-11:10	**T10.O5** – MOVING BEYOND MORTALITY: A METABOLIC FRAMEWORK FOR EXPLORING EFFECTS OF CLIMATE CHANGE ON INTERTIDAL MUSSEL BED ZONATION Allison Matzelle, Mackenzie Zippay, Gianluca Sará, , Valeria Montalto[3], Francis Choi, Shadow Gulledge, Nicole Kish, **Brian Helmuth**
11:10-11:30	**T10.O6** – INTERTIDAL OYSTER AND MUSSEL BEDS IN A GLOBAL WARMING PERSPECTIVE. TRADE-OFFS AND MICROCLIMATIC DOWNSCALING **Folco Giomi**, Concetta Mandaglio, Monthon Ganmanee, Valeria Montalto, Alessandro Rinaldi, Gray A. Williams, Gianluca Sarà
11:30-11:50	**T10.O7** – THERMOTOLERANCE OF ADULT GREEN-LIPPED MUSSELS (*PERNA CANALICULUS*): PATTERNS OF MORTALITY AND METABOLOMIC IDENTIFICATION OF KEY BIOMARKERS **Brendon J. Dunphy**, Ellie Watts, Norman L.C. Ragg
11:50-12:10	**T10.O8** – THE INTERACTIVE EFFECTS OF OCEAN WARMING AND ACIDIFICATION ON PACIFIC OYSTER LARVAE **Frauke Bagusche**, Pierrick Le Souchu, Stephane Pouvreau, Clive Trueman, Sarah Long, Chris Hauton
12:10-12:30	**T10.O9** – PHYSIOLOGY AND BIOGEOGRAPHY: THE RESPONSE OF EUROPEAN MUSSELS (*MYTILUS* SPP.) TO CLIMATE CHANGE Elizabeth K. Fly, Rhiannon L. Rognstad, David S. Wethey, **Thomas J. Hilbish**
12:30-14:00	**LUNCH**
	Chair: Peter Marko
14:00-14:20	**T10.O10** – OPEN AIR DINING: CIRCATIDAL FORAGING PATTERNS OF THE INTERTIDAL WHELK *NUCELLA OSTRINA* IN A COMPLEX THERMAL LANDSCAPE **Emily Carrington**, Hilary Hayford, Sarah Gilman, Kristina Kull
14:20-14:40	**T10.O11** – ADAPTATION TO HEAT IN THE MEDITERRANEAN SNAIL SPECIES *XEROPICTA DERBENTINA*: STRATEGIES TO SURVIVE ELEVATED TEMPERATURES **Sandra Troschinski**, Maddalena A. Di Lellis, Heinz-R. Köhler, Rita Triebskorn

14:40-15:00 **T10.O12** – OCEAN ACIDIFICATION AND WARMING ALTER ALLOMETRY OF METABOLISM IN CHITONS: ENVIRONMENTALLY-DRIVEN CHANGES TO METABOLIC SCALING INDICATE RESPONSES TO MULTIPLE STRESSORS ARE MEDIATED BY BODY SIZE

Nicholas Carey, Julia D. Sigwart

15:00-15:20 **T10.O13** – INFERRING IMPACTS OF CLIMATE CHANGE ON MARINE POPULATIONS FROM MACARONESIA USING LIMPETS, A KEYSTONE INTERTIDAL ORGANISM, AS MODEL SPECIES

Govindraj Chavan, Fernando P. Lima, Ricardo S. Santos, Pedro A. Ribeiro

15:20-15:40 **T10.O14** – ADAPTATION OF LAND SNAILS TO STRESSFUL CONDITIONS: FROM WHOLE ANIMAL TO CELLULAR MECHANISMS

Zeev Arad

AMPHITHEATRE SOUTH

CHAIR: Julia Sigwart

08:40-09:00 **T5.O1** – SPECIES DIVERSITY OF APLACOPHORAN MOLLUSCS (SOLENOGASTRES, CAUDOFOVEATA) IN THE NORTHERN EUROPEAN ATLANTIC

Christiane Todt, Elena Gerasimova

09:00-09:20 **T5.O2** – NEW METHODS PROVIDE ANSWERS TO OLD QUESTIONS - PHYLOGENETICS AND SYSTEMATICS OF THE CAUDOFOVEATA (=CHAETODERMOMORPHA)

Nina T. Mikkelsen, Kevin M. Kocot, Kenneth M. Halanych, Endre Willassen, Christiane Todt

09:20-09:40 **T5.O3** – THE BRAZILIAN CAUDOFOVEATA: A GREAT APLACOPHORAN BIODIVERSITY BEGINNING TO BE DISCOVERED

Flávio Dias Passos, Paulo Vinicius Ferraz Corrêa, Paola Visnardi Fassina, Christiane Todt

09:40-10:00 **T5.O4** – THE FAUNA OF CAUDOFOVEATA: STATE OF THE ART

Dmitry L. Ivanov

10:00-10:20 **T5.O5** – UNIQUE EVENTS IN CHITONID REPRODUCTION

John Buckland-Nicks

10:20-10:50 **COFFEE BREAK**

CHAIR: Kevin Kocot

10:50-11:10 **T5.O6** – SEEING THE WORLD THROUGH NEW EYES: A NOVEL SENSORY ORGAN IN BASAL CHITONS (LEPIDOPLEURIDA)

L. H. Sumner-Rooney, J. D. Sigwart, E. Schwabe, M. Hess, G.P. Brennan, M. Schrödl

11:10-11:30 **T5.O7** – FUNCTIONAL MORPHOLOGY AND MOLECULAR EVOLUTION OF CHITON 'SHELL' EYES

Daniel I. Speiser, Sönke Johnsen, Todd H. Oakley

11:30-11:50	**T5.O8** – COMPARATIVE ASPECTS OF SOLENOGASTER MYOGENESIS AND THEIR IMPLICATIONS FOR MOLLUSCAN SYSTEMATICS **Maik Scherholz**, Emanuel Redl, Christiane Todt, Tim Wollesen, Andreas Wanninger
11:50-12:10	**T5.O9** – NEUROGENESIS IN SOLENOGASTRES (NEOMENIOMORPHA) **Emanuel Redl**, Maik Scherholz, Tim Wollesen, Christiane Todt, Andreas Wanninger
12:10-12:30	**T5.O10** – ACULIFERA AND THE EVOLUTION OF MOLLUSCA **Andreas Wanninger**
12:30-14:00	**LUNCH**
	Chair: Christiane Todt
14:00-14:20	**T5.O11** – THE TESTARIA CONCEPT (PLACOPHORA + CONCHIFERA) **Luitfried V. Salvini-Plawen,** Gerhard Stiner
14:20-14:40	**T5.O12** – TOWARDS A MOLECULAR PHYLOGENY OF CHITONS (POLYPLACOPHORA) USING COMPLETE MITOCHONDRIAL GENOMES Iker Irisarri, Douglas J. Eernisse, **Rafael Zardoya**
14:40-15:00	**T5.O13** – PRELIMINARY MOLECULAR PHYLOGENY OF APLACOPHORA **Kevin M. Kocot**, Christiane Todt, Nina Mikkelsen, Kenneth M. Halanych
15:00-15:20	**T5.O14** – USING MOLECULAR PHYLOGENETICS TO TEST AFFINITIES OF FOSSIL ACULIFERAN MOLLUSCS AND RECONSTRUCT THEIR CHARACTER EVOLUTION **Jakob Vinther**
15:20-15:40	**T5.O15** – ON THE BASAL RELATIONSHIPS OF MOLLUSCS **Gonzalo Giribet**
15:40-16:00	**T5.O16** – WHO ARE THE "ACULIFERA"? **Julia D. Sigwart**, Christiane Todt, Amélie Scheltema

AMPHITHEATRE IV

	Chair: Sérgio Ávila
08:40-09:20	**T6.O1** – PALEOECOLOGICAL AND PALEOENVIRONMENTAL STUDIES USING FOSSIL LAND SNAILS FROM OCEANIC ISLANDS **Yurena Yanes**
09:20-09:40	**T6.O2** – FAUNAL COMPOSITION AND ISOTOPIC SGNALS OF MOLLUSK SHELLS INDICATE SEAGRASS MEADOWS IN THE MIOCENE OF INDONESIA **Sonja Reich**, Frank P. Wesselingh, Viola Water, Willem Renema
09:40-10:00	**T6.O3** – A REVIEW OF THE HETEROBRANCH FOSSIL RECORD AND ITS MEANING FOR PHYLOGENY **Alexander Nützel**, Alex Cook, Jiří Frýda, Joachim Gründel, Andrzej Kaim

10:00-10:20 **T6.O4** – INTERTIDAL SLUGS ON THE MOVE: EVOLUTIONARY BIOGEOGRAPHY AND DISPERSAL IN *ONCHIDELLA*

Rebecca Cumming, Raisa Nikula, Jon Waters, Hamish Spencer

10:20-10:50 **COFFEE BREAK**

Chair: Ricardo Cordeiro

10:50-11:10 **T6.O5** – A GLOBAL BIOGEOGRAPHICAL ANALYSIS OF THE SHALLOW-WATER MARINE GASTROPOD FAUNA OF THE NORTH-ATLANTIC OCEAN AND THE MEDITERRANEAN SEA

Ricardo Cordeiro, António M. de Frias Martins, Sérgio P. Ávila

11:10-11:30 **T6.O6** – THE PALAEO AND NEOBIOGEOGRAPHY OF THE MARINE MOLLUSCS OF THE AZORES FROM THE MIOCENE TO THE PRESENT: PROCESSES AND PATTERNS

Sérgio P. Ávila

11:30-11:50 **T6.O7** – MOLLUSCAN MIGRATIONS IN THE MACARONESIA DURING INTERGLACIAL STAGES

A. Cabero, C. Zazo, J.A. González-Delgado, J.L. Goy, C.J. Dabrio, J. Lario, T. Bardají, C. Hillaire-Marcel, B. Ghaleb

12:30-14:00 **LUNCH**

Chair: Rüdiger Bieler

14:00-14:20 **T16.O1** – INVESTIGATING THE BIVALVE TREE OF LIFE - AN EXEMPLAR-BASED APPROACH COMBINING MOLECULAR AND NOVEL MORPHOLOGICAL CHARACTERS

Rüdiger Bieler, Paula M. Mikkelsen, Timothy M. Collins, Emily A. Glover, Vanessa L. González, Daniel L. Graf, Elizabeth M. Harper, John Healy, Gisele Y. Kawauchi, Prashant P. Sharma, Sid Staubach, Ellen E. Strong, John D. Taylor, Ilya Tëmkin, John D. Zardus, Stephanie Clark, Alejandra Guzmán, Erin McIntyre, Paul Sharp, Gonzalo Giribet

14:20-14:40 **T16.O2** – ADDING STRUCTURE TO THE BIVALVE TREE OF LIFE

Elizabeth M. Harper, John D. Taylor

14:40-15:00 **T16.O3** – BIVALVIAN TRIPTYCH: BIVALVE SEASHELLS OF WESTERN SOUTH AMERICA

Paul Valentich-Scott, Eugene V. Coan, Diego G. Zelaya

15:00-15:20 **T16.O4** – GLIDING CONVERGENCE FROM CONVERGENT, PARALLEL, AND DIVERGENT SHELL SHAPES: EVOLUTION OF COMPLEX PHENOTYPIC TRAITS IN SCALLOPS (BIVALVIA: PECTINIDAE)

Alvin Alejandrino, Dean C. Adams, Jeanne M. Serb

15:20-15:40 **T16.O5** – EVOLUTIONARY PATTERN OF SYMBIOTIC LIFESTYLE AND HOST ASSOCIATION IN THE BIVALVE SUPERFAMILY GALEOMMATOIDEA

Ryutaro Goto, Atsushi Kawakita, Hiroshi Ishikawa, Yoichi Hamamura, Makoto Kato

16:00-18:30 **POSTER SESSION**

THURSDAY, 25

Aula Magna

Chair: Timea Neusser

08:40-09:00 **T4.O6** – A PRELIMINARY PHYLOGENY AND BIODIVERSITY ASSESSMENT OF THE HAWAIIAN HELICINIDAE

Kelley Leung, Norine W. Yeung, Kenneth A. Hayes

09:00-09:20 **T4.O7** – SHELL ONTOGENY AND VARIABILITY OF SHELL MORPHOLOGY IN POPULATIONS OF *LEPTINARIA UNILAMELLATA* (D'ORBIGNY, 1835) (MOLLUSCA, PULMONATA, SUBULINIDAE)

Sthefane D'ávila, Camilla Medeiros, Cristiane Lafetá Furtado Mendonça, Roberta Lima Caldeira, Omar dos Santos Carvalho

09:20-09:40 **T4.O8** – SPATIAL PATTERNS OF CRETAN LAND SNAILS

E. Georgopoulou, K. Vardinoyannis, M. Mylonas

09:40-10:00 **T4.O9** – A COMPARISON OF METHODS FOR DELIMITING SPECIES IN A CRETAN LAND SNAIL RADIATION REVEALS SHORTCOMINGS OF EXCLUSIVELY MOLECULAR TAXONOMY

Jan Sauer, Bernhard Hausdorf

10:00-10:20 **T4.O10** – DIFFERENT EVOLUTIONARY HISTORIES IN TAXA: REASONS AND CHALLENGES. A CASE STUDY IN *TROCHULUS* (GASTROPODA: PULMONATA: HYGROMIIDAE)

Michael Duda, Luise Kruckenhauser, Helmut Sattmann, Elisabeth Haring

10:20-10:50 **COFFEE BREAK**

Chair: Cindy Bick

10:50-11:10 **T4.O11** – THE CASE OF *PYRAMIDULA PUSILLA*: ADDING THE FIRST PIECES TO THE PHYLOGEOGRAPHIC PUZZLE OF ALPINE POPULATIONS

Sandra Kirchner, Luise Kruckenhauser, Helmut Sattmann, Josef Harl, Michael Duda, Elisabeth Haring

11:10-11:30 **T4.O12** – PHYLOGEOGRAPHY OF THE LAND SNAIL GENUS *ORCULA* HELD 1837 WITH A SPECIAL FOCUS ON THE ALPINE SPECIES GROUP

J. Harl, B. Páll-Gergely, M. Duda, L. Kruckenhauser, H. Sattmann, E. Haring

11:30-11:50	**T4.O13** – MORPHOLOGICAL AND MOLECULAR ANALYSIS OF *SARASINULA* AND RELATED GENERA (GASTROPODA, VERONICELLIDAE) AND TAXONOMIC IMPLICATIONS FOR THE GROUP **Suzete Rodrigues Gomes**, Norman Barr, Oscar Obregón, Rafaela Paula de Freitas, Ana Rita de Toledo-Piza, David G. Robinson, Eliana Nakano
11:50-12:10	**T4.O14** – ADAPTATION OF FRESHWATER GASTROPODS ASSOCIATED WITH GEOTHERMAL HABITATS **Olga Aksenova**, Yuliya Bespalaya, Ivan Bolotov
12:10-12:30	**T4.O15** – TOWARDS A MOLECULAR PHYLOGENY OF ELLOBIIDAE (GASTROPODA, PULMONATA) USING A MULTI-LOCUS APPROACH **Pedro Romero**, Annette Klussmann-Kolb
12:30-14:00	**LUNCH**
	CHAIR: Dai Herbert
14:00-14:20	**T4.O16** – HISTORY OF THE DIVERSIFICATION OF SURFACE AND SUBTERRANEAN MICROGASTROPODS (ELLOBIOIDEA: CARYCHIIDAE) **A. M. Weigand**, A. Jochum, H. Fukumori, Y. Kano, A. Klussmann-Kolb
14:20-14:40	**T4.O17** – OPENING WINDOWS IN CARYCHIID TAXONOMY (ELLOBIOIDEA: CARYCHIIDAE) – A NEW PERSPECTIVE HIGHLIGHTS SOME KNOWN AND NOVEL MORPHOLOGICAL CHARACTERS IN THE SHELL AND RADULA **A. Jochum**, Yaron Malkowsky, M. Kampschulte, M. J. Heneka, A. Klussmann-Kolb
14:40-15:00	**T4.O18** – SPECIES DIVERSITY OF MANGROVE GASTROPODS IN THE INDO-WEST PACIFIC **Tricia Goulding**
15:00-15:20	**T4.O19** – OUT OF THE MARINE MESOPSAMMON, INTO THE (PAN-) PULMONATE WORLD: HISTORICAL BIOGEOGRAPHY AND HABITAT SHIFTS IN THE EVOLUTION OF ACOCHLIDIAN SLUGS **Katharina M. Jörger**, Timea P. Neusser, Bastian Brenzinger, Michael Schrödl
15:20-15:40	**T4.O20** – DIVERSITY OF *SIPHONARIA* LIMPETS (GASTROPODA: EUTHYNEURA) FROM THE INDO-WEST PACIFIC **Benoît Dayrat**
15:40-16:10	**COFFEE BREAK**
	CHAIR: Heike Wägele
16:10-16:30	**T7.O1** – PARALLEL CHANGES IN GENITAL MORPHOLOGY DELINEATE CRYPTIC DIVERSIFICATION OF PLANKTONIC NUDIBRANCHS (GLAUCIDAE: *GLAUCUS*) **Celia K. C. Churchill**, Alvin Alejandrino, Ángel Valdés, Diarmaid Ó Foighil

16:30-16:50 **T7.O2** – HIDDEN DIVERSITY IN A REEF-DWELLING SEA SLUG, *PTERAEOLIDIA IANTHINA* (NUDIBRANCHIA, AEOLIDIDA), IN THE NORTHWESTERN PACIFIC

Makiko Yorifuji, Yayoi M. Hirano, Hirohiko Takeshima, Kohji Mabuchi, Mutsumi Nishida

16:50-17:10 **T7.O3** – *AEOLIDIA PAPILLOSA* (LINNAEUS, 1761), SINGLE SPECIES OR A CRYPTIC SPECIES COMPLEX? A MORPHOLOGICAL AND MOLECULAR STUDY.

Karen Kienberger Enayati, Leila Carmona, Vinincius Padula, Michael Schrödl, Juan Lucas Cervera

17:10-17:30 **T7.O4** – TOWARDS A NEW AEOLID CLASSIFICATION: CONSEQUENCES OF THE FIRST MOLECULAR PHYLOGENY OF AEOLIDIDA (GASTROPODA, NUDIBRANCHIA)

Leila Carmona, Nicolas west, Kristen Cella, Elizabeth J. Moore, Marta Pola, Terrence M. Gosliner, Juan Lucas Cervera

17:30-17:50 **T7.O5** – SECONDARY METABOLOMICS VERIFIES RADIATION IN AN ANTARCTIC MARINE INVERTEBRATE SPECIES FLOCK

Nerida G. Wilson, J. Alan Maschek, Bill J. Baker

17:50-18:10 **T7.O6** – A COLORFUL QUESTION: THE NUDIBRANCH ´*FELIMIDA CLENCHI* SPECIES COMPLEX´ INVESTIGATED THROUGH MOLECULAR MARKERS

Vinicius Padula, Isabella Stöger, Yolanda Camacho-García, Judith Brown, Dimitris Poursanidis, Manuel Malaquias, Juan Lucas Cervera, Michael Schrödl

AMPHITHEATRE NORTH

CHAIR: José Xavier

08:40-09:00 **T13.O1** – TRIBUTE TALK: MALCOLM CLARKE'S LIFE IN SCIENCE

Paul G. K. Rodhouse

09:00-09:20 **T13.O2** – MALCOLM CLARKE AND CEPHALOPOD BEAKS: THE PAST, PRESENT AND FUTURE IN ASSESSING CEPHALOPODS IN THE DIET OF TOP PREDATORS WORLDWIDE

José C. Xavier, Yves Cherel

09:20-09:40 **T13.O3** – THE ROLE OF CEPHALOPODS AROUND SOUTH SANDWICH ISLANDS FROM TOOTHFISH DIETS

J. Seco, J. Roberts, F. Ceia, M. Guerreiro, P Alvito, J.C. Xavier

09:40-10:00 **T13.O4** – WHAT CEPHALOPODS TELL US ABOUT THEIR PREDATORS

Giambattista Bello

10:00-10:20 **T13.O5** – TROPHIC ROLE OF *ILLEX ARGENTINUS* IN THE ECOSYSTEM

Rigoberto Rosas Luis, Pilar Sánchez, Augusto C. Crespi_Abril

10:20-10:50 **COFFEE BREAK**

Chair: Liz Shea

10:50-11:10 **T13.O6** – LARGE-SCALE NON-INVASIVE SCANNING PERMITS A NOVEL APPROACH TO STUDYING CEPHALOPOD MORPHOLOGY

Alexander Ziegler, Elizabeth K. Shea, Darlene R. Ketten, Ross Mair, Cornelius Faber, T. Aran Mooney, Christian Bock, Gonzalo Giribet

11:10-11:30 **T13.O7** – IDENTIFICATION OF DEEP-SEA CIRRATE OCTOPOD HATCHLINGS USING HIGH-FIELD MAGNETIC RESONANCE IMAGING

Elizabeth Shea, Alexander Ziegler, Cornelius Faber, Tim Shank

11:30-11:50 **T13.O8** – IS THE SQUID EMBRYONIC STATOLITH HOLLOW?

Rui Rosa, Gisela Dionísio, Marta Pimentel, Katja Trübenbach, Ana Moreno, Pedro Barquinha, Mário Diniz

11:50-12:10 **T13.O9** – COMPARATIVE MORPHOLOGY OF PARALARVAL BEAKS FROM REPRESENTATIVES OF THREE MAJOR SQUID FAMILIES (CEPHALOPODA: TEUTHOIDEA)

R. M. Franco-Santos, Érica A.G. Vidal

12:10-12:30 **T13.10** – NEW DATA ON SEXUAL DIMORPHISM IN ARMS AND VERTICAL DISTRIBUITION OF *LYCOTEUTHIS LORIGERA* AND *NEMATOLAMPAS REGALIS* (CEPHALOPODA: LYCOTEUTHIDAE)

Chung-Cheng Lu

12:30-14:00 **LUNCH**

Chair: Liz Shea

14:00-14:20 **T13.O11** – TRIBUTE TALK: MALCOLM, MAN OF MEGA MAMMALS AND MONSTROUS MOLLUSKS

Clyde F.E. Roper

14:20-14:40 **T13.O12** – A MOLECULAR SEARCH FOR THE GIANT SQUID *ARCHITEUTHIS*

Inger Winkelmann, Paula F. Campos, Jan Strugnell, Yves Cherel, Peter J. Smith, Tsunemi Kubodera, Louise Allcock, Marie-Louise Kampmann, Hannes Schroeder, Angel Guerra, Mark Norman, Julian Finn, Debra Ingrao, Malcolm Clarke, M. Thomas, P. Gilbert

14:40-15:00 **T13.O13** – LULA 1000 – THE NEW SCIENTIFIC EYE ON THE AZOREAN DEEP SEA

Daniel Oesterwind, Kirsten Jakobsen, Joachim Jakobsen

15:00-15:20 **T13.O14** – ANTIOXIDANT DEFENSE AND HYPOXIA TOLERANCE OF JUMBO SQUID (*DOSIDICUS GIGAS*) THRIVING IN OXYGEN MINIMUM ZONES

Katja Trübenbach, Tatiana Teixeira, Mário Diniz, Rui Rosa

15:20-15:40	**T13.O15** – UNKNOWN LARGE PELAGIC INCIRRATE OCTOPUS FROM THE SOUTHERN OCEAN **Katrin Linse**, Paul Tyler, NERC ChEsSo consortium
15:40-16:10	**COFFEE BREAK**
16:10-17:30	**Chair: Marek Lipinski, José Xavier, Liz Shea** **Panel - Legacy of Malcolm Clarke: Importance of cephalopods in the world oceans**

AMPHITHEATRE SOUTH

	Chair: Maxim V. Vinarski
08:40-09:00	**T14.O1** – CUTTING THE GORDIAN KNOT OF NOMENCLATURE - HOW TO DEAL WITH OLD NAMES? **Gerhard Haszprunar**
09:00-09:20	**T14.O2** – FRESHWATER MOLLUSCS FROM THE SÃO FRANCISCO RIVER BASIN, NORTHEAST OF BRAZIL **Silvana C. Thiengo**, Lângia C. Montresor, Raquel S. Leal, Monica A. Fernandez
09:20-09:40	**T14.O3** – NEW IDEAS ON CHARACTER EVOLUTION IN THE UNIONIDA **Arthur E. Bogan**, Eric Chapman, Walter R. Hoeh
09:40-10:00	**T14.O4** – INCONGRUENCE BETWEEN MTDNA AND NUCLEAR DATA IN THE FRESHWATER MUSSEL GENUS *CYPROGENIA* (BIVALVIA: UNIONIDAE) **Jer Pin Chong**, John L. Harris, Kevin J. Roe
10:00-10:20	**T14.O5** – GENETIC VARIATION, POPULATION STRUCTURE, AND PATTERNS OF POST-GLACIAL COLONIZATION FOR UNIONIDAE IN THE NORTH AMERICAN GREAT LAKES **David T. Zanatta**, Jennifer L. Bergner, Andrew T. Harris, Philip T. Mathias, Mariah W. Scott
10:20-10:50	**COFFEE BREAK**
	Chair: Maxim V. Vinarski
10:50-11:10	**T14.O6** – DO CONSERVATION EFFORTS REALLY TARGET THE MOST VULNERABLE TAXA? A VIEW FROM EUROPE **Vincent Prié**
11:10-11:30	**T14.O7** – FRESHWATER GASTROPOD DIVERSITY OF EUROPEAN LAKE SYSTEMS OVER THE LAST 23 MILLION YEARS - STATE OF THE ART AND OUTLOOK **Thomas A. Neubauer**, Mathias Harzhauser, Oleg Mandic, Elisavet Georgopoulou, Andreas Kroh

11:30-11:50 **T14.O8** – MARSUPIAL MOLLUSCS AS MODELS – EVOLUTIONARY SYSTEMATICS OF AUSTRALIAN FRESHWATER GASTROPODS

Nora Maaß, France Gimnich, Matthias Glaubrecht

11:50-12:10 **T14.O9** – THE STRUCTURE OF THE COPULATORY APPARATUS AS A TAXONOMIC TOOL FOR BITHYNIID SNAILS (GASTROPODA: PECTINIBRANCHIA: BITHYNIIDAE) OF WESTERN SIBERIA

Svetlana I. Andreyeva, Nikolay I. Andreyev, Ekaterina A. Lazutkina, **Maxim V. Vinarski**

12:10-12:30 **T14.O10** – TAXONOMY AND ECOLOGY OF THE GENUS *SEMISULCOSPIRA* IN THE MOLECULAR AGE

Diarmaid Ó Foighil, Osamu Miura, Jingchun Li, Satoshi Kamiya

12:30-14:00 **LUNCH**

Chair: Maxim V. Vinarski

14:00-14:20 **T14.O11** – TAXONOMY OF *ASOLENE META* (IHERING, 1915) AND *ASOLENE SPIXII* (D´ORBIGNY, 1838) (CAENOGASTROPODA: AMPULLARIIDAE) FROM BRAZIL

Aline G. Schilithz, Kenneth A. Hayes, Robert H. Cowie, Silvana C. Thiengo

14:20-14:40 **T14.O12** – DOES ECOPHENOTYPIC PLASTICITY OBSCURE EVOLUTIONARY HISTORY? RELATIONSHIPS OF NEARCTIC *STAGNICOLA* (GASTROPODA: LYMNAEIDAE) USING GEOMETRIC MORPHOMETRIC AND PHYLOGENETIC METHODS

Samantha L. Flowers

14:40-15:00 **T14.O13** – CAN DEER SPREAD SNAILS?

Gabor Majoros

15:00-15:20 **T14.O14** – TAXONOMY, MORPHOLOGY AND DISTRIBUTION OF ANCYLINAE (GASTROPODA: PULMONATA: PLANORBIDAE) IN ARGENTINA

Ximena Maria Constanza Ovando, Luiz Eduardo Macedo de Lacerda, **Sonia Barbosa dos Santos**

15:20-15:40 **T14.O15** – LYMNAEID TAXONOMY IN THE MOLECULAR AGE: ADVANCES AND PROSPECTS

Maxim V. Vinarski, Katrin Schniebs, Peter Glöer, Anna K. Hundsdoerfer

15:40-16:10 **COFFEE BREAK**

Chair: Steffen Kiel

16:10-16:30 **T3.O1** – FOSSILS AND PHYLOGENY: COMPARING PATTERNS OF EXTINCTION AND SPECIATION

Simon F. K. Hills, James Crampton, Steve Trewick, Mary Morgan-Richards

16:30-16:50 **T3.O2** – INTO THE DEEP: A PHYLOGENETIC APPROACH TO THE BIVALVE SUBCLASS PROTOBRANCHIA

Prashant P. Sharma, John D. Zardus, Ward C. Wheeler, Ron J. Etter, Gonzalo Giribet

16:50-17:10 **T3.O3** – THE PHYLOGENY AND SYSTEMATICS OF THE NASSARIIDAE REVISITED (GASTROPODA, BUCCINOIDEA)

Lee Ann Galindo, Nicolas Puillandre, Philippe Bouchet

17:10-17:30 **T3.O4** – BEYOND RELATIONSHIPS: MINING EVOLUTIONARY HISTORY FROM THE MARINE GASTROPOD FOSSIL RECORD

Carole S. Hickman

AMPHITHEATRE IV

CHAIR: Gerhard Steiner

08:40-09:00 **T17.O1** – *HOX* AND *PARAHOX* GENE EXPRESSION DURING DEVELOPMENT OF THE TROCHID GASTROPOD *GIBBULA VARIA*: HOW IDIOSYNCRATIC ARE MOLLUSCS?

Gerhard Steiner, Leyli Samadi

09:00-09:20 **T17.O2** – POU GENE EXPRESSION IN THE CEPHALOPOD *IDIOSEPIUS NOTOIDES*

Tim Wollesen, Carmel McDougall, Bernard M. Degnan, Andreas Wanninger

09:20-09:40 **T17.O3** –LOOK OUT! REVEALING PHOTOSENSITIVE STRUCTURES AND THE CORRESPONDING MOLECULAR BASIS IN THE SCALLOP, *ARGOPECTEN IRRADIANS*

Anita J. Porath-Krause, Jeanne M. Serb

09:40-10:00 **T17.O4** – IDENTIFYING THE MOLECULAR LINK BETWEEN PHOTOSENSITIVE TISSUES AND THE EYES OF THE BAY SCALLOP, *ARGOPECTEN IRRADIANS*

Autum N. Pairett, Jeanne M. Serb

10:00-10:20 **T17.O5** – DEVELOPMENT OF THE MANTLE EDGE IN *NODIPECTEN NODOSUS* (BIVALVIA: PECTINIDAE) AND ITS IMPLICATIONS FOR UNDERSTANDING THE FUNCTIONAL ONTOGENY OF SCALLOP PALLIAL FOLDS

Jorge A. Audino, José Eduardo A. R. Marian, Sônia G. B. C. Lopes

10:20-10:50 **COFFEE BREAK**

CHAIR: Janice Voltzow

10:50-11:10 **T17.O6** – AVOIDING MISIDENTIFICATIONS BY ONTOGENY:AN EXAMPLE BETWEEN *AGATHISTOMA VIRIDULA* AND *A. HOTESSIERIANA* (GASTROPODA, TROCHIDAE, TEGULINAE)

Ana Paula S. Dornellas, Luiz Ricardo L. Simone

11:10-11:30 **T17.O7** – SHELL ORNAMENTATION: VARIX FORMATION AND GROWTH IN *NUCELLA LAMELLOSA* AND *CERATOSTOMA FOLIATUM* (MURICIDAE: GASTROPODA)

Nicole B Webster, A. Richard Palmer

11:30-11:50 **T17.O8** – TESTING A MORPHOMETRIC DISCRIMINATION BETWEEN TWO SPECIES CLUSTERS BELONGING TO THE PROTOBRANCH GENERA *LEDELLA* VERRILL & BUSH, 1897 AND *YOLDIELLA* VERRILL & BUSH, 1897, BASED ON HINGE PLATE CHARACTERS

Diniz Corrêa Paone Viegas, Natalia Pereira Benaim, Ricardo Silva Absalão

11:50-12:10 **T17.O9** – COMPARATIVE ANATOMY OF THE FASCIOLARIIDAE *PUSTULATIRUS OGUM* AND *HEMIPOLYGONA BECKYAE* FROM BRAZIL (GASTROPODA: NEOGASTROPODA: PERISTERNIINAE)

Diogo R. Couto, Luiz R. L. Simone, Alexandre D. Pimenta

12:10-12:30 **T17.O10** – GASTROENDOSCOPY: AN INSIDE VIEW OF LIVE GASTROPODS

Janice Voltzow

12:30-14:00 **LUNCH**

Chair: Gary Rosenberg

14:00-14:20 **T18.O1** – MAKING SMALL DATA BIG: A SOLUTION FOR THE PUBLISHING BOTTLENECK IN BIODIVERSITY

Lyubomir Penev, Teodor Georgiev, Pavel Stoev, Jordan Biserkov, Laurence Livermore, Jeremy Miller, David Roberts, Vincent Smith

14:20-14:40 **T18.O2** – ACTIVITIES OF THE PHILIPPINE MOLLUSK SYMBIONT INTERNATIONAL COOPERATIVE BIODIVERSITY GROUP

Gary Rosenberg

14:40-15:00 **T18.O3** – MOUNTAIN KILIMANJARO ECOSYSTEMS UNDER GLOBAL CHANGE: STORY FROM SNAILS

Christine Ngereza

15:00-15:20 **T18.O4** – MOLLUSCS ASSOCIATED WITH CORAL REEF ISLA LARGA, SAN ESTEBAN NATIONAL PARK, CARABOBO STATE, VENEZUELA

Julia Andreina Alvarez-Barco, José Gregorio Rodriguez, Carmen Teresa Rodriguez, Samuel Narciso

15:20-15:40 **T18.O5** – UNRAVELLING TAXONOMIC COMPLEXITIES IN THE ENDEMIC SOUTHERN AFRICAN GENUS, *CHONDROCYCLUS* (CYCLOPHORIDAE)

Mary L. Cole

15:40-16:10 **COFFEE BREAK**

CHAIR: David G. Reid

16:10-16:30 **T18.O6** – MANGROVE-ASSOCIATED MOLLUSCS OF SOUTHEAST ASIA: DIVERSITY AND DIVERSIFICATION

David G. Reid, Tomowo Ozawa

16:30-16:50 **T18.O7** – TAXONOMY, BIOGEOGRAPHY AND ECOLOGY OF TERRESTRIAL MOLLUSCS OF THE ATLANTIC FOREST IN PARANÁ STATE, SOUTHERN BRAZIL

Eduardo Colley

16:50-17:10 **T18.O8** – PHYLOGENY OF THE CAENOGASTROPODA – A MORPHOLOGICAL PERSPECTIVE

Luiz Ricardo L. Simone

17:10-17:30 **T18.O9** – THE PRESENT KNOWLEDGE OF THE TAXONOMY OF TRIPHORIDAE (GASTROPODA) FROM BRAZIL

Maurício R. Fernandes, Alexandre D. Pimenta

17:30-17:50 **T18.O10**– DECONSTRUCTING *DENDROPOMA:* A SYSTEMATIC REVISION OF A WORLD-WIDE WORM-SNAIL GROUP WITH DESCRIPTION OF NEW GENERA (CAENOGASTROPODA: VERMETIDAE)

Rosemary E. Golding, Rüdiger Bieler, **Timothy A. Rawlings**, Timothy M. Collins

AMPHITHEATRE III

CHAIR: Megan E. Paustian

14:00-14:20 **T19.O1** – THE LAND SNAILS OF PENNSYLVANIA, USA: LIKELY EFFECTS OF GLOBAL WARMING UPON SPECIES' DISTRIBUTIONS

Megan E. Paustian, Timothy A. Pearce

14:20-14:40 **T19.O2** – IMPACT OF ENVIRONMENTAL VARIABLES ON THE DIVERSITY OF FRESHWATER MOLLUSCS

Zahoor Pir, L. K. Mudgal

14:40-15:00 **T19.O3** – EFFECT OF TEMPERATURE ON EMBRYONIC DEVELOPMENT OF THE MARINE GASTROPOD *CHARONIA SEGUENZAE* (ARADAS & BENOIT, 1870)

Chrisa K. Doxa, Aspasia Sterioti, Pascal Divanach, Maroudio Kentour

15:00-15:20 **T19.O4** – TEMPORAL VARIATION IN REPRODUCTIVE PHENOLOGY OF *PATELLA* SPP.: PAST AND PRESENT

Maria Vale, Ana I. Neto, Gustavo Martins, Stephen J. Hawkins

15:20-15:40 **T19.O5** – δ^{18}O AND δ^{13}C RECORD OF *VIVIPARUS DILUVIANUS* (KUNTH) SHELLS FROM HOLSTEINIAN DEPOSITS AT ORTEL KRÓLEWSKI AND SZYMANOWO, EASTERN POLAND

Marcin Szymanek

15:40-16:10 **COFFEE BREAK**

Chair: Inga Reich

16:10-16:30 **T20.O1** – DON'T MISS THE TRAIT!: THE IMPORTANCE OF CONSIDERING BIOLOGICAL TRAITS FOR A BETTER UNDERSTANDING OF BENTHIC ASSEMBLAGES

Fernando Aneiros, Juan Moreira, Jesús S. Troncoso

16:30-16:50 **T20.O2** – *GEOMALACUS MACULOSUS:* WHY IS THIS LUSITANIAN SLUG SPECIES THRIVING IN A COMMERCIAL FORESTRY PLANTATION 200KM NORTH OF ITS PREVIOUSLY KNOWN DISTRIBUTION?

Inga Reich, Kim O'Meara, Rory Mc Donnell, Cindy Smith, Mike Gormally

16:50-17:10 **T20.O3** – MOVEMENTS OF THE EUROPEAN FLAT OYSTER *OSTREA EDULIS* (LINNAEUS, 1758)

Cass Bromley, **Elizabeth Clare Ashton**, Dai Roberts

17:10-17:30 **T20.O4** – WASTE RECYCLING: POTENTIALS OF RICE BRAN IN CULTIVATION OF AFRICAN GIANT LAND SNAIL *ARCHACHATINA MARGINATA* PULMONATA STYLOMMATOPHORA

B.N. Ejidike,

17:30-17:50 **T20.O5**– RESPONSE OF JUVENILE GIANT LAND SNAIL *ARCHACATINA MARGINATA* FED VARYING LEVELS OF COCOA POD HUSK

A.I. Adeyemo

17:50-18:10 **T20.O6 –** DETECTION OF *HEXAMERMIS ALBICANS* NEMATODE IN *SUCCINEA PUTRIS* AMBERSNAIL IN HUNGARY

Alexandra Juhasz

18:10-19:10 **ASM AUCTION**

FRIDAY, 26

AULA MAGNA

Chair: Terrence Gosliner

08:40-09:00 **T7.O7** – THE SYSTEMATICS OF CEPHALASPIDEA REVISITED

Trond Oskars, Manuel A. E. Malaquias

09:00-09:20 **T7.O8** – BROAD SAMPLING AND MOLECULAR PHYLOGENETICS REVEALS RAMPANT PARAPHYLY IN HAMINOEIDAE CEPHALASPIDS

Manuel A. E. Malaquias, Chin Chin Too, David Rees, Paula M. Mikkelsen

09:20-09:40 **T7.O9** – NEW INSIGHTS INTO CEPHALAPIDEAN EVOLUTION: THE PHYLOGENY OF THE PHILINACEA (GASTROPODA, OPISTHOBRANCHIA).

Terrence Gosliner, Claire Gonzalez

09:40-10:00

T7.O10 – A GLIMPSE INTO EARLY HETEROBRANCH EVOLUTION - MICROANATOMY OF MURCHISONELLIDAE

Bastian Brenzinger, Nerida G. Wilson, Michael Schrödl

10:00-10:20

T7.O11 – THE ENIGMA FROM THE DEEP – INTEGRATIVE STUDY OF A REMARKABLE HETEROBRANCH SEA SLUG FROM OFF MOZAMBIQUE

Timea P. Neusser, Bastian Brenzinger, Ellen E. Strong, Michael Schrödl

10:20-10:50

COFFEE BREAK

CHAIR: Manuel Malaquias

10:50-11:10

T7.O12 – PHYLOGENY OF SACOGLOSSA: HOW KLEPTOPLASTY AND LARVAL TYPE INFLUENCE RATES OF MOLECULAR EVOLUTION AND SPECIATION IN HERBIVOROUS SEA SLUGS

Patrick J. Krug, Jann E. Vendetti, Cynthia D. Trowbridge

11:10-11:30

T7.O13 – *PLAKOBRANCHUS OCELLATUS* (SACOGLOSSA) CONTINUOUSLY ACQUIRES KLEPTOPLASTS AND NUTRITION FROM MULTIPLE ALGAL SPECIES IN NATURE

Taro Maeda, Euichi Hirose, Yoshito Chikaraishi, Masaru Kawato, Kiyotaka Takishita, Takao Yoshida, Heroen Verbruggen, Jiro Tanaka, Shigeru Shimamura, Yoshihiro Takaki, Masashi Tsuchiya, Kenji Iwai, Shuji Shigenobu, Tadashi Maruyama

11:30-11:50

T7.O14 – FUNCTIONAL CHLOROPLASTS IN SACOGLOSSA: A NON-PLAKOBRANCHID LONG-TERM RETENTION FORM – *COSTASIELLA OCELLIFERA*

Gregor Christa, William Martin, Sven B. Gould, Heike Wägele

11:50-12:10

T7.O15 – PHOTOPROTECTION MECHANISMS IN SACOGLOSSAN SEA SLUGS

Sónia Cruz, Paulo Cartaxana, Gisela Dionísio, Ricardo Calado, João Serôdio

12:10-12:30

T7.O16 – A NEW SPECIES OF *COSTASIELLA* (OPISTHOBRANCHIA, SACOGLOSSA) FROM FLORIDA, NOT ASSOCIATED WITH *AVRAINVILLEA*.

Kathe R. Jensen

12:30-12:50

T7.O17 – CULTURING SEA SLUGS: WHY THEY MATTER?

Gisela Dionísio, Rui Rosa, Miguel Leal, Sónia Cruz, Cláudio Brandão, Gonçalo Calado, João Serôdio, Ricardo Calado

12:30-14:00

LUNCH

Chair: Jesus Troncoso

14:00-14:20 **T7.O18** – REDESCRIPTION OF *PLEUROBRANCHAEA INCONSPICUA* (PLEUROBRANCHOIDEA: NUDIPLEURA) FROM BRAZIL, WITH A PRELIMINARY EVALUATION OF THE MORPHOLOGICAL CHARACTERS USED IN THE TAXONOMY OF *PLEUROBRANCHAEA*

Juliana Alvim, Luiz Ricardo L. Simone, Alexandre Pimenta

14:20-14:40 **T7.O19** – ADDRESSING THECOSOME PTEROPODS (GASTROPODA: EUOPISTHOBRANCHIA) SOFT BODIES IN 3D MICROANTOMICAL DETAIL

Peter Kohnert, Pauline Hein, Rimas Kubilius, Bastian Brenzinger, Michael Schrödl

14:40-15:00 **T7.O20** – NUDIPLEURA OF MOZAMBIQUE

Yara Tibiriçá

15:00-15:20 **T7.O21** – ADDING A MISSING PIECE TO THE PUZZLE: "OPISTHOBRANCHS" FROM PERU

Michael Schrödl, Roberto A. Uribe, Katia Nakamura, Aldo Indacochea, Aldo S. Pacheco, Yuri Hooker

15:20-15:40 **T7.O22** – INDEPENDENT EVOLUTION OF SWIMMING BEHAVIORS IN NUDIBRANCHS INFERRED FROM NEURAL MECHANISMS

Akira Sakurai, Joshua L. Lillvis, Charuni A. Gunaratne, **Paul S. Katz**

15:40-16:00 **COFFEE BREAK**

Amphitheatre North

Chair: José Xavier

08:40-09:00 **T13.O16** – TRIBUTE TALK: IN MEMORY OF A FRIEND, TEACHER AND MENTOR

C.C. Lu

09:00-09:20 **T13.O17** – "THE SCIENTIFIC ROLE OF MALCOLM CLARKE IN THE AZORES"

José Nuno Gomes-Pereira, Rui Prieto, Verónica Neves, Filipe Porteiro, João Gonçalves, Helen R. Martins

09:20-09:40 **T13.O18** – CLIMATE CHANGE IMPACTS ON COASTAL CEPHALOPODS DIVERSITY

Joana Boavida-Portugal, François Guilhaumon, Rui Rosa, Miguel B. Araújo

09:40-10:00 **T13.O19** – DISTRIBUTION PATTERNS SHORTFIN SQUIDS (CEPHALOPODA: OMMASTREPHIDAE) IN THE PORTUGUESE NORTHWEST COAST

Sílvia Lourenço, João Pereira, Dina Silva, Catarina Cavaleiro, Ana Moreno

10:00-10:20 **T13.O20** – DISTRIBUTION OF CEPHALOPOD PARALARVAE IN TWO CONTRASTING SITES OF THE IBERIAN–CANARY CURRENT EASTERN BOUNDARY UPWELLING SYSTEM: CAPE SILLEIRO (42ºN) AND CAPE GHIR (30ºN)

Álvaro Roura, Xosé A. Álvarez-Salgado, Ángel F. González, María Gregori, Gabriel Rosón, Ángel Guerra

10:20-10:50 **COFFEE BREAK**

Chair: Marek Lipinski

10:50-11:10 **T13.O21** – CEPHALOPODS AS VECTORS OF HARMFUL ALGAL BLOOM TOXINS IN MARINE FOOD WEBS

Vanessa M. Lopes, Ana Rita Lopes, Pedro Costa, Rui Rosa

11:10-11:30 **T13.O22** – WHO KNOWS, ONLY THE HOST KNOWS; SEPIOLID SQUIDS AS EVOLUTIONARY DRIVERS OF BACTERIAL SPECIFICITY IN AN ENVIRONMENTALLY TRANSMITTED SYMBIOSIS

A. Chavez-Dozal, C. Gorman, C.P. Lostroh, **M.K. Nishiguchi**

11:30-11:50 **T13.O23** – ARM AUTOTOMY IN OCTOPUS *ABDOPUS ACULEATUS* ON MACTAN ISLAND, PHILIPPINES

Jean S. Alupay, Roy Caldwell

11:50-12:10 **T13.O24** – SQUID FLY IN A 15M DIAMETER TANK - AGAIN!

Ron O'Dor, Hassan Moustahfid

12:10-12:30 **T13.025** – CEPHALOPODS IN THE FOOD AND FEEDING NETWORK OF MARINE LIFE. LEGACY OF MALCOLM CLARKE.

M.R. Lipinski, J.C. Xavier, E.K. Shea

12:30-14:00 **LUNCH**

14:00-15:20 **Chair: José Xavier, Liz Shea, Marek Lipinski**

PANEL: FUTURE CHALLENGES IN CEPHALOPOD RESEARCH

15:40-16:00 **COFFEE BREAK**

Amphitheatre South

Chair: Suzanne Williams

08:40-09:00 **T3.O5** – CONSENSUS AND CONFUSION IN MOLLUSCAN PHYLOGENY

Julia Sigwart, **David R. Lindberg**

09:00-09:20 **T3.O6** – PATTERNS AND PROCESSES OF SPECIATION IN THE BALEARIC ISLANDS ENDEMIC LAND SNAIL GENUS *ALLOGNATHUS*

Luis J. Chueca, Josep Quintana, Mª José Madeira, Benjamín J. Gómez-Moliner

09:20-09:40

T3.O7 – MOLECULAR PHYLOGENY OF THE PHILIPPINE BRADYBAENIDAE (PULMONATA: STYLOMMATOPHORA)

Gizelle Batomalaque, Jordan Ferdin Halili, Emmanuel Ryan de Chavez, Ian Kendrich Fontanilla

09:40-10:00

T3.O8 – MOLECULAR SYSTEMATICS OF *PYRAMIDULA* (GASTROPODA, PULMONATA)

Oihana Razkin, Benjamín J. Gómez-Moliner, Alberto Martínez-Ortí, Nikos Poulakakis, Katerina Vardinoyannis, Mª José Madeira

10:00-10:20

T3.O9 – NEWS FROM THE PAST ▯ OLIGOCENE CONTINENTAL MOLLUSCS OF OMAN

Eike Neubert, Dirk van Damme

10:20-10:50 **COFFEE BREAK**

Chair: Steffen Kiel

10:50-11:10

T3.O10 – LOST AND FOUND: THE EOCENE FAMILY PYRAMIMITRIDAE (NEOGASTROPODA) DISCOVERED IN THE RECENT FAUNA OF THE INDO-PACIFIC

Yuri Kantor, Pierre Lozouet, Nicolas Puillandre, Philippe Bouchet

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T3.O11 – PHYLOGENY OF VENERID BIVALVES, AS INFERRED FROM A COMBINED ANALYSIS OF MOLECULAR AND MORPHOLOGICAL DATA

André F. Sartori, **Paula M. Mikkelsen**, Rafael Robles, Nick Matzke, Rüdiger Bieler, David I. Jablonski, Scott J. Steppant

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T3.O12 – CENOZOIC CLIMATE CHANGE, TECTONICS AND DIVERSIFICATION IN THE DEEP-SEA: EVOLUTION OF DIVERSITY IN THE GASTROPOD FAMILY SOLARIELLIDAE (TROCHOIDEA)

S. T. Williams, L. M. Smith, D. G. Herbert, B. A. Marshall, A. Warén, S. Kiel, P. Dyal, K. Linse, C. Vilvens, Y. Kano

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T3.O13 – INTRODUCTION TO THE TREATISE'S PARACLADISTIC CLASSIFICATION OF THE BIVALVIA

Joseph G. Carter

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T3.O14 – PHYLOGENOMIC RESOLUTION OF RELATIONSHIPS WITHIN BIVALVIA (MOLLUSCA)

Vanessa Liz Gonzalez, Gonzalo Giribet

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Chair: Gonzalo Giribet

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T3.O15 – LOOKING UP TO ´DOWN UNDER´ - PHYLOGENY & BIOGEOGRAPHY OF AUSTRALIAN THIARIDAE

F. Gimnich, T. V. Rintelen, N. Maaß, M. Glaubrecht

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14:40-15:00 **T3.O17** – PATTERNS OF LINEAGE DIVERSIFICATION IN THE FAMILY PINNIDAE

Sarah Lemer, Gonzalo Giribet

15:00-15:20 **T3.O18** – BRIDGING THE GAP IN FOSSIL AND RECENT MELANOPSIDAE - A CASE STUDY IN EVOLUTIONARY SYSTEMATICS

Elisabetta Lori, Matthias Glaubrecht

15:40-16:10 **COFFEE BREAK**

AMPHITHEATRE IV

CHAIR: Alexandre Lobo-da-Cunha

08:40-09:00 **T21.O1** – HYPOXIA TOLERANCE OF JUMBO SQUIDS (*DOSIDICUS GIGAS*) IN THE EASTERN PACIFIC OXYGEN MINIMUM ZONES: PHYSIOLOGICAL AND BIOCHEMICAL MECHANISMS

Katja Trübenbach, Brad A. Seibel, Rui Rosa

09:00-09:20 **T21.O2** – EVALUATION OF THE GLUTATHIONE S TRANSFERASE RESPONSE TO SEASONALITY, POLYCYCLIC AROMATIC HYDROCARBON (PAH) AND HEAVY METAL POLLUTANTS IN *SACCOSTREA CUCULLATA* (BIVALVIA: OSTREIDAE), ALONG THE IRANIAN COAST OF THE PERSIAN GULF

Asadi Nariman, B. Nabavi Mohammad, Bargahi Afshar, Safahieh Alireza, Miroliaei Mehran, Tavasolpour Ehsan

09:20-09:40 **T21.O3** – OXIDASES AND DEHYDROGENASES METABOLIZING MANNITOL AND OTHER ALCOHOLS IN THE DIGESTIVE GLAND OF GASTROPODS

Alexandre Lobo-da-Cunha, Diogo Carvalho, Gonçalo Calado

09:40-10:00 **T21.O4** – PLATINUM-INDUCED SHELL INTERNALIZATION IN THE RAMSHORN SNAIL *MARISA CORNUARIETIS*

Leonie Marschner, Julian Staniek, Silke Schuster, Rita Triebskorn, Heinz-R. Köhler

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Robert Cameron

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Roland C. Anderson

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Martin P. Garwood

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Lindsey Dougherty, Sönke Johnsen

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Richard Stafford, Gray A. Williams, **Mark S. Davies**

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C. D. G. Borges, C. P. Doncaster, T. P. Crowe, S. J. Hawkins

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Gustavo M. Martins, Afonso L.C. Prestes, Ana I. Neto

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Thomas F. Duda, Jr.

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ABSTRACTS

K1 – Opening Address to the World Congress of Malacology2013

NEW FRONTIERS IN BIODIVERSITY DISCOVERY IN THE OCEANS: BRIMSTONE, CHAMPAGNE AND A TOUCH OF GOLD

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The last two decades have seen some remarkable discoveries of strange habitats in the deep ocean. With each new discovery, we learn more about geochemical and geophysical processes of the planet that create both challenging conditions and curious opportunities for life. While animals collected from "extreme" environments have broadened our understanding of evolutionary relationships within groups like the Mollusca, closer examination of their affiliations with, and adaptations to, their particular habitats may give insight into responses we may expect from related taxa faced with rapid ocean change from human influences. For examples, limpets at hot vents respond to high temperature variability with conservative behaviour while shallow water snails live closer to their limits in a warming ocean. And the discovery of beds of mussels living around liquid CO_2 vents let us explore the consequences of a low pH world. Volcanoes of back-arcs provide interesting challenges to animals, such as violent eruptions and lakes of molten sulphur. As much as these discoveries fascinate the scientists, they also are captivating to public audiences who can share in the lessons that the deep ocean offers.

K2 – Closing Address to the World Congress of Malacology2013

IT STARTS LIKE THIS:
THE INTERPRETATION OF MOLLUSCAN DIVERSITY

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We study molluscan diversity at a multitude of scales in time and space, and for a variety of different purposes from conservation management to understanding the processes of and constraints on evolution. An essential feature of any analysis is the way in which we choose to define diversity. The definition of the entities we choose to treat is also critical to the kinds of question we ask and the conclusions we draw. I will start with simple faunistic inventories at various scales and move to more complex analyses designed to detect processes and constraints, examining the way in which our analyses are dependent on the nature of the entities we recognise. While taxonomic categories are the most obvious source of such entities (with their numerous problems of equivalence and definition), they are not the only ones, and I will consider also the ways in which we define or conceptualise other aspects of diversity, and how these affect the kinds of conclusions we draw. Some promising ideas are compromised by uncertainty over the commensurate nature of the entities we use. While my examples will be drawn mainly from terrestrial molluscs, the questions raised have a more general application: where are the limits to the questions we can ask studying molluscs alone?

T1

LIVING IN THE EXTREME: MOLLUSCA OF CHEMOSYNTHETIC HABITATS

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Molluscs are major constituents of many marine habitats where chemosynthesis supports high biomass, often in settings of extreme physico-chemical conditions. Hydrothermal vents, cold seeps, hypoxic basins, carcass falls and other organic materials have yielded molluscan taxa that may show shared traits and common ancestors. Molluscan diversity is high and functional roles are often key components of ecosystem processes. Hypotheses of origination can be tested through phylogenetic analysis and by examination of the fossil record. Adaptations to these unusual conditions are expressed in physiological, morphological and behavioural traits, including symbioses. The fragmented nature of the habitats has sparked many studies of life history traits and biogeography and the application of emerging modeling approaches as well as ever-improving molecular tools. Ocean exploration continues to find new settings for molluscan assemblages and new relationships of these animals within chemosynthetic communities. This symposium encourages submissions that explore varied aspects of mollusks at chemosynthetic habitats to promote a confluence of information that will explore the origin and nature of the fauna and their adaptations.

T1.O1

A CONCEPTUAL MODEL OF CHEMOSYMBIOSIS EVOLUTION IN THE THYASIRIDAE

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Factors leading to the establishment and maintenance of long-term, stable associations between bivalves and chemoautotrophic bacteria are not well understood; examining relatively simple chemosymbioses could provide insights on how such relationships might evolve. In the Thyasiridae, some, but not all species form symbioses with sulphur-oxidizing gammaproteobacteria that are maintained extracellularly among gill cell microvilli. Symbionts likely receive reduced sulphur, carbon dioxide and oxygen for autotrophic production from the animal's burrowing and ventilation activities, and are periodically engulfed and digested by the host's epithelial cells. Recent work on asymbiotic and symbiotic thyasirids from a fjord in Newfoundland, Canada has revealed an unexpected degree of diversity among these thyasirids as well as among their symbionts. Notably, a cryptic species complex similar to *Thyasira gouldi* was

discovered in fjord, comprised of four operational taxonomic units (OTU). Within this complex, two OTUs are symbiotic, while the other two are not, and phylogenetic trees suggest that symbiont loss rather than symbiont gain has occurred in this group. We compared the burrowing and ventilation behaviour of symbiotic and asymbiotic thyasirids in experimental setups, and found strikingly similar patterns among the studied taxa. Based on these findings, we propose how thyasirid symbioses might become established, and how transitions between asymbiotic and symbiotic conditions could take place in this family.

T1.O2

POPULATION STRUCTURE IN THREE POPULATIONS OF THE 'SCALY-FOOT GASTROPOD' INDICATE LACK OF CONNECTIVITY BETWEEN HYDROTHERMAL VENTS OF CENTRAL INDIAN RIDGE AND SOUTH WEST INDIAN RIDGE

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Connectivity and population structure across all three known populations of the 'scaly-foot gastropod' *Chrysomallon squamiferum* are investigated using a 489bp fragment of cytochrome oxidase *c* subunit I (COI) gene. Population genetics analyses 20~38 individuals from each population reveals significant differentiation between the population in Dragon vent field on the Southwest Indian Ridge (SWIR) and the two populations in Kairei and Solitaire vent fields on the Central Indian Ridge (CIR). This is indicative that as the only confirmed vent field on SWIR, the genetic diversity in Dragon field is highly unique. Dragon field is within the area of the first upcoming deep-sea hydrothermal vent mining by the Chinese government, and the results from the present study have profound implications on the potential ecological impact of such mining activity. This study is also the first to document genetic differentiation of a vent-endemic species across two oceanic ridges in the Indian Ocean. In addition, the uniqueness of Dragon vent field in terms of biodiversity is highlighted by a number of new species discovered there as well as striking difference in population structure from other Indian Ocean vent fields.

T1.O3

A MORPHOLOGICAL APPROACH TO THE EVOLUTIONARY HISTORY OF BASAL HETEROBRANCH FAMILIES (GASTROPODA: ECTOBRANCHIA)

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Whereas molecular data and analyses have substantially improved our understanding of phylogenetic relationships, morphology still is valuable (a) as an independent

data-set for direct phylogenetic analysis and (b) to "tell the tree", i.e. to describe the evolutionary novelties and processes during diversificatiy of a taxon and (c) to infer the characters of its stem species. Accordingly, we investigated several families of basal heterobranch gastropods mostly based on semi-thin section series and computer-aided 3D-reconstructions.

Based on current knowledge the Ectobranchia (Valvatoidea) include Hyalogyrinidae, Xylodisculidae, Cornirostridae (all marine forms), and Valvatidae (the only family in freshwater habitats). For a better understanding of not only ectobranch but also basal heterobranch relationships we consulted characters of further basic "allogastropods", namely Architectonicidae, Mathilidae, Omalogyrinidae, and Orbitestellidae. Some preliminary results of these studies are presented:

All Ectobranchia are diagnostically characterized by their extendable bipectinate gill, which is a secondary structure rather than a primitive type of ctenidium as formerly believed and thus considered as a synapomorphy. Accordingly, the Orbitestellidae are to be excluded from the Ectobranchia, a result, also being supported by recent molecular studies: they entirely lack a gill and show a radically different genital system with a pedally innervated penis. The rhipidoglossate radula of Hyalogyrinidae probably is a retained plesiomorphic condition, thus the taenioglossate radulae of several heterobranch taxa is a matter of convergence to Caenogastropoda, and the Ectobranchia do probably represent the first extant offshoot of Heterobranchia.

It is quite likely that some more principal extant clades of basal heterobranchs do exist, many species based on shell descriptions alone need anatomical investigations. Accordingly, our current main goal is to widen the data-base and to correlate the morphological data with the results from the various molecular analyses towards an integrative approach of phylogeny.

T1.O4

SEASONAL VARIABILITY IN A DYNAMIC SYMBIOTIC RELATIONSHIP: *THYASIRA AFF. GOULDI* AND ITS CHEMOSYNTHETIC BACTERIAL SYMBIONTS

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The Thyasiridae (Bivalvia: Mollusca) constitute an unusual family of chemosymbiotic bivalves, displaying a remarkable degree of variation in the extent of morphological adaptations associated with the hosting of symbiotic chemosynthetic bacteria. Within the family, phylogenetic conservation of a symbiotic relationship with chemosynthetic bacteria and associated host adaptations is low, with striking inter-specific variability in both nutritional strategy and the possession of symbionts existing within a single genus (*Thyasira*). In addition, symbiotic thyasirids are mixotrophic and may exhibit significant temporal variation in the importance and metabolic contribution of symbiotically-derived nutrition, though the extent of this temporal variability in host nutritional strategy remains poorly characterized. In this study, we investigated the possibility of a naturally occurring seasonal trend in the nutritional strategy and symbiont abundance of *Thyasira aff. gouldi*.

Thyasira aff. gouldi is a mixotrophic, symbiotic thyasirid found in the organically enriched sediments of Bonne Bay, Newfoundland (Canada). Though it possesses the crucial adaptations to maintaining a symbiotic relationship with extracellular chemosynthetic bacteria, such as enlarged gills with extensive abfrontal expansion of the gill filaments, it retains and partially relies upon its ability to feed on particulate organic matter. We investigated the possibility that the relative nutritional importance of the symbiosis in *Thyasira aff. gouldi* varies seasonally by quantifying the abundance of bacterial symbionts associated with host gill bacteriocytes. The abundance of extracellular thiotrophic symbionts showed significant temporal variation, with a minimum during the months of early spring (April-May) after which the population of bacterial symbionts steadily increased towards a maximum during the late summer and early fall (August-October). This naturally occurring seasonal variability in symbiont abundance highlights the nutritional flexibility of thyasirid bivalves, and illustrates the marked effect of naturally occurring environmental variation on the nutritional strategy of the host's nutritional strategy.

T1.O5

TAXONOMIC REVIEW OF *TURBONILLA* (GASTROPODA: PYRAMIDELLIDAE) COLLECTED THROUGH THE MD55 EXPEDITION, OFF SE COAST OF BRAZIL

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Knowledge on taxonomy and diversity of the marine gastropod family Pyramidellidae from Brazil has grown considerably in recent years, summing up to 50 species recorded. However, these studies were mostly restricted to species from the continental shelf (0-200 m). This study is a taxonomic review of the species *Turbonilla* collected during the MD55 expedition in 1987, off the SE Brazilian coast (about 20° S), including the seamounts chain of Vitoria-Trindade, in a total of 22 stations from depths of 15 to 3.450 m. Forty-seven taxa were recognized, of which 16 were already previously reported for Brazil, one had its distribution expanded to the south Atlantic, and thirty correspond to new taxa. Although there is a substantial increase in number of species for the Brazilian fauna of *Turbonilla*, we can still expect greater richness since there are many places still not explored, especially the deep-sea.

T1.O6

ENVIRONMENTAL IMPACTS ON THE EVOLUTION OF METHANE SEEP MOLLUSKS

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New mollusk taxa have colonized chemosynthetic ecosystems through most of Earth history. But was the timing of these colonizations stochastic or characterized by certain important events that interrupted long periods of evolutionary stasis? Addressing this question through a combination of fossil and molecular data starts to reveal a dynamic history of colonization and radiation that is linked to global environmental changes.

T1.O7

ARE EVOLUTIONARY STRATEGIES FOR A LIFE ON SUNKEN WOOD COMMON OR DISTINCT IN DEEP-SEA LIMPETS?

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Numerous molluscan taxa have colonized chemosynthetic and biogenic substrates in the deep sea, but one clade, the Lepetelloidea, stands out as having diversified and specialized to live on an incredible variety of such substrates. The Lepetelloidea are small vetigastropod limpets that have thus far been found on substrates ranging from hydrothermal vents, cold seeps, sunken wood, and whale bones to polychaete tubes, chondrichthyan egg cases, crab carapaces, leaves, algal holdfasts, sponges, and fish bones among other organic falls. Historically, this superfamily was divided into families based on morphological characters, which tended to unite taxa that lived on common substrates. Recent molecular evidence (see poster by Kano *et al.*) has indicated that several of these families are polyphyletic and that some of these substrates have been colonized independently several times. Lineages that are now known to have independently colonized the same substrate, such as wood, may have adapted to that habitat via common or distinct evolutionary pathways. To test between these two pathways, semi-thin serial sectioning and light microscopy were employed to examine the internal anatomy of several independently wood-inhabiting lineages. Identifiable alimentary tract characters from newly sectioned species and previously published data have been compared to evaluate the level of disparity across lineages inhabiting similar and distinct substrates. The patterns observed from this analysis will help to elucidate the pattern of evolutionary strategies implemented to specialize to organic substrates and whether common or distinct morphologies have evolved for a life on wood in particular.

T1.O8

EVOLUTION AND RADIATION OF NEOMPHALINE GASTROPODS: TRUE ANTIQUITY AT HYDROTHERMAL VENTS?

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The hydrothermal vent fauna was once considered to be dominated by phylogenetic relicts, being isolated from other deep-sea faunas that rely on photosynthesis. Neomphalid limpets along with stalked barnacles represented 'living fossils' in vents with assumed connections with extinct Palaeozoic groups. Recent studies using molecular and fossil data reject the general antiquity and instead suggest considerable changes in the taxonomic composition of vent communities through time, as in the case for ambient deep-sea habitats. However, the evolutionary origin of the iconic *Neomphalus* has not been investigated in a phylogenetic context.

Here we present the first comprehensive phylogeny of Neomphalina based on four gene

sequences from 45 ingroup species belonging to 25 genera. Bayesian and maximum-likelihood reconstruction of tree topology and ancestral character states revealed that (1) Neomphalina comprise three monophyletic families with unresolved relationships to one another; (2) the newly defined Neomphalidae include basal seep taxa and terminal vent clades; (3) Melanodrymiidae inhabit vents, seeps and sunken-wood with an indeterminate polarity; and (4) Peltospiridae are endemic to vents mostly near active chimneys. (5) Cocculinoidea forms its sister clade, supported solely but strongly by 18S sequences; wood and other organic substrates as habitats for all cocculinoids pose an interesting possibility that the common ancestor of the two clades lived in such a reducing environment. (6) Molecular clock analyses based on Eocene fossils for ingroup nodes and/or older calibration points for outgroups suggested that the first split within Neomphalina dates back at least to the early/middle Cretaceous, radiation of the vent-endemic Peltospiridae also in the Cretaceous and split between Neomphalina and Cocculinoidea in the Palaeozoic or early Mesozoic. Despite the absence of direct and unequivocal Mesozoic fossil evidence, the Neomphalina seem to represent a relatively old vent group that was not wiped out by the global anoxia in the Cretaceous and Palaeogene.

T1.P1

GASTROPODS FROM UPPER CRETACEOUS (91 MILLION YEAR OLD) HYDROTHERMAL VENT DEPOSITS FROM CYPRUS

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The Troodos Ophiolite from Cyprus is a 91 million year old (Upper Cretaceous; Turonian) piece of Tethyan ocean seafloor that contains numerous hydrothermal vent deposits. Three of these (Kambia, Kinousa and Memi) contain relatively well-preserved pyritized vent gastropods. Some of these were illustrated in Little *et al*. (1999) but never described in detail and new material found after this publication added several new relatively well preserved specimens. The gastropod fauna in Cypriot vents is dominated small specimens with a gross cerithioid morphology and identified as such in Little et al. (1999). However, a new provannid-like protoconch specimen strongly supports these gastropods being provannids. The gastropod preliminarily identified by Little *et al*. (1999) as an"epitoniid" is much rarer and might be related to *Paskentana*, a supposed Jurassic/Cretaceous provannoid. Some new specimens found in the Cypriot vents are reminiscent of extinct seep-restricted family Hokkaidoconchidae, which are ancestral or a sister group to the Provannidae. Another single partial specimen might be related to *Abyssochrysos*? *giganteum* known from Early Cretaceous seeps in California. The most intriguing feature of the Cypriot vent gastropod fauna is a total lack of vetigastropods, either limpet-shaped or spiral shaped, which are very common in modern vent communities.

T1.P2

SUPERTREES HELP ILLUSTRATE PATTERNS ACROSS BROAD TAXONOMIC, YET FINE ECOLOGICAL SCALES: THE CASE OF BIVALVE AND GASTROPOD COLONIZATION OF CHEMOSYNTHETIC HABITATS

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Molluscs are capable of inhabiting nearly every part of the biosphere and are second only to arthropods in animal diversity. As such, there are many questions we can ask regarding patterns of molluscan diversification and many researchers have contributed knowledge in the form of phylogenies focused at various taxonomic and geographical scales. Some ecological and evolutionary questions require a finely sampled phylogeny, especially if the morphological and/or ecological characters of interest are highly variable within and across clades. However, if one wants to investigate patterns of character evolution across a large group, such as all bivalves or all gastropods, it is a daunting task to collect enough shared sequences or common morphological characters with which to construct such massive trees. The implementation of supertree algorithms offers one solution by combining phylogenies produced from disparate datasets and tree building methods and the resulting tree(s) can be used to test a variety of questions beyond what any one source tree can provide. We compiled 15 published bivalve phylogenies and 16 published gastropod phylogenies of both molecular and morphological origin and used the supertree program “Rainbow” to generate supertrees for each class. Here, we illustrate patterns of bivalve and gastropod lineages inhabiting unique deep-sea habitats: hydrothermal vents, cold seeps, whale falls, and sunken wood. This exercise allows us to visualize the multiple colonization and specialization events that have occurred over bivalve and gastropod evolution and the higher proclivity of some clades towards specializing and/or diversifying within these habitats. The supertree approach is a rigorous way to produce consensus trees that reflect the current knowledge of bivalve and gastropod relationships, which can be used to address questions of broad taxonomic and fine ecological scales.

T1.P3

ILLUMINATING RELATIONSHIPS AND HABITAT SHIFTS IN THE LEPETELLOIDEAN LIMPET RADIATION INTO DEEP-SEA ORGANIC AND CHEMOSYNTHETIC HABITATS: A MOLECULAR APPROACH

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Sunken wood and whale carcasses in the deep-sea have attracted increasing attention due to their ecological and faunistic similarity to hydrothermal vent and cold seep

environments. Such organic substrates are often regarded as ‘stepping stones’ in the evolutionary invasion of vents and seeps. The Lepetelloidea represent the most diverse lineage among animal groups in terms of their utilization of different deep-sea organic substrates that include wood, leaves, sunken algal holdfasts, whale and fish bones, chondrichthyan egg cases, polychaete tubes, detrital cephalopod beaks and sponges among others. While none have been found from ambient inorganic substrates, some inhabit vents and seeps. Their patelliform shells are relatively similar to each other, while the radulae show conspicuous modifications aligned with particular habitats, which led to the introduction of eight families and ten subfamilies for <100 described species.

Here we present the first molecular phylogeny of Lepetelloidea, based on five gene sequences from approximately 60 species (23 genera) covering all extant families and subfamilies. Bayesian and maximum-likelihood reconstruction of tree topology and ancestral character states suggests that the Lepetelloidea (1) arose from a zeugobranch ancestor with the Lepetodriloidea as the sister taxon, (2) bear the true gill or ctenidium while the right one has been lost several times, and (3) once had a loosely coiled shell as exhibited by the basal-most *Helicopelta*. (4) The highly apomorphic radulae do not offer suitable information for deep phylogeny, but reflect dietary diversification and convergent evolution on similar substrates. Finally, (5) each of the wood, whale carcass, seep and vent environments is inhabited by multiple lineages, and (6) the habitat shifts have been too frequent to allow a rigorous estimate of ancestral conditions, although vent and seep lineages tend to appear as terminal clades, possibly supporting the stepping-stone hypothesis.

T1.P4

GASTROPODS AND BIVALVES OF THE EAST SCOTIA RIDGE VENT ECOSYSTEMS

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In 2009 the UK ChEsSO consortium (Chemosynthetically-driven ecosystems in the Southern Ocean) discovered hydrothermal venting at the East Scotia Ridge segments E2 and E9. During expeditions in the following years these vent sites hosting black smokers were explored using the ROV Isis and the macrofauna sampled. In 2010 an investigation of the Kemp Caldera at the southern End of the South Sandwich Arc discovered white smokers in a vent field as well as a natural whale fall. At the E2 and E9 vent sites only gastropods were present comprising four species of *Lepetodrilus* sp., Peltospiridae sp., Provannidae sp. and Skeneidae sp. The Kemp Caldera venting sites hosted the same species of *Lepetodrilus* sp., a *Pyropelta* sp. and the two bivalves species, one each of Thyasiridae and Vesicomyidae. Specimens of Osteopeltidae were found on the whale fall next to *Lepetodrilus* sp. and *Pyropelta* sp. Here we present taxonomic and ecological information on the gastropod and bivalve species discovered.

T1.P5

POPULATION CONNECTIVITY AND SPECIATION OF VENT MUSSELS FROM THE MID-ATLANTIC RIDGE: AN INTERDISCIPLINARY APPROACH

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Knowledge about the genetic connectivity of populations and the mechanisms underlying speciation is an important requirement for biodiversity conservation. However, despite the fact that such information is generally sparse for deep sea biota, the demands for mining of seafloor mineral resources are increasing. Using mussels of the genus *Bathymodiolus* as a model system and integrating expertise from various research disciplines, the present study aims to elucidate patterns of gene flow between hydrothermal vent populations of the Mid-Atlantic Ridge. To characterize the level of genetic exchange on ecological time scales, we will genotype mussels with species-diagnostic SNP markers designed from high-throughput transcriptomic data. By performing hybridization experiments, we will study patterns of reproductive isolation between *B. azoricus* and *B. childressi* from shallower sites. Moreover, we will measure larval survival and behaviour of *B. azoricus* under a variety of environmental conditions to identify factors that influence the spreading of propagules between vents. The results from the ecophysiological experiments will be incorporated into larval dispersal studies performed with Lagrangian simulations utilizing a high-resolution model of the global ocean under realistic forcing. By comparing the outcomes of the genetic, biophysical and ecological approaches, we expect that this work will make fundamental contributions to a better understanding of population connectivity and diversification in the deep sea as well as help to manage anthropogenic threats to hydrothermal vent ecosystems.

T1.P6

SHELL SHAPE IN THE CRYPTIC AND PARTIALLY CHEMOSYMBIOTIC *THYASIRA* AFF. *GOULDI* COMPLEX

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Thyasirid classification is challenging due to the paucity of diagnostic shell characters in this group; most classifications rely on shell outline, which is thought to vary considerably within a species. Many thyasirids have wide species ranges, but this may be artifact of grouping together different species having subtle morphological differences (i.e., cryptic species). Recently, a complex of species associated with *Thyasira gouldi* was discovered in a subarctic fjord in Newfoundland, Canada. Four operational taxonomic units (OTUs) were found to coexist at this site, with OTUs 1 and 2 being chemosymbiotic and OTUs 3 and 4 asymbiotic. Closer examination suggested that subtle differences in gill thickness and colouration exist between OTUs, and that symbiotic OTUs can reach larger sizes. Here, we examine whether shell shape and

prodissoconch length might also differ between symbiotic and asymbiotic *T*. aff. *gouldi* OTUs. Using a dissecting microscope, we photographed the prodissoconch and the left valve of individuals whose genetic identity had been previously confirmed (N = 37). We used the software Shape to perform elliptical Fourier analysis of the shell contours, normalizing the data for size and orientation. Principal components analyses (PCA) were run on the Fourier coefficients, followed by cluster analyses. Prodissoconch lengths were not significantly different between OTUs. A first cluster analysis revealed two groups: one containing two-thirds of all examined symbiotic individuals, while the second contained a mixture of all OTUs. A further, finer analysis of the second group (including more detailed shape information) provided a better separation of OTUs within this group. Reconstructions of shapes representing extremities of the first two PCA axes revealed features that distinguish the asymbiotic and symbiotic *T*. aff *gouldi* shells; whether they reflect differences in longevity or adaptations to symbiosis requires further investigation. Outline analyses may be useful for distinguishing other cryptic species in the Thyasiridae.

T1.P7

A NEW GENUS OF LARGE HYDROTHERMAL VENT-ENDEMIC GASTROPOD (NEOMPHALINA: PELTOSPIRIDAE) WITH TWO NEW SPECIES SHOWING EVIDENCE OF RECENT DEMOGRAPHIC EXPANSION

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Recently discovered hydrothermal vent fields on the East Scotia Ridge (ESR, 56-60°S 30°W), Southern Ocean and the South West Indian Ridge (SWIR, 37°S 49°E), Indian Ocean each host a new species of peltospirid gastropod. The two species highly resemble each other and morphological and molecular (mitochondrial cytochrome c oxidase subunit I, COI) characterisation indicate they are sister species of a previously undocumented genus of peltospirid gastropods, and *Gigantopelta* gen. nov. was erected within the Peltospiroidae to house them. The two new species were named *Gigantopelta chessoia* (ESR) and *Gigantopelta aegis* (SWIR). They attain an extremely large size for the clade Neomphalina, reaching 45.7mm and 44.2mm in shell length, respectively. Their esophageal gland is markedly enlarged, presumably as an adaptation to housing endosymbiotic bacteria. The digestive system is also reduced probably as a result of reliance on symbiotic chemoautotrophic bacteria for nutrition. *G. aegis* has a thick sulphide coating on both the shell and the operculum of an unknown but likely defensive function. The analysis of a 579bp fragment of COI gene indicate divergence between the two newly described species of *Gigantopelta* was 4.43%. Population genetics analyses using COI (370bp) of 30 individuals of each species confirms their genetic isolation and indicate recent rapid demographic expansion in both species.

T1.P8

ENDOSYMBIOTIC BACTERIA IN THE HOT-VENT GASTROPOD *LURIFAX VITREUS* (HETEROBRANCHIA: ORBITESTELLIDAE)

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Molluscs of chemosynthetic habitats (e.g. hot-vents, cold seeps, whale or wood falls) frequently harbor ecto- or endosymbiotic bacteria, which use hydrogen sulfide or methane as energy source. Such bacterial symbionts may substantially contribute to the energy metabolism of the host. Among the Gastropoda so-called "bacteriocytes" (tissues with intracellular bacteria) have been demonstrated in certain taxa of Neomphalida, Veti- or Caenogastropoda, but not yet in higher gastropods (Heterobranchia).

As part of our studies on basal heterobranch families we also examined the Orbitestellidae on the basis of semi-thin section series and computer-aided 3D-reconstructions. We noticed an atypical "granular-glandular" epithelium in the posterior mantle cavity within *Lurifax vitreus*. We examined this special epithelium thereafter by means of ultra-thin sections and TEM.

Despite the poor fixation (70% ethanol) we could provide first evidence of an epithelium consisting entirely of true bacteriocytes within basal Heterobranchia. Within the vacuoles of the bacteriocytes we found two morphotypes of probable gram+ bacteria (thick cell membrane and a filamentous electron-dense center). We also could depict various stages of cleavage. Although distinct digestive vacuoles were not found, we detected bacteria in various stages of degradation.

The position of the prominent epithelium with the bacteriocytes in the posterior mantle cavity is so far unique: All hitherto known endosymbiotic bacteria within Gastropoda were found either in ctenidia (Neomphalidae, Peltospiridae, Provannidae) or directly associated with the gut (Bathyphytophilidae) or spread in the haemocoel (Lepetellidae). In contrast, a parallel case might exist in the monoplacophoran *Laevipilina antarctica* with likewise pallially situated bacteriocytes. Future studies on other genera of Orbitestellidae should clear up, whether the bacteriocyte system is restricted to hot-vent inhabitants or more wide-spread in the family.

T2

TEMPO AND MODE IN LAND SNAIL EVOLUTION: THE ORIGINS AND LIMITS OF DIVERSITY

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This symposium aims to go beyond the cataloguing of land mollusc diversity in different regions (a task far from complete) and to look at the mechanisms of diversification at different geographical, historical and taxonomic scales. New molecular phylogenies related to environmental history illuminate our understanding of speciation, and especially the roles of refugia and island colonisation and history on the rate of diversification. The contrasts and concordances among molecular, anatomical and conchological variation tell us something about the nature of the evolutionary forces involved. Population genetic studies tell us about the balance of drift, migration and selection among populations of the same species. Changes in faunal composition and diversity can be studied directly via the fossil record. Ecologically, studies on life histories, microhabitat preferences and morphological spectra at many scales help us establish the assembly rules for local faunas. New modelling techniques enable us to understand the interplay between historic, contingent events such as Pleistocene climate changes and present ecological constraints on species' distribution and occupancy. Invited talks and posters contribute to all these approaches.

T2.O1

DIVERGENT MITOCHONDRIAL CLADES OF SNAILS WITH A *TROCHULUS HISPIDUS* PHENOTYPE. HOW TO CONFINE A SNAIL SPECIES?

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For studying evolution it is compulsory to recognize species. However, for some taxa, this is not straightforward. An example is the *T. hispidus* complex in which species delimitation was proven to be difficult.

Hence we took a broad approach including individuals of *T. hispidus* from 129 locations covering a broad geographic distribution with a focus on the Eastern Alps and surrounding areas for morphological and genetic investigations. From 387 individuals a fragment of the mitochondrial COI gene was analyzed. We also included related taxa in our study: *T. oreinos*, *T. striolatus*, *T. coelomphala*, *T. clandestinus*, *T. biconicus*, *T. villosulus* and *T. villosus*. From 100 selected individuals representing different COI clades we analyzed a fragment of the mitochondrial 12S and 16S genes. Furthermore, nuclear sequences (including parts of the 5.8S, ITS2 and 28S) were analyzed.

The mitochondrial variation of specimens determined as *T. hispidus* (on the basis of morphological and anatomical examination) was exceptional high (max. p distance 18% in COI). The COI sequences of *T. hispidus* revealed nine distinct clades. Seven clades can be assigned to restricted, partly overlapping geographic regions, while two clades show a widespread distribution with no clear geographic patterns. In several cases quite divergent clades occur even at the same sampling locality.

In the combined COI-16S-12S tree some related species, which are morphological well differentiated, are intermixed with *T. hispidus* clades. Hence *T. hispidus* is paraphyletic. The nuclear sequences do not differentiate between any of the mitochondrial clades, except *T. oreinos*. Thus, the nuclear data provide no argument for species status of any of the *T. hispidus* clades. For final conclusions on the existence of cryptic species and species delimitation it will be necessary to investigate possible gene flow between all syntopic clades in detail.

This work has been funded by the Austrian Science Foundation (P19592-B17).

T2.O2

ENVIRONMENTAL CHANGES IN THE COURSE OF TIME: CONSTRAINTS ON ECOLOGICAL SPECIATION IN *MURELLA MURALIS*

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Land snails offer not only the opportunity to admire the wide spectrum of colour and shapes of their shells, but foremost to understand how and why evolutionary processes proceed and lead to diversity. The debate about speciation and diversification currently focuses on the relative importance of factors driving population differentiation. While many studies are increasingly producing results on the importance of selection, little is known about the interaction between drift and selection. Another point that deserves empirical exploration is how and to what extent historical factors affect speciation in interactions with selection and in the presence of environmental changes. To investigate these questions, we quantified variation on a fine geographical scale analysing morphological (shell) and genetic datasets coupled with environmental data in the land snail *Murella muralis* (Müller 1774), endemic to the Mediterranean island of Sicily. The species exhibits an impressive morphological diversity with shell shapes that vary from globular to keeled-flat, even over relatively restricted geographical areas. This spectacular variation in shell shapes has been documented in many other groups of land snails, especially in the Mediterranean area (at least 18 species), however its evolutionary causes are not yet understood. Analysis of a fragment of the mitochondrial DNA Cytochrome Oxidase I gene (COI) and eight nuclear microsatellite loci showed that genetic variation is highly structured at a very fine spatial scale by local palaeogeographical events and historical population dynamics. Molecular clock estimates provided a framework of palaeogeographical events responsible for the observed geographical variations and migration routes. Finally, we showed for the first time well documented lines of evidence of selection in the past, which explains

divergence of land snail shell shapes. We suggest that time and environmental changes in the course of time acted as constraints on the ecological speciation.

T2.O3

PHYLOGEOGRAPHY OF *CIRCASSINA FRUTIS* (GASTROPODA: HELICOIDEA: HYGROMIIDAE) IN THE CAUCASUS REGION

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The *Circassina frutis* complex endemic to the Caucasus region and the Eastern Pontus is unique among hygromiid land snails by exhibiting a polymorphic dart apparatus, i.e. either a complete dart apparatus with a dart sac plus an accessory sac and glandulae mucosae is present or one or both of these structures are reduced. Based on the different configurations of the dart apparatus, three groups are distinguished, which are usually classified as subspecies. The geographic distributions of these groups interdigitate in Western and Central Georgia. We investigated phylogenetic and phylogeographic patterns inferred from mitochondrial COI and 16S rDNA sequences across most of the range of *C. frutis*. None of the formally recognized taxa proved to be monophyletic in the mitochondrial tree. However, a subdivision in geographically coherent clusters largely corresponding to the morphologically defined groups was observed. Several processes might have caused the inconsistencies between the morphologically defined taxa and the pattern in the mitochondrial gene tree: 1) gene flow between different groups in contact zones or as a result of anthropogenic dispersal, 2) incomplete lineage sorting, and/or 3) independent reduction of parts of the dart apparatus, Moreover, the pattern of inheritance might be affected by sexual selection, because the presence of a complete dart apparatus presumably increases the likelihood of successful paternity. Multi-locus (AFLP) markers will further elucidate the phylogeographic structure of the *C. frutis* complex and, thus, increase our understanding of the processes involved at the brink between subspecific diversity and speciation.

T2.O4

SPECIES DIVERSIFICATION IN THE SOUTH ASIAN LAND-SNAIL GENUS *CORILLA* (PLECTOPYLOIDEA: CORILLIDAE)

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Using a multi-gene, molecular systematic approach we are studying species diversification in the land-pulmonate genus *Corilla*. This snail is a putative Gondwanan relict, with extant species being restricted to the rainforests of Sri Lanka (10 species) and the Western Ghats of India (1 species). Of the 10 nominal morphological species recognised from Sri Lanka, all of which are endemic to the southern and central parts of the island, 4 occur in lowland rainforest (*Corilla adamsi*, *C. carabinata*, *C. colletti* and *C. lesleyae*), and 6 in montane rainforest (*C. beddomeae*, *C. erronea*, *C. fryae*, *C. gudei*, *C.*

humberti and *C. odontophora*). To date, molecular analyses have been focussed on three mitochondrial markers, 16S rRNA (~480 bp), NADH dehydrogenase 1 (ND1, ~470 bp), and cytochrome oxidase 1 (CO1, ~680 bp), the nuclear gene-region ITS1 (ribosomal internal transcribed spacer 1), and the adjacent 1460 bp-long region of the ribosomal RNA gene cluster. Preliminary phylogenetic analyses of molecular data from 9 morphospecies of *Corilla* and 2 outgroup taxa (*Sculptaria* and *Plectopylis*) are ongoing; these are based on Neighbour Joining, Maximum Likelihood, and Bayesian approaches. Initial results indicate that *Corilla* is a strongly-supported clade, and that at least 5 of the 9 species of *Corilla* included in our study are monophyletic. They also suggest that species diversification in the genus may have involved climatic/habitat niche shifts between the montane and lowland zones of Sri Lanka, on at least two separate occasions.

T2.O5

GETTING THE PHYLOGENY OF *THEBA* STRAIGHT AND CAN FOSSILS MEANINGFULLY BE INTEGRATED IN ORDER TO DATE INTERNAL NODES?

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Three years ago a phylogenetic analysis of the land snail genus *Theba* based on COI and ITS1 suggested that the genus evolved and initially radiated on the Canary Islands before colonizing the African continent and from there the Iberian Peninsula. However, node support was only moderate and the signal of the nuclear gene fairly weak. Therefore, we decided to add more samples and analyze AFLPs. The resulting trees now turned the picture upside down and indicate a continental origin of *Theba*. The Canary Islands were largely colonized in the order of their appearance. Based on geometric morphometrics we compared shell morphologies of ancestral taxa reconstructed at internal nodes and of fossils with the aim to infer the phylogenetic position of the fossils to be used for calibrating the tree. However, convergence and punctuated equilibrium indicate that fossil shells cannot be unambiguously placed on a phylogeny. Thus, only island ages could be used for calibration.

T2.O6

A SHORT HISTORY OF THE GENUS *LEIOSTYLA*

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Extant species (46), included in the genus *Leiostyla* or in the genera *Leiostyla* and *Euxinolauria*, inhabit the Caucasus with adjacent areas (14 species) and the Macaronesian islands (Madeira: 28 species, Azores: 2 species, Canary Islands: 2 species). The two areas are refuges where relic Tertiary forests have been preserved. One species is found on the western fringes of Europe and northern fringes of Africa. The fossil record from central-western Europe includes four species from deposits dated as Upper Miocene to very early Pleistocene which would suggest a once continuous range, with subsequent extinction of most European species. Anatomical studies made it possible to distinguish a few phylogenetic lineages; each inhabits both areas, and each area holds representatives of more than one lineage. This indicates radiation and dispersal preceding the extinction in the intervening area. Our phylogenetic analysis used COI and 18S sequences of 24 species of *Leiostyla* (52% of all extant species) and *Lauria* as out-group. Biogeographical and anatomical information as well as fossil record, combined with sequence analysis, revealed the following history of *Leiostyla*. The genus came into existence in the Early Tertiary or even earlier, in central-western Europe. Its subsequent radiation and differentiation into several phylogenetic lineages was accompanied by dispersal, the Macaronesian islands being colonised repeatedly, starting ca. 15 million years ago. During the Pleistocene glaciations the European members of the genus, except *Leiostyla anglica*, became extinct.

T2.O7

EVOLUTIONARY HISTORY OF A VANISHING RADIATION: THE PACIFIC ISLAND TREE SNAIL FAMILY PARTULIDAE

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Partulid tree snails are endemic to the high islands of Oceania. The family contains three genera, each with highly distinctive distributions, and half of its nominal species diversity occurs on a single Eastern Pacific hot spot archipelago, the Society Islands. Partulidae has experienced catastrophic extinction in recent decades primarily due to misguided biological control programs involving introduced snail predators. Museum, captive (zoo) and recently sampled field specimens were used to genotype 54 of the ~128 recognized species, including many extinct or extirpated taxa, from 14 archipelagos that span the familial range. The goal was to flesh out broad scale (range wide) and fine scale (within-Society Islands) phylogenetic relationships of *Partula* and *Samoana*, the two widespread genera. Our data indicate that the genus *Partula* is paraphyletic: Palauan members are phylogenetically distinct from their congeners and are sister to the derived genus *Samoana*. These two genera have experienced very different diversification patterns across Oceania. Originating at the western edge of the familial range, *Samoana* is a relatively recent arrival to eastern archipelagos (Society, Austral, Marquesas) where it exhibits a stepping-stone phylogenetic pattern and has proven much more adept than *Partula* at both intra- and inter- archipelago colonization. The pronounced east-west geographic disjunction exhibited by the genus *Partula* is recovered in our gene trees, indicating that it may stem from a single long-distance dispersal event. *Partula*'s high nominal taxonomic diversity in the Society Islands is a product of a long history of within-archipelago diversification, but the results are inconsistent with a progression rule model of speciation developed for Moorean and Tahitian taxa. The importance

of isolation for partulid diversification is evident in time-calibrated phylogenetic trees where remote archipelagoes least impacted by continental biotas bear the oldest clades. This also explains their rapid collapse following anthropogenic introduction of continental predators.

T2.O8

TRUNCATELLOIDEAN GASTROPODS INFORMING GEOLOGY: CONTINUOUS EMERGENCE OF ISLANDS OF VANUATU ALREADY SINCE THE MID PLIOCENE

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The archipelago of Vanuatu situated at the border of Australian and Pacific plates has a complex history of sea level fluctuations. These fluctuations were caused by tectonic events including volcanism as well as glaciation cycles. Recently, the biota of the archipelago has been estimated to be not older than 2 Myr. However, the geological literature is fairly ambiguous when it comes to the question since when the islands have remained above sea-level. We reconstructed the phylogeny of truncatelloidean freshwater gastropods from seven islands of the archipelago based on one nuclear and two mitochondrial fragments. The phylogeny was time calibrated using a substitution rate published for COI of confamilial taxa from New Zealand. The phylogenetic analysis revealed three clades. Species from all islands except Erromango forming the youngest clade with an age of 0.68 Myr were hardly differentiated probably due to incomplete lineage sorting. The age of the sister clade with two species from Erromango was estimated to 2.62 Myr, and the most basal split concerning species from Espiritu Santo had an age of 4.81 Myr. These data provide a completely new frame for the analysis of origin and evolution of Vanuatu's biota.

T2.O9

AN OUTSTANDING RADIATION OF HELICINIDS ON THE GAMBIER ISLANDS, FRENCH POLYNESIA: EXTINCT BEFORE ITS DISCOVERY

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While the land snail families Partulidae, Achatinellidae, Endodontidae, and Amastridae are known as highly vulnerable to alterations of their environment with significant numbers of already extinct species, the operculate Helicinidae so far did not share this „fame" except for certain Hawaiian representatives.

Recent studies that further complete the systematic revisions of the land snail fauna of the Gambier Islands revealed a remarkable radiation of ten helicinids on this small island group, with up to seven species co-occurring in a single locality and up to eight species on a single island. Nine of the ten species are new to science, most are minute and, at 1.5 mm, rank among the smallest, if not the smallest, species in the family world-wide. However, this radiation had already become

extinct (nine of ten species) several decades before the expansion of the predatory snail *Euglandina rosea* in the Pacific, and even before the species were collected for scientific study, i.e. mainly by the Bishop Museum *Mangarevan Expedition* in 1934 and by the second author in 1997. For all Gambier Island land snails revised so far it is found that massive extinctions of these endemics had already taken place in the 19th century, but have remained largely unrecognised and undocumented. The new case of the lost helicinid radiation increases the number of documented global mollusc extinctions by almost 2 %. But not just species were lost: Several of the newly recognised helicinids have apertural barriers and one has opercular apophyses – character states not previously documented in any Pacific species in the family. Whereas the only surviving Gambier species belongs anatomically to the genus *Sturanya*, relationships of the other – conchologically diverging – species can now only be discussed by indirect evidence.

T2.O10

PATTERNS OF GENETIC RELATEDNESS AMONG POPULATIONS OF THE GENUS *CERION* (CERIONIDAE: GASTROPODA: MOLLUSCA) IN THE FLORIDA KEYS

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The family Cerionidae has long been known for its exceptional morphological diversity and the profusion of species level taxa, especially in the Recent faunas of Cuba, the Bahamas, and Cayman Islands. Fossil records of the family date to the Oligocene of western Florida, yet it is limited to a single species, *Cerion incanum* (with four subspecies or forms) in the Recent fauna of Florida that inhabits near shore vegetation along a crescent-shaped, archipelago of islands spanning 240 km that extends from Key Biscayne to Key West. A number of authors have suggested that *C. incanum* is not directly descended from the species of the Florida Oligocene, but rather from Cuban Cerion that recolonized southern Florida following the inundation of this region during the interglacial high stands during the Pleistocene. More recently, 13 non-native species from the Bahamas, Cuba, Puerto Rico, and Curaçao were intentionally introduced into the Florida Keys and Dry Tortugas between 1912 and 1924 by Paul Bartsch as part of a long-running and well-documented series of experiments. Some of these introductions persist today as pure colonies, others as hybrids with the native *C. incanum* or with each other. We report on the relationships of *Cerion incanum* and its constituent taxa based on partial sequences of the cytochrome *c* oxidase I and 16S rDNA genes from 17 populations spanning the geographic range of the species that include the type localities of all described subspecies and forms. These data are used to determine the spatial scale and patterns of genetic connectivity across the entire range of this species, and correlate these patterns to the geology and origin of the Florida Keys.

T2.O11

ADAPTATION IN LAND SNAIL SHELL SHAPE - 30 YEARS SINCE GOODFRIEND

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The shell shape of land snails is exposed to a wide diversity of selection pressures. These include abiotic ones (damage from falling, overheating, desiccation) as well as biotic ones (predation by shell crushing or drilling predators, for example). Since the last review of adaptation in land snail shell shape (Goodfriend, 1986. *Syst. Zool.*), much new work has appeared. In this presentation, we aim to review the advances made in the past three decades. In addition, we also aim to advocate a change in our perspective on the adaptive evolution of land snail shells. In contrast to earlier approaches, we do not just take an atomistic approach, examining shell shape response to individual selection pressures, but we also address how land snail shells show an integration and compromise among multiple, simultaneous demands from the environment. We hope this approach will provide a better understanding of how a limited set of adaptive inputs can allow the evolution of such a tremendously diverse set of conchological outcomes. Since land snail systematics is still very much focused on shell shape and form, we think our approach will provide a valuable tool for those involved in malacological biodiversity studies.

T2.O12

LAND SNAIL RICHNESS AND ABUNDANCE ALONG A SHARP ECOLOGICAL GRADIENT AT TWO SAMPLING SCALES: DISENTANGLING RELATIONSHIPS

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The abundance of individuals and the species richness of samples of land snails are usually positively correlated. This correlation may be an artefact of sample size, but it may also reflect the similarity in microhabitat preference of many species. Biotic interactions (competition) might also influence this relationship: an upper limit to co-existence at a particular scale. Here, I model the relationships between abundance, richness and environmental factors in the snail faunas of treeless fens. There is a broad range of calcium content in such fens, best estimated by water conductivity; this variation accounts for much of the difference in faunal richness and composition among such fens. The models considered two scales of sampling: (i) a 12 litre sample collected at 4x4 m^2 plot (187 samples) capturing at least 80% of the site's known species pool, and (ii) a sampling of 25x25 cm^2 plot (115 samples) usually capturing less than 40% of the site's species pool. At the larger scale, species richness was better predicted by conductivity than by abundance, but this was reversed at the smaller scale, although the sampling in the latter was theoretically total at the quadrat level. In both cases, the best fit model indicated

a unimodal relationship between richness and abundance. At small scales, not all species are represented, even when abundance is high. When the sampling effect was removed by using complete site arrays, the number of species responded to mineral richness gradient more tightly than total densities did; a substantial part of the total variation related exclusively to environmental conditions, even though there remains a significant increase of species richness with increasing number of individuals. The hump-shaped relationship between the numbers of live individuals and species raises a classical question about interspecific competition in land snail assemblages.

T2.O13

DISCOVERING FACTORS RESPONSIBLE FOR THE EXISTENCE OF TERRESTRIAL MOLLUSCAN ASSOCIATIONS AND ROLE OF SOME OF THOSE FACTORS IN SPECIATION.

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Molluscs with similar ecological preferences co-occurring in a certain biogeographical region form an association in a particular type of habitat. It is important to note that these are molluscan habitats, which are not necessarily the same for other organisms. Thus, recognition of the associations should derive from the analysis of molluscan co-occurrence and not from our understanding of environmental factors and/or distribution of other organisms (plants for example). It is also important to recognise and to separate ecological and biogeographical components in the results of such analyses.

The results of co-occurrence analyses of terrestrial molluscs of some areas of Kopet Dag (Central Asia), central part of Northern Caucasus, Northern Mozambique, Laos, Cebu (Philippines) and Nimba (West Africa) show that amplitudes of fluctuations in humidity and temperature seem to be the main factors responsible for the existence of terrestrial molluscan associations. Although those associations comprise different species in different biogeographical regions, the following types of associations often can be recognized. Mountains at higher altitudes are inhabited by associations of molluscs that can tolerate low temperatures and often represented by the relicts of glaciofluvial phases of the Quaternary. Molluscs that can tolerate (and/or to avoid) regular desiccation usually form associations in open areas (grasslands and rocky slopes), while molluscs more sensitive to changes in humidity usually form associations in forested areas. Associations of forested areas often reflect different stages of damage/recovery of native habitats since fluctuations of humidity are usually higher in degraded and secondary forests. Limestone and non-limestone areas (as well as different substrate types in general) could support separate molluscan associations in the same region.

Natural selection often favours extremes of size variation when larger molluscs have survival advantages on open surfaces and smaller molluscs have survival advantages in micro cavities and crevices.

T2.O14

SYMPATRY WITHOUT CO-OCCURRENCE: EXPLORING THE PATTERN OF THE DISTRIBUTION OF TWO *HELIX* SPECIES IN GEORGIA USING ECOLOGICAL NICHE MODELING APPROACH

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Two species of the genus *Helix* (Mollusca: Gastropoda) are widespread in Georgia. One species *Helix lucorum* has Mediterranean distribution whereas the other – *Helix buchii* is Caucasian endemic typically associated with broadleaf forest. In spite of their sympatry within Georgia, they never co-occur. Furthermore, in contrast with *H. buchii*, *H. lucorum* is manly found in areas subject to human disturbance. With these two congenerics there is another large helicoid species (*C. calligera*) which also is widespread in Georgia. *C. calligera* is usually found with both species of *Helix*. Based on the pattern of distribution these three species it can be assumed that interspecific competition might play a pivotal role in shaping the distribution of two *Helix* species. In order to test this hypothesis, I used predictive ecological niche models (ENM) based on the Maximum Entropy algorithm. ENMs showed that the niches of these species in Georgia are significantly different but not fully separated (~15-36% overlap). The distributional pattern of *H. lucorum* should not be considered truly natural in Georgia and may be a synanthropic phenomenon. The fact that these two *Helix* species never co-occur could be a result of competitive relationship and the lack of natural habitats for *H. lucorum* whereas *H. buchii* usually avoids anthropogenic disturbance. However the competition remains most useful informative assumption to explain the distributional pattern of *H. lucorum*.

T2.O15

PREDATION ON GREEK *ALBINARIA* (PULMONATA: CLAUSILIIDAE) AS A POSSIBLE DRIVER OF SPECIATION

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Albinaria is an extremely speciose genus of over 100 land snail species, containing an impressive diversity in conchological and anatomical characters. Yet this *Albinaria* radiation cannot easily be explained by niche differentiation, as all species occur in rather similar limestone habitats in Greece and surrounding countries, feeding on algae. Interestingly, *Albinaria* populations usually occur allopatrically, with small distributional ranges, resulting in mosaic distributions. This may indicate that competitive interactions between populations, due to exploitation of the same niche, prevent sympatrical occurrences. The allopatric distributions might also imply that each *Albinaria* population is adapted to its own unique local environment, but there appears to be much too little ecological differentiation between the ranges of *Albinaria* species for this to be plausible.

So the *Albinaria* radiation might be driven by mechanisms unconnected to the abiotic environment, such as predatory pressure, sexual selection or genetic drift.
This project aims to assess the contribution of predation to the speciation within the genus. *Albinaria* snails are mainly preyed upon by carnivorous *Poiretia* snails and *Drilus* beetle larvae. Small, circular holes are also regularly found, but the maker of these holes remains unknown. The distinctive predation marks enable us to estimate predation rates in *Albinaria* populations by collecting empty shells. Samples were taken at rare zones of overlap or hybridization between two species. The species pairs were selected to differ in conchological characters. *Poiretia* predation rates reached up to 21%, *Drilus* predation up to 25% and circular hole predation up to 36%. Species with high rib prominence showed significantly higher *Poiretia* predation rates versus species with low rib prominence, as well as dextral species versus sinistral species. There were many other significant differences in predation rates between species, but these did not show consistent patterns connected to conchological characters.

T2.O16

REFUGIAL POPULATIONS OF GLACIAL RELICT *VERTIGO* SPECIES IN CENTRAL EUROPE

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During the Quaternary glaciations many cold-adapted species experienced broader distribution in central Europe, comparing to their modern distribution which is usually restricted to northern Europe and isolated refugia at lower latitudes. In this contribution we focus on snail fauna of groundwater-fed fens – habitats which can serve as typical refugia for glacial relict species. Nevertheless, fens belong to the most seriously threatened habitats of the temperate zone, and probably because of their fragmentary character we still know only a little about their biota. Recent researches have shown that fens harbor highly diverse mollusc assemblages, and yet the majority of fen areas remain unexplored. However, between 2010 and 2012 we discovered several new isolated occurrences of glacial relict *Vertigo* species living in fens. *V. geyeri*, traditionally referred to as boreo-alpine species, was found at more than 20 sites in Polish lowlands and 15 sites in Bohemian-Moravian Highlands. The species is restricted to open calcareous fens with stable water regime, similarly to *V. genesii* which is however confined to higher altitudes. In central Europe, *V. genesii* was known only from the eastern Alps, until a few isolated populations in the western Alps were discovered. *V. lilljeborgi*, unlike the majority of the European land snail fauna, prefers rather calcium-poor conditions. Except the northern Europe, the species was known from only five isolated sites. However, in 2012 new occurrences were documented in the Alps and in the Czech Republic. Although formerly regarded as European endemics, these *Vertigo* species were also found to occur in central Asia, which suggests their much larger ranges during the Late Glacial. With respect to the rarity and high conservation value of central European populations of these species, negative influences affecting their refugial and globally threatened habitats will be discussed as well.

T2.O17

CEPAEA – CHANGES IN SPECIES DISTRIBUTIONS AND MORPH FREQUENCIES ON THE MARLBOROUGH DOWNS

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In 1960 and 1961 Arthur Cain and John Currey surveyed *Cepaea* on the Marlborough Downs, an area of diverse habitats in central southern England. Focussing primarily on morph frequencies in *C. nemoralis*, they identified so-called "area effects" in which one morph predominated regardless of habitat type. Their paper, published in 1963 became a classic, prompting a considerable body of work attempting to understand the reasons for this unexplained pattern. In 1985, Cowie and Jones re-surveyed the area. The range of *C. nemoralis* had declined and it was being replaced, especially in lower locations, by its congener *Cepaea hortensis*. The area effects were still intact but morph frequencies in both species had changed overall, more so in *C. nemoralis* than *C. hortensis*, with paler forms increasing in frequency.

We re-surveyed the area in 2008 and 2009. The most striking change was the continued and dramatic expansion of *C. hortensis* and decline of *C. nemoralis*. Morph frequencies have continued to change, in the same directions as between 1960/61 and 1985, although the trend in *C. hortensis* is slight.

Changes in colour and banding patterns in *C. nemoralis* have also been modeled using a 3-locus Wright-Fisher model. Using a Bayesian approach, we are able to make inferences about selection coefficients and effective population sizes in the sampled populations.

While the change in morph frequencies is consistent with a hypothesis based on global warming, the change in species distributions, with the more cold-adapted species, *C. hortensis*, expanding its range, is contrary to a global warming hypothesis, and possibly explained by habitat changes.

T2.O18

RAPID EVOLUTION IN LAND SNAILS

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Land snails are proverbial for their low dispersal abilities. In such species, active migration in response to unfavourable environmental change is less effective than in more mobile ones, and adaptation is likely to play an important role. Recent studies report on shifts in the genetic composition of land snail populations occurring within a few decades or an even shorter time. Evolutionary changes in shell colour and banding pattern in response to climatic changes have been shown in *Cepaea nemoralis*, *C. hortensis* and *Theba pisana*. In *Mandarina anijimana*, changes in shell shape, size and colour occurred as a result of

habitat shift in response to increased predation pressure. Growing evidence indicates that in the land snails evolutionary changes on contemporary time scales might be more a commonplace than an exception. In changing environments such highly localised genetic changes might be more important for snails than shifts in distribution, and they are facilitated by the low rate of gene flow even among populations that may be only hundreds of metres apart.

T2.O19

UPSTREAM OR DOWNSTREAM? LAND SNAIL, *VENTRIDENS LIGERA* (SAY, 1821) POPULATION STRUCTURE IN THE POTOMAC RIVER WATERSHED

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Organisms that live in or near watercourses often disperse with the flow of the water and therefore experience asymmetric gene flow. Land snails have limited ability to disperse over land and those living near streams and rivers may disperse downstream. I analyzed genetic diversity in land snail, *Ventridens ligera*, populations over 300 km of the Potomac River watershed to determine if gene flow is asymmetric. A low level of genetic differentiation (mean .ST < 0.0494) was present between the rivers flowing into the Potomac River however no clear gradient of increasing genetic diversity with downstream flow was found suggesting that gene flow is occurring both upstream and downstream. Based on this finding, I suggest that *V. ligera* are rafting downstream on plants or debris reaching more distant habitats in combination with limited terrestrial movement to nearby habitats upstream, downstream or further from the river.

T2.O20

INVENTORYING THE LAND MOLLUSCAN FAUNA OF NIGERIA RAINFOREST: THE STORY SO FAR

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The loss of tropical rainforest and its biodiversity is one of the principle drivers of modern day extinction. Knowledge of the Afrotropical land mollusc faunas, previously perceived to be grossly under sampled, is gradually increasing. In Nigeria, over 100 species have been recorded. Many species are still in the identification process and many new species continue to be described. Mean alpha diversity differ between forest types based on land usage. Species richness ranged from 4 to 34 species and from 8 to 422 individuals per plot. Primary forest and forests on limestone hills are the most species rich while agricultural plantations (oil palm and rubber) have the least molluscan diversity. Threats to land molluscs include deforestation, conversion of rainforest to oil palm plantation, urbanization, pollution and limestone quarrying. Conserving the remaining limestone hills and old-growth forest in national parks will help in protecting many species that are threatened.

T2.O21

USING PREDICTIVE MODELS OF SPECIES DISTRIBUTION AS A TOOL FOR ECOLOGY AND CONSERVATION OF MADEIRAN LAND SNAILS

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The Madeiran archipelago comprises one of the most diverse mollusc faunas of oceanic Islands, with 254 *taxa* (67 % endemic), including many single Island endemics dispersed in a wide range of habitats. This fauna has engaged substantial changes in its composition during time, due to climate change, habitat loss and fragmentation. Despite 200 years of work on Madeira land snails, there is still a lack of knowledge on distribution (mostly on endemic and threatened species) and on the significant factors, processes and variables distressing this distribution.

To overcome the typical sparseness of distributional data, species distribution models where applied via MAXENT software, which related species distribution with the geographic and/or environmental predictors by means of maximum entropy algorithm. 114 endemic species were modelled, employing twenty-two predictive variables and biological data from the BIOBASE (Madeira Archipelago Biodiversity database).

New potential distribution areas were identified for all the species studied, and in 63% of the cases the presence of the species on these areas was validated.

The model suggests a marked geographic differentiation on Madeira fauna, recognizing 5 distinct faunas within costal, forest and alpine regions. It also validates the influence of shell size and form on habitat and surface selection and the apparent anthropophilic influence on endemic distribution.

For 56 rare and threatened species, new distribution areas were identified, that can be used on a species translocation program. For conservation prioritization purposes, species distribution was evaluated according to two climate scenarios on two different periods (2040-69 and 2070-2099), targeting those species with greater probability of survival.

In conclusion, predictive models of species distribution emerge as a valuable tool for tackling the lack of distributional information on Madeiran land snails, helping to identify ecological and geographical patterns at a regional scale and allowing the development of species conservation strategies and measures under current and future climates.

T2.O22

BIOGEOGRAPHICAL PATTERNS IN THE LAND SNAIL FAUNA OF THE CAUCASUS REGION

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The Caucasus region is one of the most important biodiversity hotspots worldwide. About 330 land snail species are known from the Caucasus region, of which

approximately 75% are endemic. We compiled the distribution data of the Caucasian land snails from museum collections, own field work and published locality data. For several species we found a considerable extension of their known range. Based on this comprehensive dataset, we analysed factors influencing the distribution of diversity across the region and tested whether there are non-random distribution patterns. Biogeographic elements that are characterized by endemic species with similar ranges were delimited. We discuss whether these elements reflect barriers that shaped the endemic fauna by causing vicariance events. We show that the geographic ranges of the Caucasian land snails are nested and that the centres of nestedness might indicate the location of Pleistocene refugia. The origins of the Caucasian land snail fauna as well as the importance of the Caucasus region as a source for the colonization of adjacent areas are outlined.

T2.O23

PALAEOBIODIVERSITY AND PALAEOBIOGEOGRAPHY OF EUROPEAN SNAILS: A PLEISTOCENE PERSPECTIVE

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Quaternary climatic cycles have had a strong effect on species distributions in general and on continental molluscs expansion in particular. During glacial periods most non-marine molluscs vanished from North-West Europe but during interglacial periods they progressively spread from refugia to recolonize these once periglacial territories. Interglacial malacofaunas thus provide a good means of evaluating biogeographical and biodiversity changes during the Pleistocene. In Northern France calcareous tufas and fluvial sequences have yielded rich molluscan successions allowing the reconstruction of faunal history for different interglacial periods from the Middle Pleistocene up to the Holocene. Specific assemblages of land and aquatic snails, including several species that are now extinct or beyond their modern range, can be recognized for each temperate episode. Detailed Pleistocene malacological successions are described from two thick tufa sequences, one of Middle Pleistocene age dated to Marine Isotope Stage (MIS) 11 (424-374 ka) and a second from the Last Interglacial correlated with MIS 5e (~125 ka). At both sites the appearance of forest species occurs as successive events related to the present-day geographical ranges of the component species. Those of the earliest forest phase at the beginning of the interglacial consist of species with North and West European ranges. Species with Central European distributions appear just before the warmest phase, whereas Eastern and Southern European species appear only later during the optimum itself. Comparison of French data with other European malacological successions from similar contexts shows that total number of species decreases between MIS 11 and the Holocene, and is especially marked for shade-demanding species. Geochemical analyses from the tufa sequences at Caours (MIS 5e) and La Celle (MIS 11) have confirmed the coincidence of maximum diversities with the warmest temperatures.

T2.O24

DEVELOPMENT AND LOSS OF LAND SNAIL DIVERSITY DURING THE LATEGLACIAL AND HOLOCENE: A PERSPECTIVE ON THE MODERN FAUNA OF NW EUROPE

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The pattern of colonization of land snails during the Lateglacial and Holocene (the last 13,000 years or so) is now reasonably well known from NW Europe. Records from the Lateglacial are derived mostly from stratified colluvial sequences that have formed on Chalk bedrock. The more informative Holocene successions are those obtained from tufa deposits, since rich assemblages of land snails lived on, and were entombed by, the actively accreting tufa surface. Such deposits therefore provide faithful reflections of the living communities from which the fossil assemblages were derived. Some of the Lateglacial and tufa sequences are waterlogged and have furnished pollen records, which provide the vegetational background to the observed faunal successions. Many waterlogged sequences have also yielded material suitable for radiocarbon dating, so that detailed chronologies are now available from many sequences. The highest diversities were attained during the mid Holocene (6000-8000 ^{14}C yr BP), when up to 35 species were recovered from a single sample. This pattern is also true of northern France, although there are some differences in species composition. These mid Holocene assemblages are richer than the most species-rich localities in Britain where maximum values rarely exceed 30 species. The same situation appears to be true of Northern France, although the differences in diversity between mid Holocene and modern forest assemblages are less marked, although there are still some significant differences in species composition. Several species that were once widespread during the mid Holocene (e.g. *Vertigo pusilla*, *V. alpestris*, *Leiostyla anglica*, *Ena montana*) are now much less common, but it is not clear whether such declines result entirely from human-induced changes in landscape or whether climatic or other factors are involved.

T2.O25

PUNCTUATED EQUILIBRIUM ALIVE OR PLAIN ISLAND SPECIATION?

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Punctuated equilibrium, a theory of phenotypic change and stability proposed as an alternative to the Darwinian paradigm of gradual evolution over time, systematized

Darwin's acceptance of two tempos on the evolutionary process and stressed the gradual nature of the change phase. Species are interpreted as individual entities which are born, age and die, reflecting various degrees of stability during those stages: a brief pulse of variance at birth – punctuation –, followed by a long period of reduced variance – stasis. PE was proposed within a paleontological framework and the speciation process underlying it was peripatry. The surge of the peripatric event was later associated to strong environmental disturbance. Our work on the Azorean endemic oxychilid pulmonate subgenus *Drouetia* suggests that this may be an appropriate model to explore the conditions and predictions inherent to PE: it lives in all islands and exhibits abundant intra- and inter-island phenotypic variability. The archipelago constitutes an appropriate setting: spread along 600 km, clustered in three groups of islands, their ages varying from 250 Ky to 8 My. Peripatric (intra-island) events can be related to volcanic activity. Inter-island dispersal will be evaluated as a factor accounting for intra-island variability, and its impact on the tenets of punctuated equilibrium assessed.

The 5 islands of the Central Group (ages 250 Ky to 2.5 My) show a complex pattern of 2-3 cryptic species-level taxa per island, with inter-island dispersal playing a major role in intra-island variability; in this situation, Darwin's original "island speciation model" appears to hold an appropriate explanation. Flores (Occidental Group, 2.15 My) shows four morphologically distinguishable species-level taxa, one of which widely spread and very variable. São Miguel (Eastern Group, 4 My) has various species-level taxa reflecting the complex volcanic history of the island; the youngest clade is anatomically very variable and widespread. Both situations may be interpreted as cases of punctuation as proposed by the PE model. Santa Maria (Eastern group, 8 Ma) has three morphologically and anatomically distantly related species with low intra-species phenotypic variability, as well as the related monotypic, little variable subgenus *Atlantoxychilus*; such inter-taxon morphological difference and intra-taxon low morphological variability is interpreted as a stasis phase.

(Acknowledgement: Project PTDC/BIA-BDE/73467/2006 – Speciation in *Drouetia*: evidence of punctuated equilibrium? (Fundação para a Ciência e a Tecnologia, Portugal).

T2.O26

THE PUNCTUATED EQUILIBRIUM THEORY: EVIDENCE FROM GASTROPODS REVIEWED

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Punctuated equilibrium evolution (PEE) was established by Eldredge and Gould in 1972 as "a model for discontinuous tempos of change (in) the process of speciation and the deployment of species in geological time". This model summarized the paleontological observation that phylogenetic lines in the fossil record often show long periods of morphological stasis, punctuated by rapid morphological change associated with speciation events. PEE is frequently seen as a contrast to phyletic gradualism and triggered much debate on pattern and process of speciation in general.

Since its proposal, PEE has been debated intensively and the search for examples continues. A recent re-examination of the foundational Plio-Pleistocene Turkana Basin molluscs casts doubt about their supporting the theory because the rapid morphological changes in the record were shown to represent multiple invasions of unrelated taxa rather than changes from ancestor to descendant. This example shows that various issues, not in the least sampling problems, may bias our perception of the tempo of evolutionary changes.

Our paper discusses modes of evolution (and hence evidence for PEE) in freshwater gastropods, both modern and fossil. We particularly focus on Lake Ohrid (Recent, Macedonia), the Turkana Basin (Plio-Pleistocene, Kenya), the Vienna Basin (Late Miocene, Austria) and the Steinheim Basin (Middle Miocene, Germany). We demonstrate how difficult it is to establish high-resolution stratigraphic sequences with appropriate time-control; how sedimentation rates and sedimentary gaps bias observations on phenotypic change; what role taphonomy plays, including preservational bias, reworking, sorting and transport; what problems there are to recognise biological species in fossil material or to discern genuine evolutionary events from phenotypic variability, and finally to confidentially establish ancestor-descendant relationships, both in cases of anagenesis and cladogenesis.

T2.P1

DEVELOPMENT OF THE MOLLUSCAN DIVERSITY IN THE FLOODPLAINS OF THE PARIS BASIN (FRANCE) BETWEEN 8500 BC AND 1400 AD

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Rescue archeology has developed considerably in France over the last thirty years. In this context, the Paris Basin has been the subject of numerous investigations due to its significant economic development in recent decades. As a result of this extensive fieldwork, a broad multidisciplinary approach combining geology with several biological proxies has then been undertaken. Among these biological proxies, studies of continental molluscs enable the reconstruction of extremely small-scale environmental changes both in a spatial and temporal sense. Today, an important set of malacological data has been carried out in the valleys of the Paris Basin and it is thus possible to follow the development of the biodiversity in this region through time. Looking at the Holocene in more detail, i.e. the ten last millennia, when the first Neolithic settlers arrived in the Paris Basin around 5200 BC, the landscape is dominated by clear woodlands. These provide a patchwork of habitats for snails that form diversified assemblages. From the end of the Neolithic until the end of the Iron Age, a dramatic and continuous decrease of the diversity is registered. The number of species does not decline significantly at first but the specimens collected become actually more and more unevenly distributed between the different species identified. Species from wet grassland thrive at the expense of shade-demanding taxa. Secondly, the biodiversity declines with a dramatic decrease of the number of species. This impoverishment of the malacological diversity thus results from a comparable homogenisation of vegetation broadly observed in the Paris Basin floodplains. Whether the climate is primarily responsible of the moistening of ecosystems, the important homogenisation of landscapes expresses an anthropogenic stress caused by the maintaining of open spaces for agropastoral activities.

T2.P2

SUCCESSION OF LAND SNAIL ASSEMBLAGES IN QUARRIES OF BOHEMIAN KARST, CZECH REPUBLIC

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Succession of land snail assemblages was studied in 18 abandoned limestone quarries of different age in Bohemian Karst, Czech Republic. The number of species in studied quarries increases in the time. The less species were found in the oldest quarries. This trend was probably caused by habitat diversity decline although it is not conclusive. The best predictors of mollusk species composition are type of surrounding vegetation, light and age. It is important to take into account correlations of the other environmental variables with light and the cover of tree layer. Compositions of mollusk assemblages of north and south-facing slopes differ, but these differences diminish with ongoing succession. Quarries represent suitable model sites for the study of succession.

T2.P3

RECENTLY ADAPTED OR RELIC SURVIVORS? THE PHYLOGEOGRAPHY OF *HELIX* FROM THE APENNINES (ITALY) TO NORTH EUROPE

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The evolutionary history of the snail *Helix* is yet unknown. Its type species, the Roman snail *H. pomatia*, thought to be of South European origin, is widespread in Europe. There are three main hypotheses to explain its present distribution: (1) a spontaneous post-glacial re-colonisation of Central and Northern Europe from South European refugia; (2) repeated human mediated translocations since the Roman Epoch; (3) the concurrence of these two events.

At the smaller scale of the Apennines (peninsular Italy), *Helix* is a diverse group displaying broad shell variation, but two main categories can be recognised: a coloured (= hazel to yellowish) shelled one and a pale (= pale hazel to whitish) shelled form. Both types are distributed along a broad range of altitudes, i.e. from 300 to 2100 m above sea level. Over the time, these two forms and their variants have been considered different

species/subspecies scattered along the Apennines but a stable taxonomic arrangement has not been reached so far.

To test the validity of the current systematics of *Helix* and to reconstruct the phylogeography of the Roman snail, we analysed morphological (shell and genitalia) and molecular (mitochondrial and nuclear markers) data. The phylogeography of the Roman snail does not support a scenario in which human-mediated translocations played a significant role. Moreover, contrary to the expectations, shells do not correctly identify species, whereas molecules and morphology of genitals do. Phylogeographic analyses of *Helix* from the Apennines support a scenario in which more than one species is involved and where the pale form is a relict that survived the Pleistocene glaciations. The coloured form is a derived condition related to habitats at lower altitudes.

T2.P4

LAND SNAIL SPECIES OF PORTO SANTAN ISLETS: THE LIFE PROJECT EXPERIENCE

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The Porto Santo Island is one of the world's biodiversity hotspot as far as land snail conservation is concerned. Dispersed on a total area of 232 ha, the Porto Santan Islets (PSI) enclose 33 *taxa*, where 30 (90.8%) are endemic to the archipelago and eight (24.24%) are exclusive. Some of these species, like *Hystricella turricula* (Cima Islet) and *Idiomela subplicata* (Baixo Islet), have a very restricted distribution, with a range less than 500m^2. Several of those exclusive species have an unfavorable conservation status being listed as endangered, both on International and Regional Red Lists.

The LIFE Project "*Halt the loss of European Biodiversity through the recovery of habitats and species of the PSI and surrounding marine area* (LIFE09 NAT/PT/000041 - LPSI)" has the purpose to guarantee that the ecosystems on the Nature 2000 Network site of PSI (PTPOR0001 – Habitat 1250) reach a stable, favorable and self-sustainable conservation status. Taking place between 2010 – 2014, one of the main aims of the LPSI is to create conditions in order to enable the recovery of European priority land snail species such as *Caseolus calculus*, *Caseolus commixtus*, *Idiomela subplicata* and *Hystricella turricula*.

The main ecological and conservation actions for land snails include (1) the establishment of monitoring schemes to assess the *taxa* response to the concrete conservation actions implemented on the PSI, (2) revision and improvement of the current taxonomical knowledge of the terrestrial molluscs fauna of the PSI, (3) elaboration of Action Plans for each of the species listed in the Habitats Directives; (4) improvement of the expansion of the severely endangered endemic land snails populations (*C. calculus, C. commixtus, H. turricula, I. subplicata)* (5) Setting a network of "shelters" and exclusion areas in order to reduce and/or prevent the predation of land snails by seagulls and mice, (6) Building a strong support of the general public and awareness regarding the land snail species and ecosystems in question.

T2.P5

MORPHOLOGICAL CONVERGENCE AND MOLECULAR DIVERGENCE OF *TROCHULUS STRIOLATUS* AND *T. MONTANUS* WITH THEIR RELATIONSHIP TO SYMPATRIC CONGENERS (GASTROPODA: PULMONATA: HYGROMIIDAE)

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In molluscs shell morphology has played an important role in the differentiation of species since ever. However, extensive morphological variation and lack of readily available diagnostic characters often invite taxonomic confusions among closely related species, such as in the genus *Trochulus*. Two nominal species *Trochulus striolatus* (C. Pfeiffer, 1828) and *T. montanus* (Studer, 1820) are indistinguishable on the basis of sole conchological traits and show only subtle differences in the reproductive system. Therefore, we performed molecular and morphological analyses to establish robust species limits among the species. The canonical discriminant analysis (CDA) of shell characters confirms the strong similarity between the species. At the same time, the shell morphology shows a high variability among and within populations of both species so that distinct forms can be distinguished. Similarly, the analysis of genital morphology shows that differences in genital morphology are continuous and practically negligible among the species. On the contrary, phylogenetic analysis based on sequences of the mitochondrial cytochrome oxidase I (COI) gene shows clear genetic divergence between *T. striolatus* and *T. montanus*. Phylogenetic tree based on 167 individuals of *Trochulus* species (114 sequences of our own and 53 retrieved from the GenBank database) consists of two major clades. The first one groups *T. striolatus*, *T. sericeus* and *Trochulus* sp. The second clade comprises *T. montanus*, *T. clandestinus*, *T. caelatus*, *T. sericeus* and a large series of unidentified *Trochulus* sp. Thus, we can conclude that *T. montanus* is most closely related to *T. clandestinus* and *T. caelatus*; they form a monophyletic group. However, it is difficult to determine the systematic position of *T. sericeus* since the specimens morphologically resembling this taxon are placed in both main clades of the phylogram as significantly different. For final conclusions on *T. sericeus* detailed studies, including a larger number of individuals/markers are required.

T2.P6

FOCUSED ON MORPHOMETRY OF EUROPEAN *PUPILLA* SPECIES (FLEMING, 1828)

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Pupilla snails are typical fossils of the glacial loess assemblages in which several taxa of this genus usually co-occur. Some of such species of loess fauna survived ends of

the Last Glacial in Central Europe at rare and isolated habitats such as rocky steppes (*P. sterrii, P. triplicata*) or tufa-forming fens (*P. alpicola*) but *P. muscorum* actually became one of the most common species in grasslands including urban lawns. Other *Pupilla* species known from fossil record got extinct in Central Europe but still occur in steppes of Central Asia. According to modern molecular studies, a new species of *Pupilla* (*P. pratensis*) was validated but more taxonomic revisions within this genus are likely to follow. Our study compares shell characters of Central European fossil specimens with recent snails for better insight into variability of known taxa and possible differences between them. We used a unique collection of Quaternary material collected by Dr. Vojen Ložek from the area of the Czech and Slovak Republics, and recent *Pupilla* species from this region. We will present results of comparison of classical morphometry with the geometric morphometric approach (Elliptical Fourier Analysis).

T2.P7

SNAILS DO IT – BUT SOMETIMES THEY DON´T NEED TO DO IT! SELFING IN GEOGRAPHICALLY SEPARATED POPULATIONS OF *CYLINDRUS OBTUSUS* (GASTROPODA: PULMONATA: HELICIDAE)

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Cylindrus obtusus is a hermaphroditic landsnail, endemic in the Austrian Alps, which is restricted to high elevations (1600 to 2500 m asl) and limestone. It has a quite patchy distribution area which may become even further reduced in the future due to global warming. Previous investigations revealed geographic differences in the genital apparatus: All specimens from the more western populations had one stylophore and two equally developed mucus glands more than twice the length of the stylophore. In contrast, in individuals from the eastern margin of the species distribution, one or two mucus glands were found and the size ratio between stylophore and mucus gland(s) was highly variable. To find out whether these anatomical differences reflect a genetic differentiation, which might be an indication for distinct glacial refugia, we investigated a 650 bp fragment of the COI sequence (200 individuals) and 9 microsatellite loci (500 individuals from 29 populations) from samples covering the whole distribution range of the species. The COI sequences showed a geographic differentiation between eastern, central and western populations. The microsatellite analysis reveals a high differentiation between the populations implying restriction of gene flow. Remarkable nearly all individuals from the eastern populations, which are variable in their genital morphology, are homozygous in all microsatellite loci (although different alleles were found within populations). The most plausible explanation for this finding is an altered mode of reproduction. For further investigations quantitative measurements of the mucus glands and the stylophore were taken from more than 70 individuals collected from 16 populations. The results confirm the east-west division suggesting possible functional differences. To assess the functionality of the mucus glands, a comparative histological investigation of was performed. This work has been funded by the Austrian Science Foundation (P19592-B17).

T2.P8

WHY SUCH A GREAT DIVERSITY OF REPRODUCTIVE STRATEGIES IN BALEINAE (GASTROPODA: PULMONATA: CLAUSILIIDAE)?

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Baleinae are one of five clausiliid subfamilies represented in Europe; they include 7 genera with 51 species. Life cycles of 10 of the species (ca. 20%) have been studied to date, both in the laboratory and in the field. They are iteroparous, long-lived, of determinate shell growth and delayed reproductive maturity. The species vary in their reproductive strategies: 4 are oviparous, 3 retain their eggs for various periods of time, 3 are viviparous. Three (among them viviparous species and egg retainers) are capable of self-fertilisation. The spermoviduct and free oviduct section do not differ anatomically or histologically between oviparous and viviparous species (except *B. perversa* with its simplified structures inside the gonoduct). The spermoviduct is composed of 3 partly open canals (semitriaulic system): autospermiduct, allospermiduct and oviduct; below the separation of vas deferens the oviduct with the accompanying allospermiduct forms the uterus. The structure of spermoviduct and free oviduct makes possible egg retention/viviparity, but only some species use these structures to retain eggs. Reasons for the diversity of reproductive strategies may be sought in environmental conditions. Egg retention/viviparity are probably favoured by high humidity of montane and submonate forests, areas adjoined by water bodies or subject to the effects of oceanic climate. All the studied viviparous and egg-retaining Baleinae occur in such areas and their distribution ranges do not include typically continental or Mediterranean regions. The simplified structure of the closing apparatus in *Balea perversa* from oceanic climates is a particular adaptation to viviparity. The conical shell shape (like in juveniles of other Baleinae), compensatory growth after the onset of reproduction and small size, indicate neoteny which may have evolved in a high-humidity environment.

T2.P9

PINNING DOWN *TENUISTEMMA* (PULMONATA: UROCOPTIDAE): LOCAL EVOLUTION OF AN EXTREME SHELL SHAPE

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The Cuban land snail genus *Tenuistemma* (Pulmonata: Urocoptidae) is characterised by a strongly attenuated almost needle-like shell, a shape unique within the family Urocoptidae. The genus has an exceptionally small geographic distribution: it is known

from one species, *Tenuistemma lateralis*, which is confined to the summit of El Yunque mountain in the Nipe-Sagua-Baracoa massif in SE Cuba.

Genus-level molecular phylogenetic studies showed that *Tenuistemma* is very closely related to the genus *Pleurostemma.* That genus has a cylindrical shell, like most Urocoptidae. *Pleurostemma* is far more diverse and wide-spread than *Tenuistemma*, with three recognized species with a combined distribution covering most of the Nipe-Sagua-Baracoa massif surrounding the range of *Tenuistemma*.

This more detailed study includes multiple specimens of *Tenuistemma lateralis*, and it examines *Pleurostemma* at the species and subspecies level. For each specimen, partial sequences of the mitochondrial cytochrome oxidase I gene and sequences of five clones of the multi-copy nuclear internal transcribed spacer 2 (ITS2) region were obtained. Surprisingly, phylogenetic analyses of both markers independently nest *Tenuistemma lateralis* not only within *Pleurostemma,* but within the species *Pleurostemma perplicata,* where it forms clade with *Pleurostemma perplicata yunquensis*. This subspecies occurs parapatrically with *Tenuistemma lateralis* on El Yunque mountain. Unless one assumes intergeneric introgressive replacement of both mitochondrial DNA and ITS2 copies in *Tenuistemma lateralis,* these results indicate that *Tenuistemma lateralis* evolved from *Pleurostemma perplicata yunquensis* on El Yunque mountain.

T2.P10

PREDATION BY BEETLES (COLEOPTERA: ELATERIDAE: DRILINI) MAY DRIVE SHELL EVOLUTION IN *ALBINARIA* (PULMONATA: CLAUSILIIDAE)

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Albinaria is a genus of rock-dwelling clausiliid land snails with high conchological diversity. The ca. 100 species occupy largely allopatric ranges throughout Greece and Turkey. We have investigated the possible role of predation by the dominant natural enemy, larvae of the beetle genus *Drilus*, in shell evolution in tis genus. In this poster we outline the diversity, distribution, and behaviour of *Drilus*. We also provide preliminary results on predation-related selection pressures on shell traits in several Greek *Albinaria* populations.

T2.P11

VARANID LIZARD PREDATION DRIVES HABITAT-USE AND SHELL SHAPE SHIFTS IN THE TROPICAL ISLAND LAND SNAIL, *HELICOSTYLA PORTEI* (BRADYBAENIDAE: HELICOSTYLINAE)

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Evolution of anti-predator adaptation, which can lead to speciation, varies from morphological to behavioral modifications. In this study, we demonstrated how the varanid lizard, *Varanus olivaceus*, affected the ecomorphology of the island endemic land snail, *Helicostyla portei*. Land snails were surveyed from Polillo (with predator lizard), and Patnanungan (without predator lizard) Islands in the Philippines. Shells were analyzed using geometric morphometrics based on 14 landmarks, while habitat-use was discriminated by the sitting position (on tree trunk, leaves or vines) of the snail. The relationship among shell morphology, habitat-use and other environmental variables (island, altitude, tree density, canopy cover, leaf litter depth) were tested using generalized linear mixed model. Land snails on the island where predator is present have larger shell size and wider body whorl with narrower aperture. More snails were found on leaves, followed by vines and rarely on tree trunks. Land snails on the island without the lizard have more extensive size range and narrower body whorl but wider aperture. Habitat-use among snails shifted in the absence of the predator, wherein tree trunk became the most preferred, followed by leaves and vines. This suggested that predation induced habitat-use variation resulting in change in shell shape. The significant relationship between habitat utilization and shell form indicated that *H. portei* exposed to predator selection favored characters more adapted to sites inaccessible to the lizard, whereas in the absence of the predator, shells showed relaxed phenotype more adapted to tree trunk. The lack of relationship between habitat-use with other environmental variables further supported the hypothesis. Our study revealed that snail-eating varanid lizards could drive rapid morpho-ecological plasticity among tropical land snails.

T3

MOLECULAR PHYLOGENETICS AND PALEONTOLOGY

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The evolution of life has been intimately linked to environmental changes throughout Earth's history. Combining molecular and paleontological data, especially through the use of time-calibrated molecular phylogenies, has recently opened vast new opportunities for evolutionary biologists and paleontologists to investigate these links. But much remains to be learned about how best to use fossils in calibrations and how to deal with extinct taxa and clades, to name just a few issues. This symposium aims to bring molecular biologists and paleontologists together to exchange the latest results and to enhance communication on methodological issues and developments on questions that may only be answered with each other's expertise. The symposium is not restricted to work that explicitly address this issue, but is also open to molecular phylogenetic and paleontological studies addressing evolutionary and phylogenetic questions.

T3.O1

FOSSILS AND PHYLOGENY: COMPARING PATTERNS OF EXTINCTION AND SPECIATION

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The rich Cenozioc marine mollusc fossil record of New Zealand provides a wealth of paleontological data for integration and comparison with molecular datasets. We have utilised fossil occurrences of living species together with sampling probabilities (of fossils) to generate calibration distributions for the inference of a time-calibrated molecular phylogeny of the volute genus *Alcithoe* (Gastropoda). Our selection of calibration species eliminates the taxonomic uncertainty associated with the assignment of extinct species to internal nodes in the phylogeny. Calibration prior distributions are derived from measured uncertainty from the fossil record. This approach yielded a well-supported tree with divergence times that are consistent with the fossil record. The pattern of diversification implied by the molecular phylogeny indicates that most *Alcithoe* speciation has occurred relatively recently. However, this appears to be at odds with the fossil record, in which more taxonomic diversity is observed to have occurred in the past. This observation leads to the question: to what extent does the diversification pattern seen for the living species reflect the history of diversification for the whole clade? Using our time-calibrated molecular phylogeny and diversification rates for New Zealand Mollusca calculated from paleontological data, we examine

the diversification process in the *Alicthoe* lineage during the Cenozoic. By comparing the *Alcithoe* molecular phylogeny with trees simulated using various diversification models we test for scenarios that can reproduce trees similar to the inferred molecular tree. The models tested are derived from measurements of origination and extinction from the fossil record data and capture increasingly complex parameterisation of the diversification process. Our results show that for *Alcithoe*, diversification of the living taxa is not representative of the complete evolutionary history of the lineage. Appropriate modelling using the paleontological data is however sufficient to recover a diversification process that can generate phylogenies consistent with the molecular tree.

T3.O2

INTO THE DEEP: A PHYLOGENETIC APPROACH TO THE BIVALVE SUBCLASS PROTOBRANCHIA

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A molecular phylogeny of Protobranchia, the subclass of bivalve mollusks sister to the remaining Bivalvia, has long proven elusive, owing to the deep-sea habitats of many constituent lineages and ensuing methodological challenges for preserving genetic material. After numerous collecting campaigns, we obtained representatives of all extant protobranch families and investigated the internal phylogeny of this group, using sequence data from five molecular loci (16S rRNA, 18S rRNA, 28S rRNA, cytochrome *c* oxidase subunit I, and histone H3). Model-based and dynamic homology parsimony approaches to phylogenetic reconstruction unanimously supported four major clades of Protobranchia, irrespective of treatment of hypervariable regions in the nuclear ribosomal genes 18S rRNA and 28S rRNA. These four clades correspond to the superfamilies Nuculoidea (excluding Sareptidae), Nuculanoidea (including Sareptidae), Solemyoidea, and Manzanelloidea. Salient aspects of the phylogeny include (1) support for the placement of the family Sareptidae within or sister to Nuculanoidea; (2) the non-monophyly of the order Solemyida (Solemyoidea + Manzanelloidea); (3) and the non-monophyly of most nuculoidean and nuculanoidean genera and families. We also re-examined the fossil record of Protobranchia and inferred clade divergence times using simultaneous estimation of tree topology and node ages. The chronogram of Protobranchia, in concert with analyses of diversification rates, demonstrates the signature of the end-Permian mass extinction in the phylogeny of extant protobranchs, manifested as an anti-sigmoidal net diversification curve, with marked upturn in diversification subsequent to ca. 260 Ma.

T3.O3

THE PHYLOGENY AND SYSTEMATICS OF THE NASSARIIDAE REVISITED (GASTROPODA, BUCCINOIDEA)

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Nassariidae are a group of scavengers that are diversified on soft bottoms as well as on rocky shores, and are the subject of numerous research papers in ecology, ecotoxicology, paleontology and one species is even a model organism in biology. A weak and/or apparently continuous variation in shell characters has resulted in a confused taxonomy, with complex synonymy lists. Over 1,320 nominal Recent species have been established, of which 420 are regarded as valid. Above species level, the state of the art is equally hazy, with four subfamilies and seven genera currently considered valid, and many other names in the graveyard of synonymy. Two global phylogenies – including fossils - have been based on shell morphology, and a single molecular phylogeny is based on fewer than 20 species. We have conducted a molecular analysis based on three 3 mitochondrial (COI, 16S, 12S) and two nuclear (28S, H3) markers. Our dataset includes 215 putative nassariid species, comprising 6 of the 7 genera considered valid, and 24 nominal genera are represented by their type species. The monophyly of the Nassariidae as classically construed is confirmed, and a previous hypothesis that included *Phos* and *Nassaria* in the family is rejected. Within the Nassariinae, the tree unexpectedly demonstrates that species from the Atlantic and the Indo-Pacific form two clades, and thus represent two independent diversification events. This result will have a profound impact on nassariid taxonomy, especially with regard to the validity of genus-level names. Additionally, we have disclosed a number of species complexes, and many cryptic species remain to be discovered and described in the family.

T3.O4

BEYOND RELATIONSHIPS: MINING EVOLUTIONARY HISTORY FROM THE MARINE GASTROPOD FOSSIL RECORD

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The gastropod shell is a funeous bioinorganic structure, recording a broad range of historical information. Biological, physical, and chemical records encoded in shells persist through millions of years in the fossil record. They provide a more complete evolutionary history and richer spectrum of environmental data than can be inferred from the molecular sequences of living taxa and their extant outgroups. This is especially important to the evolutionary understanding of taxa with early origins, long geologic ranges, and a hyperdiversity of extinct taxa. It is also important to understanding phenomena such shifts in ecology and biogeographic distribution, migration and invasion, and responses to mass extinction and climate change. Two paleontological examples of enriched evolutionary understanding are the fossil record of micro-vetigastropods of morphologically similar species of *Liotella* Iredale, 1915 and

Brookula Iredale, 1912 and the fossil record of deep-sea lineages in the vetigastropod family Colloniidae Cossmann, 1916.

The first example is remarkable because fossil shells typically are better preserved than the shells of extant species in museum collections and because there is are no published molecular sequence data, anatomical data or observations of live animals. The second example is remarkable because generic diversity is concentrated in the Cenozoic fossil record and because the family is closely allied morphologically to higher taxa that were even more diverse in the Mesozoic. Cenozoic deep-water genera first appear in forearc hydrocarbon seep settings that are more easily sampled in the exposed terrestrial rock record than in the deep-water settings of fluid expulsion from modern substrates where extant populations occur. In both examples, it is taphonomic history and peculiar taphofacies that provide special opportunities for paleontologists and evolutionary biologists to join forces to bring the maximum amount of data to bear on evolutionary questions.

T3.O5

CONSENSUS AND CONFUSION IN MOLLUSCAN PHYLOGENY

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Monophyly of the eight Recent molluscan classes is undisputed, but relationships between these groups and patterns of radiation have remained elusive. Molecular, fossil and anatomical data show apparently contradictory evidence for branching patterns within Mollusca. Arguments about traditional (morphological) phylogeny focus on a small number of topological concepts but often without regard to proximity of particular classes. In contrast, molecular studies have proposed a number of radically different, inherently contradictory, and controversial sister-relationships. The traditional reductionist model of the 'hypothetical molluscan ancestor' has hampered the resolution of molluscan topology; some hypotheses rejected as artifacts (e.g., Serialia) continue to find additional support and cannot be dismissed conclusively. We assembled a dataset of 40 unique published trees describing molluscan interrelationships. We used these data to ask several questions about the state of resolution of molluscan phylogeny compared to a null model of the variation possible in random trees constructed from a monophyletic assemblage of eight terminals. More than half of the unique trees that have been proposed from morphological inference are not statistically different from each other. Morphological topologies are on average significantly different to molecular topologies. Within the available molecular topologies, only four studies to date have included the deep-sea class Monoplacophora; but more than a third of all trees do not significantly differ from each other. The inter-nodal distance is consistently close between a few taxon pairs, particularly the Monoplacophora and the chitons, Polyplacophora. Others have rare or non-existent occurrence of proximate placement, such as the vermiform Caudofoveata and Bivalvia. We also derive morphological and molecular supertrees from all available molluscan phylogenies, which can serve as a basis for future hypothesis testing.

T3.O6

PATTERNS AND PROCESSES OF SPECIATION IN THE BALEARIC ISLANDS ENDEMIC LAND SNAIL GENUS *ALLOGNATHUS*

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The genus *Allognathus* Pilsbry, 1888 (Gastropoda: Helicoidea), is endemic to the Balearic Islands. It is present in all the main islands of the archipelago, Majorca, Minorca, Ibiza and Formentera, and also in some small islets. The genus contains two subgenera *Allognathus s. str* and *Iberellus*.

The subgenus *Allognathus* is monotypic, while 7 taxa are considered within *Iberellus* in the CLECOM classification. Differences of *Iberellus* taxa are based mostly on shell morphology and geographic distribution. There are not diagnostic differences in the reproductive apparatus. Due to its endemicity and its distribution in the different islands, it is a group of high interest both, in terms of evolution and biogeography.

For this study, some populations belonging to all taxa considered within the genus were studied by means of DNA sequenciation, two mitochondrial genes (COI and 16S rRNA) and two nuclear gene fragments (ITS2 and 28S rRNA). The analysis of the four-concatenated DNA gene fragments recovered the monophyly of *Allognathus grateloupi*. As many as six haplogroups were obtained within *Allognathus (Iberellus)*. However, the taxonomic validity of the six lineages will be discussed on the basis of the morphological, biological and phylogenetic species concepts. *A. (I.) hispanicus horadadae* and *A. (I.) hispanicus palumbariae* were not separated lineages. We also analyzed the evolution of the genus and discussed about the origin of species within the archipelago, contrasting vicariant and dispersal processes as a means of explaining their current patterns of distribution. We considered several possible scenarios based on the most relevant paleogeographic events occurred in western Mediterranean, since the Oligocene (30 Million Years Ago): i) fragmentation and drift of the Hercynian belt, ii) landbridge connection between the Iberian Peninsula and the Balearic islands during the Langhian-Serravallian, iii) the Messinian Salinity Crisis, and iv) sea level fluctuations occurred during the Plio-Pleistocene.

T3.O7

MOLECULAR PHYLOGENY OF THE PHILIPPINE BRADYBAENIDAE (PULMONATA: STYLOMMATOPHORA)

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The Philippines has more than 200 species of land snails, with 80 recorded endemic species. Of these endemics, more than 50 percent belong to the family Bradybaenidae. Despite this great diversity, little taxonomic research has been done on the Philippine species. The shell morphology of the bradybaenids resembles that of other families such as the Helicidae and Camaenidae. Previous molecular research on these groups suggests that the Bradybaenidae and the Camaenidae are nested together. This study is the first large-scale attempt to include Philippine species to test the monophyly on the Bradybaenidae based on three genes—the nuclear ribosomal (r) RNA gene cluster, and the mitochondrial cytochrome c oxidase subunit I (CO1) and the 16S rRNA genes. A total of 30 species were collected from 20 different sites all over the Philippines. Of the 30, 29 species are native to the Philippines, while one species (*Bradybaena similaris*) is introduced. Of the 29, 11 species are endemic to the Philippines. The phylogenetic analyses, based on each of the three genes and their combination, were consistently nesting the Bradybaenidae within the Camaenidae. Furthermore, the monophyly of the Philippine native species (all under subfamily Helicostylinae) was highly supported based on the nuclear rRNA gene cluster. This study supports the claim that the Bradybaenidae and Camaenidae are confamilial. It is thus recommended that both families be flagged for taxonomic revision, and lumped into a single family.

T3.O8

MOLECULAR SYSTEMATICS OF *PYRAMIDULA* (GASTROPODA, PULMONATA)

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Pyramidula is a genus of terrestrial gastropods whose distribution extends to almost all Europe, Mediterranean area, Central Asia and Japan. Species have a trochoid shell, from high to flattened, with a broad umbilicus. They are small, not exceeding 3 mm in diameter, inhabiting on limestone rocks. It includes six morphospecies in the European and adjacent distribution range: *P. pusilla* is the most widespread and common in Europe; *P. rupestris* occurs in the entire Mediterranean region and Central Asia; *P. umbilicata* has a Lusitanian-atlantic distribution; *P. jaenensis* is an endemism of the Iberian Peninsula; *P. chorismenostoma* with the body whorl separated from the rest of the shell is present in Greece, Crete, Aegean islands and Western Turkey. *P. cephalonica* occurs in Croatia, Greece and Turkey. There is a controversy about a seventh form (*P. hierosolymitana*) from Israel, which some authors consider as a different species.

Until now, the identification of the species of this genus has been based exclusively on shell parameters, particularly shell high and diameter and umbilicus width. These parameters are highly correlated and they could be not enough to resolve the taxonomy, thus the need of complementary characters becomes evident.

The aim of the present study was to review the taxonomy and phylogeny of the genus using molecular markers, specifically the sequences data from two mitochondrial (COI and 16S rRNA) and one nuclear gene fragment (5.8S - ITS2 - 28S rRNA). The results

based on the analysis of 258 specimens (258 sequenced for the two mitochondrial gene fragments and 47 for the nuclear DNA) collected along its western Palaearctic distribution area are presented. As many as 6 phylogroups were obtained within the genus. We compared these phylogenetic groups with the morphospecies currently considered, giving new insights on the taxonomy and evolution of this genus.

T3.O9

NEWS FROM THE PAST – OLIGOCENE CONTINENTAL MOLLUSCS OF OMAN

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The Zalumah Formation in Dhofar, Oman, of Terminal Eocene age (c. 35 Ma) contains a highly diversified and well preserved land and freshwater snail fauna. It constitutes the earliest known terrestrial malacofauna of the Afrotropical Region, an area, where the paleontological knowledge is extremely fragmentary and virtually non-existent, at least for this period. On the one hand, the fossil assemblages show close affinities with the Modern intertropical African fauna, but on the other hand are distinctly linked to the snail fauna that radiated on Soqotra after the Soqotra Plate broke away from Oman in Oligocene times. The palaeo-environmental setting appears to be one of extensive freshwater swamps rather than lakes or rivers with a very marked seasonal difference in dry and rainy season water level. There are no indications of water currents and the snails probably were deposited in fine limey mud. We conclude that the extraordinary richness of preserved shells may be the result of a climate that was not fully tropical. The Omani fossil snail fauna appears to be quite diversified and contained species from the families Ampullariidae, Pomatiidae, Succineidae, Achatinidae, Cerastidae, Subulinidae, and Helicarionidae. The assemblages yielded 11 species with 9 of them being described as new to science: *Lanistes tricarinatus* n. sp., *Lanistes thaytinitiensis* n. sp., *Cyclotopsis praecursor* n. sp., *Succinea omanensis* n. sp., *Limicolaria omanensis* n. sp., *Achatina sculpturata* n. sp., *Cerastus pseudoena* n. sp., *Cerastus praeinsularis* n. sp., *Trochozonites arabica* n. sp. Today, Achatinidae and Ampullariidae are missing in the malacofauna of the Arabian Peninsula as well as in Soqotra.

T3.O10

LOST AND FOUND: THE EOCENE FAMILY PYRAMIMITRIDAE (NEOGASTROPODA) DISCOVERED IN THE RECENT FAUNA OF THE INDO-PACIFIC

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The evolutionary history of the predatory/scavenger Neogastropoda is a classic example of a successful, post Cretaceous radiation of marine snails. Most neogastropod families

have a continuous record from the Cretaceous or Paleogene to the Recent. However, the fossil record also contains a number of obscure nominal families with unusual shell characters that are not adequately placed in the current classification. Some of these are traditionally regarded as valid, and some have been “lost” in synonymy – for good or for weak reasons. One such «lost» family is the Pyramimitridae, established by Cossmann in 1901 for the Eocene genus *Pyramimitra*, and currently buried in the synonymy of Buccinidae. As part of our routine work on deep-water molluscs from the tropical Indo-West Pacific, we examined several species of inconspicuous, small turriform gastropods that revealed a unique radula so far unknown in Neogastropoda. Although one of the Recent species had previously been described as an “aberrant” species of Terebridae, overall the shell characters identify them as members of the “extinct” family Pyramimitridae. Molecular data (12S, 16S, 28S, COI) confirm the recognition of Pyramimitridae as a distinct family, although no sister group was identified in the analysis. Likewise, neither the radular morphology, nor the anatomy reveal the relationships of this enigmatic, “living fossil” family. Pyramimitrids occur in the Recent fauna at bathyal depths of the Indo-Pacific from Taiwan to Madagascar and New Zealand, with three genera and nine species (all new except one).

T3.O11

PHYLOGENY OF VENERID BIVALVES, AS INFERRED FROM A COMBINED ANALYSIS OF MOLECULAR AND MORPHOLOGICAL DATA

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Represented by approximately 800 Recent species, Veneridae is the largest family of bivalves and one of the most important ecologically and economically. Nevertheless, venerid systematics is poorly understood, with published classifications differing widely in their concept and boundaries between species, genera, and subfamilies. In recent years, morphological and molecular inferences of venerid phylogeny have led to progress in our understanding of the higher-level relationships, particularly of the composition and relationships of subfamilies. However, none of the previous studies used combined molecular and morphological data sets, nor did they attempt to integrate the rich fossil record of venerids into their analyses.

With the aim of exploring biogeographic, stratigraphic, and methodological questions, our multidisciplinary team has assembled the largest venerid datasets to date, comprising scorings for 71 discrete morphological characters from extant and fossil representatives, as well as sequences for three nuclear (H3, 28S, 18S) and two mitochondrial genes (16S, COI). Preliminary analyses of our dataset indicate support for Tapetinae, Dosininae, Gemminae, and Gouldinae, with some possible outliers. Representatives of Chioninae are recovered in a mixed clade with Venerinae only, not Dosiniinae as suggested by previous studies. Relationships of Meretricinae, Callistinae, Pitarinae, and Sunettinae are problematic, with a larger mismatch between trees and prevalent taxonomic classifications. Our results also confirm that Turtoniinae and Petricolinae are nested within Veneridae, and thus do not represent separate families. Dense sampling within some generic units allowed us to test the validity of some long-debated species and subgenera, thus providing the starting point for a much-needed revision of these groups.

T3.O12

CENOZOIC CLIMATE CHANGE, TECTONICS AND DIVERSIFICATION IN THE DEEP-SEA: EVOLUTION OF DIVERSITY IN THE GASTROPOD FAMILY SOLARIELLIDAE (TROCHOIDEA)

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The modern Indo-West Pacific Ocean (IWP) is the largest biogeographic marine province and is renowned as a hotspot for biodiversity. A maximum, in terms of species richness, is observed for many shallow-water marine organisms in the central IWP, with biodiversity declining with increasing distance from the centre. Recent expeditions have also revealed high levels of biodiversity among deep-sea gastropod molluscs. While many hypotheses exist about the mechanisms that may have led to the present high biodiversity levels in shallow-water IWP communities, little is known about the age or origin of tropical deep-sea biodiversity. We used a deep-sea radiation of vetigastropods as a tractable model to test key hypotheses about origins and to determine the factors driving diversification in the deep sea. We show that an abrupt period of global warming during the Palaeocene Eocene Thermal Maximum leaves no molecular record of change in diversification rate in solariellids. Conversely, diversification in a major clade is congruent with a period of global cooling at the Eocene-Oligocene transition approximately 33.7 Mya. Increased nutrients made available by contemporaneous changes to erosion, ocean circulation, tectonic events and upwelling may explain increased diversification, suggesting that food availability may have been a factor limiting exploitation of deep-sea habitats.

T3.O13

INTRODUCTION TO THE TREATISE'S PARACLADISTIC CLASSIFICATION OF THE BIVALVIA

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Parsimony analysis has proven to be an indispensable tool for analyzing character evolution in the Bivalvia, but its associated cladistic (phylogenetic) systematics does little to facilitate discussion of ancestor-descendant relationships. This is largely because cladograms do not portray ancestor-descendant relationships, and cladistic taxonomy precludes the formal recognition of paraphyletic groups. The exclusion of paraphyletic groups is appropriate for organisms with a poor fossil record (e.g., Hexapoda), and for some organisms with a rich but relatively character poor fossil record (e.g., Gastropoda), but it is less appropriate for groups, such as the Bivalvia, with an excellent fossil record that is rich in potentially phylogenetically informative characters (e.g., shell, hinge and ligament morphology, muscle scars, and ligament and shell microstructure). The fossil record suggests that paraphyly is too widespread among the bivalve orders, superfamilies and families to be ignored in a comprehensive, formal classification of the Bivalvia: 50% of protobranchian, 29% of pteriomorphian, and 25% of heteroconchian orders are paraphyletic, and 50% of these paraphyletic orders are extant. For these same three groups, 57%, 36%, and 37% of the superfamilies are paraphyletic, and 75%, 21%, and 32% of these paraphyletic superfamilies are extant; also, 39%, 39%, and 32% of the families are paraphyletic, and 22%, 17%, and 27% of these paraphyletic families are extant, respectively. The paraphyletic nature of these orders, superfamilies, and families is commonly hidden in molecular phylogenetic studies by their necessary exclusion of stem group members, wherein the paraphyly generally lies. The revised classification of the Bivalvia for the Treatise on Invertebrate Paleontology differs from a purely cladistic approach in formally recognizing paraphyletic groups, although at miminal taxonomic ranks. These are defined with the same rigor as monophyletic clades, but by the presence of specified apomorphies and by the absence of apomorphies that define their descendent clade or clades.

T3.O14

PHYLOGENOMIC RESOLUTION OF RELATIONSHIPS WITHIN BIVALVIA (MOLLUSCA).

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With an estimated 20-30,000 species, bivalves represent the second largest living class of molluscs. Phylogenomic approaches have recently been employed to obtain robust resolution of molluscan relationships, but conflicts in morphological and molecular datasets persist within major molluscan lineages, particularly Bivalvia. Recent investigations reveal general congruence of the phylogenetic placement of major bivalve lineages, however support for several critical basal nodes is lacking. Here we provide the first phylogenomic reconstruction of Bivalvia toward resolving deep divergences within this group. All five major lineages of bivalves (Archiheterodonta, Euheterodonta [including Anomalodesmata], Palaeoheterodonta, Protobranchia, and Pteriomorphia) were sampled resulting in 34 newly sequenced bivalve transcriptomes, in addition to 4 transcriptomes from representatives of 3 other molluscan lineages. This constitutes the most comprehensive phylogenomic dataset to date for inference of deep relationships within Bivalvia. Subsequent analyses obtained robust resolution of bivalve lineages.

T3.O15

LOOKING UP TO ´DOWN UNDER´ - PHYLOGENY & BIOGEOGRAPHY OF AUSTRALIAN THIARIDAE

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Freshwater gastropods are suitable for biogeography studies because they tend to preserve distribution patterns over long periods of time. The origin of Australian faunal elements and the directionality and timing of colonizations are controversial. We present here preliminary results of an ongoing study on freshwater Thiaridae (Caenogastropoda: Cerithioidea) with focus on the Australian continent. Based on own collections, relevant type material and the comparison with material in major Australian museum collections we document their geographical distribution (with over 1000 records) with references ranging from world-wide patterns to smaller scaled drainage-based characteristics. As to the thiarids we tested whether they are either an "appendage" of the SE Asian biota, or originated on the Australian continent since ancient times. We applied molecular phylogenetic techniques analyzing mitochondrial 16S rRNA and cytochrome oxidase I gene sequences as well as histone H3 subunit and 28S rRNA gene sequences for representative thiarids from all over the world. Corroborating the morphologically distinguished genera and species, we identify a total of eleven distinct genetic clades in Australia of which four represent species being endemic to the continent. The molecular data does not support the monophyly of all extant Australian thiarids. The distribution cannot be explained by simply a single colonization event from Asia to Australia, neither vice versa. The molecular dating of the gene trees by calibration points using fossils could give enormous insights regarding the timing of colonization events but is a difficult task due to ambiguous assignments.

T3.O16

FREELOADING TO FREE-LIVING: PHYLOGENY, DIVERSIFICATION AND MORPHOLOGICAL EVOLUTION OF THE MEGADIVERSE MARINE BIVALVE SUPERFAMILY GALEOMMATOIDEA

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The interplay of abiotic and biotic factors has shaped the planet's biodiversity through time. However, studies of contemporary marine lineage diversification are typically framed within abiotic hypothesis-testing contexts only and have collectively lagged behind terrestrial studies in developing an integrated framework that includes a meaningful biotic perspective. The marine bivalve superfamily Galeommatoidea is a particularly apt group for addressing this deficiency because it contains large numbers of obligate commensal as well as free-living species and is therefore amenable to comparative approaches. The evolutionary pathways of free-living and commensal clams are both affected by abiotic factors, but the commensal species are influenced by an additional biotic factor: their ecological interactions with their hosts. We are interested in understanding how commensal and free-living lifestyles have shaped galeommatoidean macroevolutionary trajectories and what are their relative contributions to the superfamily's present-day "megadiverse" status. To do so, we constructed a global, multi-gene molecular phylogeny of Galeommatoidea incorporating hundreds of morphospecies. Phylogenetic reconstructions revealed the existence of multiple commensal clades and one major free-living clade. Ancestral state reconstruction indicated that the commensal lifestyle is likely to be the ancestral trait of galeommatoidean clams. Macroevolutionary analyses showed that the free-living lineages collectively have a higher diversification rate compared to the commensal clades. Furthermore, quantitative analysis of clam morphologies suggested that the free-living group also exhibited higher morphological disparity. Given that the commensal lifestyle in Galeommatoidea is an adaptation to living in sediments and that the free-living lifestyle is tightly associated with living in hard-bottom habitats, these findings imply that by colonizing hard-bottom habitats, galeommatoideans were able to escape a "host-commensal" evolutionary constraint and undergo an accelerated diversification as free-living lineages. Our data point to a key role played by biotically-complex coral reef hard bottom habitats, in particular, in driving this exceptional evolutionary radiation of free-living galeommatoideans.

T3.O17

PATTERNS OF LINEAGE DIVERSIFICATION IN THE FAMILY PINNIDAE

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Species of the family Pinnidae, commonly called fan or pen shells, are widely distributed in shallow waters of temperate and tropical seas. Altogether, *51* species are commonly recognized, based on morphological characters, but the number of valid species requires further scrutiny. For the first time, a multi-gene phylogenetic analysis of *c.* 20 Pinnidae species using 4 genetic markers (COI, 16S rRNA, 18S rRNA and 28S rRNA) was produced in order to resolve the phylogeographic structure of this family and to clarify the phylogenetic relationships among species, their evolutionary history and their divergence time. Using historical and geological data (e.g., sea level fluctuations, or emergence of physical barriers to dispersal) we tackled the means by which natural variation and speciation are generated. In parallel, focusing on present environmental conditions for each species (e.g., currents, temperature or salinity clines) and species life history traits (e.g., age of maturity, reproduction time), we elucidated the means by which variation is maintained through time and space. Our results show three distinct major clades corresponding to three genera: *Atrina* being the sister group to the two other genera *Pinna* and *Streptopinna* which are paraphyletic. The phylogenetic relationships between *Atrina vexillum*, *A. pectinata* and *A. rigida* are still unclear at this stage of the analysis. Apart from the species *Streptopinna saccata,* all Indo-Pacific species display a clear separation among their Indian Ocean and Pacific Ocean populations. Within those species, *P. muricata* shows a sub-separation between the Red sea and the Mozambique Chanel. Within the Western Atlantic species, *A. rigida* populations appear to be divergent between Florida, Panama and the Caribbean arc whereas *P. carnea* shows homogenous distribution in the same area. Variations in species distribution highlight the influence of past and contemporary biogeographical barriers and the complex evolutionary history of each species, which will be further discussed.

T3.O18

BRIDGING THE GAP IN FOSSIL AND RECENT MELANOPSIDAE – A CASE STUDY IN EVOLUTIONARY SYSTEMATICS

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According to the vicariance approach in historical biogeography the phylogenetic pattern in a given taxon is causally linked with the sequence of spatial separation events. In this context the well-documented palaeogeography in the Mediterranean region of the northern Tethys margin provide an ideal setting for such studies, as well as freshwater gastropods of the Melanopsidae provide a well-suited model case. Fossil and Recent melanopsids have been studied by taxonomists since nearly two centuries now, leaving us with several different opinions on their systematics while a decisive and comprehensive solution is still lacking. In addition to the merely taxonomic description of biological diversity, however, a resolved phylogeny is of paramount importance. At the same time the rich fossil record of melanopsids, with a plethora of specific names, and in particular the Messinian history of the Mediterranean provide multiple calibration markers. In a two-fold approach (i) we have mapped the continuous occurrence and distribution of chronospecies through space and time, from the Cretaceous and middle Eocene to Recent, documenting shifts in range and morphology of taxa comprising the entire Mediterranean region; (ii) we have carried out a comprehensive mtDNA analyses (using the gene fragments of COI and 16S) of Recent specimens of the various taxa - from generic to species level - from the entire distributional range in comparison with anatomical data, viz. evaluating radula characters for their potential in providing additional phylogenetic signal. Based on the backbone molecular phylogeny we used geometric morphometric analyses of shells to bridge the methodological gap between the above palaeontological and zoological approach in order to link the biogeographical-stratigraphical data with the molecular phylogenetics. In the conceptual framework of evolutionary systematics the results yield more reliable facts that substantiate the reconstruction of the complex evolutionary history of this equally enigmatic and fascinating cerithioidean model.

T3.P1

NEW INSIGHTS FROM A LOST WORLD - UNLOCKING THE POTENTIAL OF MUSEUM COLLECTIONS USING HISTORICAL SPECIMENS

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Natural history museums and collections are dedicated to the documentation of current and past biodiversity. In light of the increasing biodiversity crisis, the study of this biological diversity at all levels and the underlying evolutionary forces is becoming even more urgent. Museum collections worldwide house between 1.5 and 3 billion specimens and due to their archive function play a central role in the study of biodiversity and evolution. Their potential for taxonomy, phylogeny and phylogeography is even higher when modern molecular genetic methods, such as ancientDNA techniques, could be applied also to those specimens most valuable for an array of reasons, e.g. being types, topotypical material or representing populations today not accessible or extant any longer. We tested a non-destructive aDNA extraction protocol and developed primers for historical mollusk specimens and sequence enrichment techniques to be explored for use in malacological collections. We found the protocol suitable for DNA extraction in more than 50 historic samples of various dried materials (shells, operculum and dried tissue) from different families, in particular used here for Thiaridae including Paludominae and for Planorbidae, which were as old as nearly 150 years. We will present case studies from SE Asian and Australian Thiaridae where it was possible to recover informative sequences and perform phylogenetic reconstructions. For example, we found that (i) historic specimens of *Ripalania queenslandica,* collected over a century ago in Papua New Guinea and housed in the Berlin museum, cluster with *queenslandica* sequences from Australia indicating that this thiarid is actually not endemic to the continent, (ii) *Neoradina prasongi* from southern Thailand is an independent lineage distinct both from *Melanoides* and *Stenomelania*, (iii) *Paludomus* is not strictly an Oriental taxon, and (iv) the rare and eu-viviparous *Simulathena papuensis* might be a thiarid instead of a planaxid.

T3.P2

VETIGASTROPODA (MOLLUSCA: GASTROPODA) FROM THE PLIO-PLEISTOCENE OF THE PHILIPPINES

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An extremely well-preserved Plio-Pleistocene mollusc fauna was found in the north-western Philippines. The heteropod and pteropod species in this fauna were previously studied and their species number was found to be higher than in any other fauna found to date. Subsequently, several vetigastropod families were studied and systematically described. The paleoenvironmental and paleobiogeographical character of the fauna is explored; in the fauna indicates relatively deep water (c. 200–300 m paleodepth) depositional settings. Twenty six species of gastropods were studied, three of which are described as new, viz. *Halystina conoidea, Calliotropis arenosa* and *Ethminolia wareni*. An additional number of four new combinations are proposed, viz. *Pseudotalopia taiwanensis* (Chen, 2006), *Solariella segersi* (Poppe, Tagaro & Dekker, 2006), *Zetela tabakotanii* (Poppe, Tagaro & Dekker, 2006) and *Ilanga konos* (Vilvens, 2009). Thirteen species are known living and another five are possibly ancestors of modern species, giving the fauna an overall modern resemblance. Most modern species occur around the Philippines. In addition, two of the species are shared with Neogene deposits from western Pacific islands. The new fauna offers insights into the character of deep water Indo-West Pacific mollusc faunas prior to the onset of the Quaternary ice ages. The fauna also contains many other mollusc species still waiting to be studied.

T3.P3

PATTERNS OF LAND SNAIL SUCCESSION IN CENTRAL EUROPE OVER THE LAST 15.000 YEARS: MAIN CHANGES ALONG ENVIRONMENTAL, SPATIAL AND TEMPORAL GRADIENTS

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Location of Central Europe at a transition of climatic zones and between continental and alpine glacial ice sheets gives this area a high potential to understand postglacial spreading and distribution of species in the entire temperate Europe. Within Central Europe, the Czech Republic and Slovakia belong to regions with the densest network of Holocene mollusc successions, enabling a fine spatial resolution. From more than 300 existing profiles we selected 91 the most important sites for radiocarbon dating and a detailed palaeoecological analysis in order to cover variation of habitat types, altitude, type of deposit, and time span over the last 15.000 years. We seek for the main patterns of species richness and compositional changes since the Late Glacial; also in reaction to biogeographically boundary between the Continental and Atlantic Europe. On the basis of 828 mollusc assemblages recorded in samples of all lithologically distinct layers of each succession we modelled changes of species richness within the main ecological groups of land snail in order to find differences between general and local development across the elevation and geographical position. We found significant changes along the age for both species richness and proportional representation of species classified into the main ecological groups. We observed that proportional representation of forest and open country species reversed just at the Pleistocene/Holocene transition. Changes of species richness were rather small across the study area and elevation, contrary to changes in species composition. MDS ordination based on presence/absence data distinguished four main patterns of species composition associated with the number of forest species in assemblages, position of site along the west-east direction, moisture of site, and age of samples. We described general patterns of the Central European mollusc succession, which seems to be, however, rather unique for Central Europe.

T3.P4

PATTERNS OF DISPARITY AND DIVERSITY: INDUCED MORPHOLOGIC VARIATION OF VENERID BIVALVES (BIVALVIA: VENERIDAE) OF THE INDO-PACIFIC

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Studies of modern taxonomic richness look increasingly to the fossil record for information about the formation and maintenance of biodiversity. As a hotspot of modern diversity in marine habitats, the Indo-Pacific has been recognized as a persistent center of origination for the majority of the Cenozoic. In this context, I am investigating the evolution of venerid-bivalve biodiversity throughout the Indo-Pacific with the goal of understanding causal mechanisms for the development of the tremendous molluscan diversity observed in terms of both species richness (ie. *biodiversity*) and morphologic variation (i.e. *disparity*).
I hypothesize that closely constrained biotic interactions, such as the agonistic relationship between venerid bivalves and their predators, shell-drilling gastropods, may cause directional changes in shell shape and form as a heritable phenotypic response. Further, this evolutionary response may contribute to genetic differentiation and promote speciation within pre-existing clades. Here, I report an assessment of morphologic variation, by utilizing both landmark and outline morphometric techniques, among Neogene venerid genera from the Indo-Pacific. I constrain these analyses in a stratigraphic and geographic context, taking into account the frequency of drilling predation as a potential function of morphological variation.
Morphometric analyses of venerid genera demonstrate that taxa are randomly distributed throughout shape space with respect to geographic and temporal distributions. However, when predation instances (i.e. drilled specimens) are superimposed on the ordination in shape space, a bias in prey selectivity is observed.

T3.P5

ARCHAEOMALACOLOGICAL STUDY OF LA GARMA B CAVE (CANTABRIA, SPAIN)

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La Garma B is one of the caves in La Garma Archaeological Complex (Omoño, Ribamontán al Monte, Cantabria). Two multiple burial phases were defined during the 1995-1999 archaeological excavation, one dated to *c*. 3000-2500 cal BC and corresponding to the early Copper Age (layer C), and another one dating to *c*. 2200-1600 cal BC and ascribable to the early Bronze Age (layer A). Most of the archaeological content of the cave corresponds to the latter, including human remains, mammal bones and molluscs, as well as pottery, lithic implements and some metal objects.

This contribution studies the archaeomalacological evidence (marine and terrestrial molluscs) in this burial cave from different points of view: taxonomy, taphonomy, technology, stratigraphy and spatial distribution. The marine species are dominated by limpets (*Patella intermedia*, *Patella ulyssiponensis* and *Patella vulgata*). Topshell *Osilinus lineatus* and the mussel *Mytilus* sp. are also present, but to a lesser extent. The marine molluscs were gathered on the coast, currently located about 5 km from the cave. A total of 12 terrestrial snails taxa have been found. *Cepaea nemoralis* is the more abundant and dominant species, and the only one that appears to have been gathered to be eaten. It shows a high proportion of apices among the MNI, which can be indicative of a poor state of conservation of the remains, perhaps derived from the humidity of the site. *Discus rotundatus* is the second more abundant land snail species. Its small size makes it unlikely that it was used as food. Yet its occurrence might be also indirectly derived from human activity. Snails of this species are frequently adhered to fallen leaves, so they might have been undeliberately introduced in the cave with some kind of vegetal matter. Finally, the relevance of malacological analysis in funerary archaeological contexts will be discussed.

T3.P6

ADAPTIVE RADIATION OF NERITOID GASTROPODS: TRANSITIONS BETWEEN MARINE AND FRESHWATER ENVIRONMENTS IN THE ONTOGENETIC CYCLE AND PAST EVOLUTIONARY HISTORY

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The transition from marine to freshwater habitats is one of the most significant steps in animal evolution. The Neritoidea are common and diverse members of the gastropod superorder Neritimorpha in rocky shores, seagrass beds, submarine caves and deep-sea hydrothermal vents and cold seeps, as well as in mangrove swamps, estuaries, rivers, streams and lakes. Interestingly, a previous phylogenetic reconstruction of this superfamily based on morphological characters suggested multiple habitat transitions from marine to freshwater, although the robustness of the tree topology was not tested and the history of their radiation has remained largely elusive.

Here we present a comprehensive, well-supported phylogeny of Neritoidea based on four gene sequences (5 kbp in total) from approximately 60 species representing most extant genera in Neritidae, Phenacolepadidae and Neritiliidae. Bayesian and likelihood reconstruction not only confirms the repeated invasions of freshwater by marine ancestors but also suggested multiple reinvasions of the sea from limnic habitats. A very plausible explanation for such frequent and unusual habitat shifts is the euryhaline nature of most limnic neritoids in their amphidromous life cycle: hatched larvae are swept downstream to the sea and metamorphosed juveniles settle at river mouths and then migrate upstream. Morphological and ontogenetic traits that would be adaptive in amphidromy have also been acquired in parallel. The most striking case concerns four independent losses of shell coiling and functional operculum to better facilitate upstream migration, resulting in the near-identical appearance of the polyphyletic *Septaria*. Our global investigation on the settlement size of neritoid planktotrophs revealed specific size ranges for individual clades that are useful in classifying fossils, although two amphidromous lineages were found to have independently acquired the smallest settler sizes, presumably to reduce probability of abortive dispersal through shorter metamorphic competence time while retaining ability of occasional long-distance trips with an extended delay period.

T3.P7

DEVELOPMENT AND CHARACTERIZATION OF MICROSATTELITE LOCI FOR THE HARVESTED LIMPETS *PATELLA CANDEI* (D'ORBIGNY, 1839) AND *PATELLA ASPERA* (RÖDING, 1798) USING 454 SEQUENCING

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There is growing consensus that anthropogenic activities are impacting the structure and functioning of marine ecosystems and that these can have profound community-level effects, particularly when targeting keystone species. Limpet harvesting in Azores (NE Atlantic) has been taking place probably since the islands were first colonized. These species are highly exploited and the stocks in most islands have declined steadily with catastrophic effects on coastal communities. They are a locally important resource but also ecologically important species and require prioritizing conservation strategies. Such strategies should be supported by reliable data on the structure and dynamics of their populations, so that ecological hotspots are identified and protected. Characterizing the genetic diversity and structure of marine exploited populations is thus of paramount importance to identify such units of conservation. Here we describe and develop species-specific microsatellite markers for the harvested limpets *Patella candei* and *Patella aspera* using whole genome shotgun 454 sequencing. A total of 309 bioinformatic-validated pairs of primers were obtained from *P. aspera* microsatellite-enriched library. The optimization of the amplification conditions of selected microsatellites (simplex and multiplex reactions) was performed in a gradient thermal cycler to optimize locus-specific amplification conditions and test their utility as genetic markers. Forty pairs of primers were tested, and about 28 revealed to be polymorphic. Using the same procedure, a total of 107 pairs of primers were validated for *P. candei* of which 15 turned out to be polymorphic. These novel genetic markers can be used to study the population genetic structure and evolutionary history of both patellid species e.g. levels of genetic variability within and between populations, and thus to contribute for stock conservation and management along their distributional area.

T3.P8

MOLECULAR SYSTEMATICS AND EVOLUTION OF THE HELICOIDEA (GASTROPODA, STYLOMMATOPHORA) OF THE WESTERN PALEARCTIC

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The Helicoidea, Rafinesque, 1815, is the most diverse group of the terrestrial molluscs of the Western Palaearctic, with its distribution center being located in the Mediterranean region where it locally can represent more than half of the molluscan biodiversity. It contains several families and genera of uncertain phylogenetic relationships.

The classification of the Helicoidea is mainly based on the morphology of shell and reproductive system, but there are still some controversies between the main classification systems. In addition the analysis of the possible ways of evolution within the Helicoidea requires other sources of information. In this work we are using the molecular techniques to progress in the resolution of the taxonomy, phylogeny, and evolution of this interesting group.

The main objectives of this work were to determine the phylogenetic relationships between the genera distributed throughout the Western Palearctic, as well as to clarify the phylogenetic relationships between some of the worldwide distributed families. We also studied the evolution of several organs used extensively to the classification of the Helicoidea.

We show the results of the analysis of 121 species belonging to 9 families (Sphincterochilidae, Elonidae, Helicodontidae, Trissexodontidae, Hygromiidae, Helicidae, Bradybaenidae and Humboldtianidae). One mitochondrial gene (16S rRNA) and one nuclear gene fragment (5.8S - ITS2 - 28S rRNA) were selected for this study in order to compare the new sequences with those obtained previously by other authors. The validity of the taxa considered in the main classification systems were contrasted with the phylogenetic tree obtained. Afterwards, we used the phylogenetic information to evaluate the evolution of different organs of the reproductive system, including the following: diverticulum of bursa copulatrix, dart sac with dart, accessory sac, mucous glands, as well as the relationship of the ocular retractor muscle and genital system.

T3.P9

PHYLOGENY OF PALAEOZOIC GASTROPODS INFERRED FROM THEIR ONTOGENY: HOW MANY HIGHER-LEVEL CLADES LIVED DURING PALAEOZOIC ERA?

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Gastropods are not only one of the most diverse groups of living animals occuring in marine, freshwater as well as terrestrial environments, but also have a rich fossil record extending back to the Cambrian. Because a third of all gastropod families are extinct, understanding of gastropod evolution and phylogeny necessarily involves study of both fossil and living species. Knowledge of the latter can be obtained from anatomical, morphologic, and molecular data, but for extinct forms virtually the only data source is the shell; typically it presents us with few characteristics. For both living and fossil gastropods, elucidation of ontogenic strategies is of prime importance in understanding the high-level phylogeny of this enormously diverse group. The analysis of Palaeozoic gastropods presented here relies heavily on ontogenies based on shell characteristics. It is argued that these results coordinate well with phylogenies of living gastropods inferred from the wider aggregate of anatomical, morphological, and molecular data. On the other hand, the analysis has highlighted problems with published phylogenies of living gastropods and, moreover, has produced evidence for the existence of several order-rank and long-lasting gastropod lineages forming an important part of Palaeozoic gastropod faunas but which failed to cross the Permian–Triassic boundary. Clearly, for understanding the phylogeny of the Gastropoda, it is imperative that the history of fossil gastropod clades be included.

T3.P10

MITOCHONDRIAL GENOMES OF EIGHT SPECIES IN VETIGASTROPODA (MOLLUSCA: GASTROPODA)

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Mitochondrial DNA sequences have been commonly used in the studies of molecular phylogenetics and evolutionary biology. The gene order of mtDNA in animal kingdom

is generally conserved at high taxonomic levels but can be somewhat variable across taxa in Mollusca. Gene order variation may provide useful phylogenetic information for resolving evolutionary relationships of the deep branching lineages within taxa. The Vetigastropoda, one of the mollusk orders, is a highly diverse group containing thousands of living species. Its phylogeny is still poorly resolved and mitogenomics does not bring decisive insights beacuse only 6 complete mt genomes belonging to 3 families have been determined up to now. In this study, long PCR and primer walking method were used to acquire the whole mt genomes of 8 additional vetigastropods, including two Turbinidae species, *Lunella granulata* (Gmelin, 1791), *Astralium haematragum* (Menke, 1829), two Trochidae species, *Chlorostoma argyrostoma* (Gmelin, 1791), *Omphalius nigerrima* (Gmelin, 1791), one Angariidae species, *Angaria delphinus* Linnaeus, 1758, one Stomatellidae species, *Stomatella planulata* (Lamarck, 1816), one Pleurotomariidae species, *Perotrochus hirasei* (Pilsbry, 1903), and one Fissurellidae species, *Variemarginula punctata* (Adams, 1852). The size of these mt genomes is approximately 13,475 – 19,554 bp and each mt contains 13 protein-coding genes, 2 ribosomal RNAs and 21 to 22 transfer RNAs. The gene order of these eight mt genomes was compared with others published vetigastropod mt genomes, mainly from the family Haliotidae. The phylogenetic analyses were also conducted to provide a new perspective on the relationships among the main lineages of this group. Yet, more gastropod mt genomic data are needed for a better understanding on the gastropod mitochondrial evolution, especially within the Vetigastropoda.

T3.P11

MOLECULAR PHYLOGENY AND REVISION OF AUSTRALIAN *MELO* SPECIES (VOLUTIDAE)

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Volutidae from the genus *Melo* are commonly known as Baler or Bailer shells. This derives from the function they fulfilled for some indigenous peoples, as devices to remove water from canoes. In Australia they were also prized as water holders and for fashioning shell craft (ceremonial use). Whole shells or pieces have been traded for hundreds of miles inland. *Melo* species are found on the coast of almost all of Australia, except NSW, eastern Victoria and Tasmania. They can reach very large sizes (over 40cm), and the shells are very variable in characters such as colour and shoulder spine extensions. There are unconfirmed reports of hybridization occurring between species in regions such as Shark Bay, WA and Hervey Bay, QLD. We are using mitochondrial genes COI and 16S, and the nuclear ADP/ATP translocase gene to understand the relationships among *Melo* species. This work will assist delimiting and identifying species and their distributions, and understanding how variable some of the characters currently used to identify species can be.

T03.P12

VERTICAL TRANSMISSION OF BACTERIAL SYMBIONTS IN THE FAMILY ASTARTIDAE (BIVALVIA)

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The periostracum of the species from the family Astartidae is characterized by having a pitted surface. The presence of bacteria inside the pits has been previously reported for *Digitaria digitaria* (L., 1758) and this seems to be the general rule for the other genera of the family. In order to check the relationship between the bacteria and the bivalves, we studied the pathway of transmission using semi-thin sections and transmission electron microscopy. The presence of bacteria inside bacteriocytes inside the gonads of *Digitaria digitaria* and *Astarte cf. undata* Gould, 1841 has been observed. In *Goodallia triangularis* (Montagu, 1803), a brooding species, the bacteria appear inside the oocyte. These results point out an endosymbiosis, a mutually obligate association in which the symbiotic bacteria are maternally transferred. This is assumed to involve co-evolutionary interactions.

T3.P13

ON THE PHYLOGENETIC POSITION OF THE ENIGMATIC ABYSSOCHRYSOIDEA (GASTROPODA)

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In 1989, a French expedition in Southwest Pacific found marine snails living at depths around 2000 mlinked to hydrothermal vents. It was a surprised that these marine snails showed rather distinct morphologies and were initially recognized as Caenogastropoda with uncertain phylogenetic position. At present, these gastropods are assigned to the superfamily Abyssochrysoidea, which includes two families, Provannidae and Abyssocrysidae with 5 and 2 living genera, respectively. Previous studies place the group variously outside Hypsogastropoda based on morphology or as sister group of Littorinidae based on mitochondrial 16S gene. Thus, their exact phylogenetic relationships within Caenogastropoda remain unclear. In this study, we sequenced the complete mitochondrial genome of *Ifremeria nautilei* (Provannidae), in order to elucidate the relative phylogenetic position of Abyssochrysoidea within gastropods.
We sequenced and assembled the mitochondrial genome of *I. nautilei* using Next Generation Sequencing (Illumina). The gene order was compared to genome organization of other 14reported gastropod mitogenomes belonging to Neritimorpha, Vetigastropoda, Patellogastropoda, Caenogastropoda and Heterobranchia, and a

cephalopod mt genome. The gene order arrangement is typical of a Caenogastropoda, differing in the position of the *trnW*gene with respect to Rissoidea, Tonnoidea and Muricoidea. Phylogenetic analyses based on concatenated protein-coding genes at the amino acid level nested *I. nautilei* deep within Hypsogastropoda and closely related to Rissoidea, Tonnoidea, Conoidea, and Muricoidea. Additional analyses using concatenated nuclear genes recovered similar results.

T3.P14

HELIX STRAMINEA – A FORGOTTEN ESCARGOT WITH TRANSADRIATIC DISTRIBUTION

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Helix Linnaeus, 1758 is a genus of large land snails diverse in the Mediterranean region. Although it is probably the most familiar European snail, it has still an unsettled taxonomy. One of the problematic taxa is the widely distributed and economically important *Helix lucorum* Linnaeus, 1758. The species is conchologically very variable, with many described synonyms. In Italy two conchologically distinct forms may be encountered under this name. Whereas a typical *H. lucorum* lives in the north of the country, the form from central and southern Italy is different. It had been described as *Helix straminea* Briganti, 1825 but later it was synonymized with *H. lucorum.* Conchologicaly it resembles the Balkan species *H. vladica* (Kobelt, 1898) instead of *H. lucorum*, differing from the latter by larger protoconch and coloration pattern. To test the hypothesis that *H. straminea* is a valid species, and to evaluate its relationship to some other species from Italy and the Balkans, we have used 16S and COI phylogeny and a shell-shape analysis. According to our results, *Helix straminea* is a separate species unrelated to *H. lucorum. Helix vladica* is a junior synonym of *H. straminea,* and two problematic Balkan taxa, *H. volensis* Kobelt, 1906 and *H. vardarica* Knipper, 1939, are also likely synonymous with *H. straminea* on the basis of shell characters. The species is morphologically variable but it can be reliably identified based solely on conchological characters. It is conchologically so distinct that we could use photographs available on web pages among the sources when assessing its range. *Helix straminea* has a disjunctive transadriatic range, and it is not closely related to any other Italian *Helix*. Its closest relatives are found in the western Balkans, the distribution of haplotype groups indicate a possible colonisation of the Apennines from the south across the Adriatic Sea.

T3.P15

MOLECULAR PHYLOGENY OF THE GENUS *XEROCRASSA* IN THE BALEARIC ISLANDS

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Xerocrassa Monterosato, 1892, is a genus widely distributed in the Mediterranean area, with several species endemic to the Balearic Islands. It is present in all the main islands of the archipelago: Majorca, Minorca, Ibiza and Formentera, and it is also present on some small islets of this archipelago. Currently, there are considered as many as 10 species with 22 subspecies: two species living in Minorca, another five (with nine subspecies) in Majorca and three more in Ibiza-Formentera (with at least thirteen subspecies). Two main shell forms can be recognized in these species, i) the form of the Gymnesias (flattened with pronounced ribs and keels), and ii) the form of the Pytiusas (bigger, rounded and with less prominent sculpture).

For this work, populations belonging to nearly all taxa (including some populations of all the species) were studied by sequencing two mitochondrial DNA gene fragments (COI and 16S rRNA). A total of 65 specimens were included in the molecular work. The tree obtained recovered the monophyly of all the Gymnesian species. Nevertheless, the three species from the Pytiusas were not recovered as monophyletic groups. As a result, the intraspecific phylogroups we obtained within *Xerocrassa caroli*, *X. cisternasi* and *X. ebusitana* were in conflict with the current taxonomy of several subspecies. We discuss the new results on the basis of morphology, DNA sequencing and biogeography. Our results indicated that in some cases geographical distribution, better than shell morphology explained the phylogroups. *Xerocrassa molinae* from the Columbretes Islands (50 km in front of the Iberian Peninsula) was also included in the study, and it seemed to be phylogenetically more related to species from Ibiza than to species from the Iberian Peninsula.

T4

BIODIVERSITY AND EVOLUTION OF PULMONATE TAXA

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Many aspects of the evolution and biodiversity of pulmonate gastropods are still poorly understood. At higher levels, phylogenetic relationships among the major clades (e.g., Stylommatophora, Veronicellidae, Hygrophila, Onchidiidae) are far from being resolved, not to mention the relationships of pulmonates with respect to opisthobranchs. At lower levels, many taxa would need to be revised taxonomically, and many species remain to be discovered in the field, especially for stylommatophorans. This symposium will present some of the current research done on pulmonates. Some of the themes covered include: species diversity and field exploration, taxonomic revisions, higher phylogenetics, and macroevolution.

T4.O1

USING 'NEXT GENERATION' SEQUENCING TO RESOLVE DEEP PHYLOGENETIC RELATIONSHIPS IN THE LAND MOLLUSCS (EUPULMONATA)

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Despite much effort by systematists and phylogeneticists over the last few decades to determine the deep evolutionary relationships within the pulmonates, much remains tentative and controversial. Molecular techniques have increasingly been used to help resolve the phylogenetic relationships within many molluscan taxa over the last 20 years, however, this approach is currently restricted by the limited number of molecular markers available. This has often resulted in poor phylogenetic resolution as well as incongruence between independent studies. It is now well-established that a consensus arising from a much larger set of independently evolving nuclear loci is needed to adequately assess and resolve evolutionary relationships across all evolutionary depths. 'Next generation' sequencing (NGS) refers to a set of forefront molecular sequencing technologies which have the potential to revolutionise the field of molecular phylogenetics by allowing for rapid 'genome wide' sequencing. These techniques result in vast amounts of genomic information from which thousands of genes can be screened and identified to produce large multi-loci datasets. The broad objective of our study is to sequence and assemble multiple transcriptome datasets (i.e. mRNA, representing expressed protein coding genes) and use this information to identify a set of single copy orthologous genes which can be used to address deeper evolutionary relationships within Panpulmonata with a focus on the eupulmonates (terrestrial molluscs). So far we have sequenced and assembled transcriptomes for 45 species from across

Panpulmonata and have identified over 500 nuclear genes suitable for phylogenetic use. Here we present preliminary phylogenetic analyses arising from this work, and outline a “targeted enrichment” protocol for obtaining large multi-loci datasets from old natural history specimens.

T4.O2

SYSTEMATICS AND BIOGEOGRAPHY OF SOUTHERN AFRICA’S DWARF CANNIBAL SNAILS (PULMONATA: RHYTIDIDAE)

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The southern African radiation of the Gondwanan snail family Rhytididae has traditionally been considered to comprise two major lineages, the cannibal snails (*Natalina s.l.*) and dwarf cannibal snails (*Nata s.l.*). Having completed our revisionary studies on the larger species, our attention has turned to the dwarf species. While *Nata* (*s.l.*) is not a diverse group, species delineation is rendered complex due to limited interspecific variability, combined with significant intra-specific variability in shell form. It is also bedeviled with synonymy. To date, species discrimination based on shell characters has often been tentative and the taxonomy and systematics of the genus is much in need of revision. To address this we have used a combined approach employing both morphological and molecular data.

Morphological revisionary work suggests the existence of six distinct species (two undescribed) and molecular sequence data confirm the monophyly of these lineages. In most cases the species have somewhat restricted distributions, particularly the four endemic to the southern Cape. One species, however, is widely distributed, but it exhibits strong phylogeographic structure. At a deeper level, *Nata* (*s.l.*) appears to have diverged from the ancestral rhytidid stock at an early stage, with interspecific divergences being exceptionally deep relative to other genera within the family. Consequently, whether the southern African rhytidids, or indeed *Nata* (*s.l.*) comprise genuinely monophyletic entities remains unresolved, but this is an issue we hope to explore further by using Next Generation Sequencing methodology and by adding further taxa from Australia and New Zealand to give a broader Gondwana perspective.

T4.O3

A BIODIVERSITY HOTSPOT HOT FOR LAND SNAILS TOO: THE CASE OF MAPUTALAND-PONDOLAND-ALBANY

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Boundaries of biodiversity hotspots are often delimited intuitively based on floristic endemism and have seldom been empirically tested on species distributions, especially of endemic fauna. Here we attempted to numerically analyse the zoogeography of the malacofauna in south-eastern Africa, focusing on evaluating the delimitation of the Maputaland-Pondoland-Albany (MPA) biodiversity hotspot, while proposing a first mollusc-based numerical regionalisation for the area. We also discuss patterns and centres of land snail endemism and then assess the importance of the MPA hotspot for their conservation. A species incidence matrix for selected, taxonomically well-known and fairly uniformly and well-collected lineages of land snails and slugs (seven genera; 75 species) in 40 predefined operational geographic units was compiled from the KwaZulu-Natal Museum Mollusca database. The data matrix was subjected to two types of numerical analyses, *viz.* hierarchical clustering using the unweighted pair-group method with arithmetic averages (UPGMA) and the Parsimony Analyses of Endemicity (PAE). While the UPGMA dendrogram provides a hierarchical regionalisation of the area, UPGMA and PAE dendrograms were respectively used to determine centres and areas of endemism (COEs and AOEs). The above results, as well as geographical patterns mapped for measures of endemism (e.g. weighted endemism) support a greater Maputaland-Pondoland-Albany (GMPA) region of endemism for molluscs (more similar to the same published for vertebrates, than to the more restricted MPA hotspot). Zoogeographical regionalisation confirms a south-east Africa dominion, congruent with that of vertebrates, within which the GMPA is recognised as a province, while subordinate districts and assemblages are identified. Although the MPA hotspot is found to be valid for terrestrial molluscs, the GMPA region provides a more robustly defined zoogeographical entity and a region of conservation concern, with COEs serving as local conservation priorities. The study emphasises the importance of quantitative biogeographical methods in conservation biogeography, in addition to their uses in theoretical biogeography.

T4.O4

TOWARDS A REVISION OF A TAXONOMICALLY DIFFICULT SNAIL FAMILY: PROBLEMS WITH DEFINING NEW SPECIES OF GLESSULIDAE IN NEPAL (GASTROPODA: PULMONATA: STYLOMMATOPHORA)

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The Glessulidae Godwin-Austen, 1920 (sometimes also considered as a subfamily of the Subulinidae) is one of the most speciose achatinoid families. There are more than 160 nominal species, the majority of which have been described from India and Sri Lanka, and with fewer species reported from Myanmar, Thailand, Borneo, Sumatra, Java and Vietnam. Most of these nominal glessulid species are poorly known, which is well-illustrated by the fact that there are anatomical data for only six species. Hence, most glessulid species have been described on the basis of shell characters only. Currently, two genera *Glessula* Martens, 1860 and *Rishetia* Godwin-Austen, 1920 are recognized, though several authors only retain *Glessula*, with *Rishetia* as a subgenus.

Hitherto, only two glessulid species have been recorded in Nepal, viz. *Glessula subjerdoni* Bedome, 1906 and *Rishetia tenuispira* (Benson, 1836). Yet, newly collected specimens from all over Nepal do not only show that the Nepalese glessulid fauna is more diverse than these literature records indicate, but also suggest that both species may have been misidentified. Against this background, the present study provides new data on the reproductive anatomy of eleven glessulid taxa from Nepal (three *Glessula* and eight *Rishetia*). Several of these taxa are probably new to science, but their description as new species faces a number of practical problems that will be discussed.

T4.O5

DIFFERENTIAL SURVIVAL AMONG TAHITIAN TREE SNAILS DURING A MASS EXTINCTION EVENT: PERSISTENCE OF THE RARE AND FECUND

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The deliberate introduction of the carnivorous Rosy Wolf Snail (*Euglandina rosea*) to the Society Islands archipelago in the 1970's led to a mass extirpation of its rich Partulidae fauna, comprising approximately half of all species in this Pacific Island tree snail family. On Tahiti, the largest island in the archipelago, ongoing field surveys have encountered scattered remnant populations of two closely related species, *Partula clara* and/or *Partula hyalina*, in 38 valleys. *E. rosea* is now a potent predator responsible for the extinction of many endemic land snail species across Oceania, and understanding why these Tahitian taxa have differentially survived almost 40 years of predation pressure may have regional conservation import. A null hypothesis states that *P. hyalina* and *P. clara* have

survived because they were the most abundant and/or widespread species and that they too, will eventually be driven to extinction by the predator. We lack demographic data contemporaneous with *E. rosea*'s introduction, but H. E. Crampton's remarkable 1906-1909 survey of the island contains a wealth of demographic information for intact Tahitian valley populations. His data show that *P. clara* and *P. hyalina* were widespread but were consistently much rarer than their now-extirpated co-occurring congeners, including in the 23 valleys he surveyed a century ago that retain surviving populations. Given this result, might there be an intrinsic aspect of their biology that has allowed them to differentially persist? Crampton recorded the clutch sizes of individual gravid snails and his data show that *P. clara* and *P. hyalina* consistently had higher instantaneous mean clutch sizes per gravid female reproductive tract than their co-occuring congeners. Higher fecundities may have been a contributing factor in the differential survival of *Partula hyalina* and *Partula clara* in the valleys of Tahiti.

T4.O6

A PRELIMINARY PHYLOGENY AND BIODIVERSITY ASSESSMENT OF THE HAWAIIAN HELICINIDAE

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Hawaiian land snails are incredibly diverse with >750 species and 99% endemicity. Unfortunately they are rapidly going extinct due to habitat destruction, climate change, and invasive species. Like most Hawaiian land snails, the Helicinidae have not been studied comprehensively in more than 60 years. This family of terrestrial operculate snails consists of 500+ species distributed throughout tropical and subtropical regions of the world except for Europe. They are among the oldest known terrestrial snail families, and may be a good system to address questions of evolutionary transitions from marine to terrestrial habitats and gastropod evolution broadly. Hawaii has 14 recognized helicinid species in two genera (*Pleuropoma* and *Orobophana*) and 43 varieties. They were described from all main Hawaiian Islands, but have not been monographed since 1934 and little is known about their current distributions or remaining diversity. As part of an effort to update their taxonomic and conservation status, we have constructed a preliminary molecular phylogeny of Hawaiian helicinids using mitochondrial (COI) and nuclear (28S) sequences from material collected during recent biodiversity surveys and specimens from the Bishop Museum in Honolulu. Extensive surveys on six of the main Hawaiian Islands have so far recorded seven helicinid populations on only two islands, Kauai and Oahu. Clearly, their ranges have been drastically reduced, as has much of the original species diversity. However, species diversity is probably higher than initially estimated, with cryptic species among those described as varieties. Initial results indicated that some of the Oahu species are basal to Kauai species, despite Kauai being an older island and the expectation that older lineages are found on older islands. Analyses of molecular data also indicated that Hawaiian helicinids are distantly related to non-Hawaiian Helicinidae genera, and that Hawaiian taxa are in need of extensive taxonomic revisions.

T4.O7

SHELL ONTOGENY AND VARIABILITY OF SHELL MORPHOLOGY IN POPULATIONS OF *LEPTINARIA UNILAMELLATA* (D'ORBIGNY, 1835) (MOLLUSCA, PULMONATA, SUBULINIDAE)

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Recent studies concerning species of land snails have revealed that the shell morphometrics can provide evidence of the differentiation among populations. In many cases, the morphologic analysis combined with the investigation of molecular variability, can support changes in taxonomy of studied groups. The main objectives of this work were to describe the shell ontogeny of *Leptinaria unilamellata*, and to investigate if snails from different populations demonstrate variations in the patterns of shell morphology and shell morphometrics. It was also verified if such variations were reflected in the differences in the shell forming process. The morphological and ontogenetic pattern differences were collected among snails from four different populations, kept under the same laboratorial conditions. It was possible to distinguish characteristic shell morphometrics for snails from each location. At a few stages there were similarities in growth allometry, which indicated that the whole shell forming process is different among these morphotypes, not only the final form of the adult's shell. This fact suggests that such characteristics are primarily under genetic determination. The shell ontogeny study provided an understanding of the shell formation pattern and the structural mechanisms along the development of the molluscs that create the diversity observed. For the snails with determinate growth, species distinction is difficult during the juvenile phase, due to the great similarity of shell morphology. It is possible that shell characteristics, considered important for taxonomy can also be present from the initial developmental phases. In this sense, an in depth revision of genus *Leptinaria* is necessary. It is possible that the shell differences that justified the creation of the new *Leptinaria* species represent polymorphisms or variations related to shell ontogeny. Alternatively, superficial shell similarities might have obscured cryptic complex species, which would make more studies necessary to access the morphological and genetic variability among populations.

T4.O8

SPATIAL PATTERNS OF CRETAN LAND SNAILS

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The current work is a first approach of the potential spatial distribution of the Cretan land snails. The maximum entropy (MaxEnt) analysis was used to model the potential

distributions of 56 land snail species. MaxEnt is a machine learning method that predicts the potential distribution of a target group over a geographical region from a sample of presence localities and a set of environmental data. The effect of the environmental parameters that were used to model the potential distribution of the species is explored. Results show that temperature contributes to the explanation of the potential distributions of 35 species, while two other important factors seem to be rainfall and land cover. Moreover, species with restricted distribution range, such as *Albinaria eburnea*, have higher AUC values (higher than 0.8), while species with a broader range, such as *Cantareus aspersus* have lower AUC values (lower than 0.7). The potential distributions of most species, e.g. *Poiretia dilatata* and *Trochoidea* sp. are quite precise. However, MaxEnt does not take into account historical data, e.g. the paleogeography of the area, which is most likely affecting the distribution of some species (*Metafruticicola dictaeus*), as a result the potential distribution is not precise.

T4.O9

A COMPARISON OF METHODS FOR DELIMITING SPECIES IN A CRETAN LAND SNAIL RADIATION REVEALS SHORTCOMINGS OF EXCLUSIVELY MOLECULAR TAXONOMY

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We compared the results of different approaches for delimiting species based on single-locus DNA sequences with those of methods using binary multilocus data. As case study, we examined the radiation of the land snail genus *Xerocrassa* on Crete. Many of the methods based on mitochondrial sequences resulted in heavy under- or overestimations of the species number. The methods using AFLP data produced classifications with an on average higher concordance with the morphological classification than the methods based on mitochondrial sequences. However, the percentage of correct species classifications is low even with binary multilocus data. Gaussian clustering produced the classifications with the highest concordance with the morphological classification of all approaches applied in this study, both with single-locus sequences and with binary multi-locus data. Methods for species delimitation using genetic data search for clusters of individuals, but do not implement criteria that are sufficient to distinguish clusters representing species from other clusters. The success of morphological species delimitation results from the potential to focus on characters that are directly involved in the speciation process, whereas molecular studies usually rely on markers that are not directly involved in speciation.

T4.O10

DIFFERENT EVOLUTIONARY HISTORIES IN TAXA: REASONS AND CHALLENGES. A CASE STUDY IN *TROCHULUS* (GASTROPODA: PULMONATA: HYGROMIIDAE)

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Classical taxonomy and evolutionary phylogeny of organisms often stand in contradiction, as the first is a man-made order system, while the latter is an attempt to reconstruct evolutionary relationships. Concerning pulmonates we point out these problems on three taxa of the genus *Trochulus*, in which the terms species and subspecies are used at completely different levels. *T. hispidus* is presently treated as a species complex because of its great variability in morphology and genetics. Moreover, in mitochondrial and nuclear trees it is paraphyletic, as morphologically well-defined species are intermingled between the clades representing *T. hispidus*. Whether there are cryptic species within *T. hispdius* remains to be investigated, but even delineation of subspecies failed so far because of the lack of distinctive traits. In contrast, the differentiation of the genetically more uniform and clearly monophyletic *T. striolatus* into several subspecies is more straightforward and partially concordant with genetic differentiation. Finally, *T. oreinos* shows two morphologically and genetically widely separated subspecies, each of them displaying low variability. These inequalities are caused by different evolutionary histories as a consequence of different ecological niches, dispersal ability and glacial refugia: Both *T. hispidus* and *T. striolatus* are fast spreading, euryoecious organisms which are able to (re-)colonize habitats and survive under different climate conditions. While *T. hispidus* probably survived the Pleistocene in several glacial refugia, for *T. striolatus* one glacial refugium is assumed. *T. oreinos* differs from the other taxa, as it is a slow disperser with a narrow ecological niche. We assume that its subspecies spent at least the last glaciation close to the presently inhabited areas. Taxonomic revisions might be considered, but it should be concerned that taxonomic classifications may affect the state of protection.

T4.O11

THE CASE OF *PYRAMIDULA PUSILLA*: ADDING THE FIRST PIECES TO THE PHYLOGEOGRAPHIC PUZZLE OF ALPINE POPULATIONS

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In spite of the fact that the alpine pulmonate land snail *Pyramidula pusilla* (Vallot, 1801) is the most widespread species among the European representatives of the monotypic

family Pyramidulidae, it often remains unnoticed. One reason for this might be its relative small and inconspicuously coloured shell. The distribution of *Pyramidula pusilla* ranges from the Mediterranean area to Western and Central Europe where it inhabits sunlit calcareous rock and nourishes on endolithic lichens. Although it is quite common, the species' phylogeography has not been investigated so far. To gather first insights, we performed phylogenetic and morphometric analysis including geographic information of the sampling sites. Altogether we collected individuals at 98 different sampling sites mostly located in the Eastern Alps and investigated 357 individuals genetically, whereof 143 were also used for morphometric analysis. After extracting and sequencing a ~650 bp section of the mitochondrial *cytochrome c oxidase subunit 1* (COI) gene, we constructed a phylogenetic tree. This tree reveals at least two genetically distinct clades, which also appear differentiated in the morphometric analysis. The question whether those findings indicate the division into two kryptic species or only express a high degree of genetic and morphological variation within the Alpine population of *P. pusilla* cannot be ultimately answered and needs further studies on gene flow, reproductive barriers and nuclear markers.

T4.O12

PHYLOGEOGRAPHY OF THE LAND SNAIL GENUS *ORCULA* HELD 1837 WITH A SPECIAL FOCUS ON THE ALPINE SPECIES GROUP

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Most land snails have low active dispersal capabilities and inhabit small areas, facilitating the study of speciation processes and dispersal. In our study we performed a phylogeographic analysis of the rock dwelling land snail genus *Orcula* Held 1837, including all currently accepted species, twelve of which show an Alpine-Carpathian-Dinaric distribution and one occurring in the Western Black Sea region. Using three marker genes (*COI*, *12S* and *16S*), we set up a reliable mitochondrial phylogeny and found that the genus can be divided into three major groups: 1) the eight species with purely Alpine distribution form one clade, which is the sister group of the widespread *Orcula dolium*, 2) the second group consists of the Dinaric species *O. wagneri* and *O. schmidtii* and the Southern Carpathian *O. jetschini* and 3) *Orcula zilchi*, finally, represents the third major lineage. The Alpine species group comprises by far the largest number of species. Speciation and distribution within this group seem to be strongly influenced by the Pleistocene glaciations. Our data suggested that glacial refuges were located in the Western, north-eastern and south-eastern Alps. In addition, a comparison of mitochondrial and nuclear (*histone 3/4*) sequences indicated that hybridisation took place between some of the species during the Pleistocene but probably even up to the present.

T4.O13

MORPHOLOGICAL AND MOLECULAR ANALYSIS OF *SARASINULA* AND RELATED GENERA (GASTROPODA, VERONICELLIDAE) AND TAXONOMIC IMPLICATIONS FOR THE GROUP

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Morphological and molecular analyses were performed to delineate taxa in *Sarasinula*, a genus of terrestrial slugs of the family Veronicellidae, in view of the difficulties in differentiating its species and their long-confused taxonomy. The genus is important for agriculture and public health, including pest species and intermediate hosts of nematodes. We examined characteristics of the phallus, bursa copulatrix and coloration, and number of tubules at the digitiform gland from 428 specimens collected from 35 different countries. In addition, we sequenced fragments of the mitochondrial cytochrome oxidase I and/or 16S rRNA genes from 189 of the specimens. Phylogenetic analyses were conducted using species of *Angustipes*, *Latipes*, *Diplosolenodes*, and a new genus from Bolivia as out-groups. Based on preliminary tree searches using DNA sequences, *Sarasinula* is supported as a valid genus with four species: *S. plebeia*, *S. linguaeformis*, *Sarasinula* sp. 1 and *Sarasinula* sp. 2. The number of tubules at the digitiform gland and size of the reproductive structures can be an auxiliary character to discriminate them. *Sarasinula* n. sp. 2, with the largest size for the reproductive structures and around 15-20 tubules at the digitiform gland, probably resembles an ancestral condition in *Sarasinula*. The smaller reproductive system and smaller number of tubules (in general, not more than 9) found in *S. plebeia*, the most successful species of the genus (almost pantropical), seems to be a derived condition. *Sarasinula plebeia* is sister of the clade grouping *S. linguaeformis* and *Sarasinula* sp. 1, that are cryptic species, both with more tubules than 10 tubules at the digitiform gland. *Latipes* seems to be paraphyletic and needs to be better investigated, since *L. erinaceus* appears as sister-group of *Sarasinula* and not grouped with *L. lisei*, used as out-group as well. The new genus from Bolivia, here proposed, is a sister group of *Sarasinula* spp. plus *L. erinaceus*. *Angustipes angustipes* is supported as sister-species of the clade including *Sarasinula*, *L. erinaceus* and the new genus analyzed. *Belocaulus* is proposed here as synonymous with *Angustipes*. We support that *S. dubia* is a synonym of *S. plebeia*, and *S. marginata* is a synonym of *S. linguaeformis*. We also conclude that the black slug found in Honduras and Gulf states of the United States is *A. angustipes*, originally from southern South America east of the Andes as well as *Sarasinula*.

T4.O14

ADAPTATION OF FRESHWATER GASTROPODS ASSOCIATED WITH GEOTHERMAL HABITATS

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Thermal streams are natural incubators, where the water temperature remains more or less constant near the discharge for long periods of time. Hydrothermal systems are characterized by certain common environmental conditions, providing similar opportunities for the development of living organisms. In recent years a considerable amount of work has been done in the study of the fauna and ecology of molluscs in the thermal springs of different parts of the world. The information available on this question is fragmentary. It is our purpose on this occasion to analyze some features of the gastropod snails in thermal streams.

The authors studied the freshwater molluscs populations in geothermal streams of North European Russia, Kamchatka and Kuril Islands. Additional information has been obtained from number of publications about gastropods from other regions.

The comparative analyses reveal that in thermal streams formed similar communities of different species of gastropods (family Lymnaeidae, Planorbidae, Physidae, Thiaridae, Hydrobiidae, Neritidae etc.). These communities are characterized by high value of abundance and biomass, but very low species diversity. Molluscs in the process inhabit in thermal ecosystems acquire number of ecological, morphological and physiological adaptations. Investigations of growth, reproduction, life cycle and the effects of temperature showed that each population had a shortening of the life cycle, reducing the size of the shell and increase of number generations per year.

This study was supported by the grants of Russian Foundation of Basic Research № 12-04-31488_mol_a, № 13-04-10107_k; by the grants of Ural Branch of the Russian Academy of Sciences № 13-5-NP-11, № 12-P-5-1014, № 12-U-5-1022, № 12-45-M-2062, № 12-5-7-009; special grant from the President of the Russian Federation for state support of young scientists MD-4164.2011.5; Federal Target Program «Science and science-education specialists of innovative Russia for 2009-2013».

T4.O15

TOWARDS A MOLECULAR PHYLOGENY OF ELLOBIIDAE (GASTROPODA, PULMONATA) USING A MULTI-LOCUS APPROACH

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Ellobiidae are pulmonate gastropods occurring in intertidal, supratidal and even terrestrial habitats. The family Ellobiidae is subdivided in five subfamilies: Melampodinae, Ellobiinae, Pythiinae, Pedipinae and Carychiinae. Previous morphological and molecular work failed to support the monophyly of all of these subfamilies. Our aim is to infer a molecular phylogeny using nuclear and mitochondrial loci to assess the evolutionary relationships within this family. We used 40 samples comprising all subfamilies and sequences from Otininae (*Smeagol* and *Otina*), and Trimusculidae (*Trimusculus*), which

have been reported to be related to ellobiids. Veronicellidae (*Veronicella*) and Onchididae (*Onchidium*) were used as outgroups. A multi-locus approach was followed using six loci: three nuclear (28S, 18S and H3) and three mitochondrial (16S, 12S, COI). Trees were reconstructed using maximum likelihood (ML) and Bayesian inference (BI) on the CIPRES platform. We observed high and consistent support for the following clades: Melampodinae, Ellobiinae and Phytiinae, in both analyses. In Melampodinae, the genus *Melampus* resulted monophyletic; however, *Microtralia* and *Pseudomelampus* (Melampodinae) were closer to Otininae, although with low support. In Ellobiinae, we found two supported clades, one with the genus *Ellobium* and the other comprising the genera *Auriculinella*, *Blauneria*, *Cylindrotis*, and *Leucopythia*. In Phytiinae, two clades are also well supported: one with *Laemodonta* species and the other with *Cassidula* and *Ovatella*. Finally, *Trimusculus* was closely related to Pedipedinae forming a monophyletic clade. The phylogenetic position of *Carychium* (Carychiinae), and *Pythia* and *Myosotella* (Pythiinae) remains uncertain. Although *Carychium* and *Pythia* were grouped with high support in BI analysis, this clade is not supported in ML results. The search of a well-supported phylogeny of this family will provide a better understanding of patterns of past habitat shifts and terrestrialization.

T4.O16

HISTORY OF THE DIVERSIFICATION OF SURFACE AND SUBTERRANEAN MICROGASTROPODS (ELLOBIOIDEA: CARYCHIIDAE)

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Carychiid microgastropods (Eupulmonata, Ellobioidea) are common inhabitants of temperate biotas of the Northern Hemisphere with species frequently acting as handmaidens of taxonomists and systematists. In an integrative approach, we combine taxonomic and phylogenetic hypotheses to address species diversity and to analyze temporal and geographic diversification of epigean (*Carychium*) and subterranean (*Zospeum*) evolutionary lineages (ELs) in Carychiidae.

Until recently, carychiid snails have been identified on the basis of continuous conchological characters of the adult shell only. Following this traditional approach, we first postulated primary morphospecies hypotheses, which were then investigated by different molecular delimitation approaches (ABGD, GMYC, Statistical Parsimony, and threshold). Despite a conservative delimitation strategy, carychiid morphospecies comprise a great number of unrecognized diversity with 28 investigated morphospecies covering 43 genetically distinct ELs. Only 61% (17 morphospecies) are recovered as a single EL (= match between morphospecies assignment and genetic delimitation). In general, the non-trivial distinction between intra- and interspecific conchological variability most probably has led to past taxonomic lumping and splitting. An inferred wide distribution and variable phenotype suggest underestimated species diversity. However, by collecting morphospecies at their type locality, molecular investigations are able to link the historic morphospecies description with their respective EL. An example is presented for Japanese *Carychium*.

The first molecular phylogenetic hypothesis for Carychiidae (based on COI, 16S and H3) concurs with previous ecological and morphological investigations and reveals *Carychium* and *Zospeum* to be reciprocally monophyletic. Geographically proximally-distributed lineages are often closely related. The evolution of Carychiidae is characterized by relatively few (long distance) colonization events. Temporal diversification of lineages is best described by a constant rate model. We propose that rare founder populations initially colonized a continent or cave system. Subsequent passive dispersal into adjacent areas continuously led to *in situ* pan-continental or mountain range diversifications.

T4.O17

OPENING WINDOWS IN CARYCHIID TAXONOMY (ELLOBIOIDEA: CARYCHIIDAE) – A NEW PERSPECTIVE HIGHLIGHTS SOME KNOWN AND NOVEL MORPHOLOGICAL CHARACTERS IN THE SHELL AND RADULA

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Dependable shell characters are deficient in carychiid microgastropods (Eupulmonata, Ellobioidea). Taxonomists have relied upon variable characters such as the position and the degree of sinuosity of the parietal lamella, shell dimensions, external sculpture and aperture dentition in delimitating species. These characters are highly susceptible to phenotypic plasticity and have been subjected to a hazy history of frequently inadequate and often subjective species designations. Respecting earlier taxonomic designations based on these characters, recent molecular investigations have revealed that the morphospecies status of two European *Carychium* members (*C. mariae* Paulucci, 1878 and *C. hellenicum,* Bank & Gittenberger, 1985) comprise lineages of the hygrophilic *C. minimum* Mueller, 1774. On the other hand, these same investigations revealed that the North American morphospecies *C. stygium* Call, 1897 and *C. exile cf. mexicanum* Pilsbry, 1891 constitute a single taxon and that neither the species status of *C. stygium* nor the subspecies rank of *C. exile cf. mexicanum* hold. These investigations not only underscored the subjective splitting practice of taxonomists of yore, but also demonstrate the need for more consistent, reliable morphological characters to sufficiently designate this frequently misunderstood group.
Methods such as scanning electron microscopy (SEM) and x-ray nanotomography have enabled us to corroborate known information as well as to detect new structures. Our studies show that morphological characters such as pitting on the protoconch and interior shell resorption are consistent for the Carychiidae. A Carychium-type, rhipidoglossate radula has been investigated in one morphospecies of *Zospeum* and two morphospecies of *Carychium* (*C. stygium and C. hellenicum (C. minimum)*). Up to now, this radula type has been segregated and described in only a few carychiid members. Fine crystalline buttresses in the diaphanous shell walls of four investigated alpine *Zospeum* morphospecies have been revealed. Consistent in ten *Zospeum* and fifteen *Carychium* morphospecies are regularly angular, staple-like crystallographic wedges located on the parietal lamellae. These structures may well serve to achieve muscular traction during the positioning and

turning of the unwieldy carychiid shell. Investigation of fractures of the *C. minimum* shell has revealed an intersected cross platy laminate architecture. Information gleaned from this investigation opens still even more windows for character designation within the Carychiidae.

T4.O18

SPECIES DIVERSITY OF MANGROVE GASTROPODS IN THE INDO-WEST PACIFIC

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Mangroves are commonly found in the tropical Indo-West Pacific, with the highest tree species diversity between Sumatra and Papua New Guinea. Although mangroves are a harsh habitat with variable physical factors, animals are abundant and diverse. However, animal diversity in mangroves is still poorly known, especially for invertebrates. Rigorous taxonomy is critical to better understand mangroves as an ecosystem, better manage and preserve them, and address fundamental questions in patterns of species distribution. Our lab has been undertaking extensive fieldwork in the Indo-West Pacific, particularly South-East Asia, to collect new, fresh material of mangrove gastropods. Species (of all gastropod taxa) are being delineated using morphological and molecular data. Based on COI sequences, species are strongly separated into reciprocally monophyletic units: genetic divergences within units (<1%) are always much lower than divergences between units (>5%). Thus far, our data set contains 53 species of onchidiid slugs and 97 species of snails, many of which are ellobiids (by far the most diverse taxon of snails). Several cases of species delineation will be illustrated, using mainly ellobiids and onchidiids, two groups that are currently being revised in our lab: 1) species that are morphologically distinct and can be easily recognized in the field; 2) species that are highly variable morphologically and could easily be misinterpreted as multiple species in the field; 3) cryptic species that cannot be distinguished based on external morphology, but are clearly distinct lineages. Some nomenclatural issues will also be briefly discussed.

T4.O19

OUT OF THE MARINE MESOPSAMMON, INTO THE (PAN-) PULMONATE WORLD: HISTORICAL BIOGEOGRAPHY AND HABITAT SHIFTS IN THE EVOLUTION OF ACOCHLIDIAN SLUGS

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Molecular phylogenetics have challenged our conventional classification of euthyneuran gastropods and placed traditional opisthobranch or ‘lower heterobranch’ clades (such as Sacoglossa, Acochlidia and Pyramidelloidea) into sistergroup relationships

with established pulmonate taxa. We present a comprehensive molecular phylogeny on acochlidian slugs based on a global sampling that covers 82.5% of the described diversity and additionally nearly doubles known diversity by undescribed taxa. Our phylogenetic hypothesis is largely congruent with previous morphological analyses and provides a robust framework to trace the evolutionary history of Acochlidia. To do so, we conducted molecular clock analyses and reconstructed ancestral areas as well as the ancestral states of major ecological traits. Based on our data, the Acochlidia originated from a marine, mesopsammic ancestor adapted to tropical waters in the Mesozoic Jurassic. Early acochlidian radiation might have been triggered by isolation events due the breakup of the Panthalassa Ocean and the formation of the shallow early Atlantic and Tethys oceans. A series of vicariance events influenced the history of the two major clades with remarkably different evolutionary history. The Microhedylacea remained in stunning morphological and ecological stasis for approximately 150 million years, and are restricted to the marine mesopsammon. Molecular data reveals that the majority of microhedylacean diversity belongs to (pseudo-)cryptic species with deep genetic divergences, indicating long reproductive isolation. In contrast, the evolution of Hedylopsacea is characterized by a series of independent habitat shifts out of the marine mesopsammon, conquering semi-terrestrial and limnic habitats while reestablishing a benthic lifestyle. The major radiations and habitat shifts in hedylopsacean families occur in the central Indo-West Pacific and can be related to tectonic events in the area.

This study on acochlidian phylogeny and biogeography adds another facet to the yet complex (pan-) pulmonate evolution and highlights the various parallel pathways in which these snails and slugs invaded non-marine habitats.

T4.O20

DIVERSITY OF *SIPHONARIA* LIMPETS (GASTROPODA: EUTHYNEURA) FROM THE INDO-WEST PACIFIC

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Siphonaria limpets are common in the rocky intertidal, worldwide, except in the Arctic. There are 205 species-group names that are available and not permanently invalid. However, estimating the actual species diversity has remained challenging. Past authors have interpreted shell variation differently, resulting in different taxonomic accounts. Species diversity of *Siphonaria* limpets in the tropical and subtropical Indo-West Pacific (from eastern Africa to Hawaii) is evaluated based on DNA sequences (COI, 12S, and 16S). The current data set includes new sequences for 152 individuals: 123 individuals were collected from 93 locations across the Indo-West Pacific, and 29 individuals represent species from the rest of the world. In total, 29 species are recognized from the Indo-West Pacific, all of which are strongly supported. Potential names based on traditional taxonomy and nomenclatural issues will be discussed. Intra- and inter-specific shell variation will be discussed in the light of new molecular results: shell variation is high and overlaps a great deal between species. Geographically, no *Siphonaria* species is distributed across the entire Indo-West Pacific. Instead, quite a few species are endemic or restricted to sub-regions within the Indo-West Pacific. The biogeography of *Siphonaria* in the Indo-West Pacific will be briefly compared to other groups.

T4.P1

DNA BARCODING OF PHILIPPINE HELICARIONIDS (GASTROPODA: PULMONATA)

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DNA barcoding is a molecular method of identifying organisms based on a short length sequence of its genome. This study aimed to barcode terrestrial snails belonging to the family Helicarionidae found in the Philippines. A total of five species, namely *Ryssota zeus* (n=2), *R. sagittifera batanica* (n=5), and the Philippine endemic *Hemiglypta semperi* (n=3), *R. otaheitana* (n=7), and *R. lamarckiana* (n=4), were barcoded using the standard marker cytochrome c oxidase I (COI) gene. A further two genera, *Hemiglypta* sp. (n=3) and *Lepidotrichia* sp. (n=3), were also included. Helicarionid individuals were obtained from various sites in the Philippines (Batanes, Bicol, Leyte, Mindoro, and the Polilio Group of Islands). Highest sequence divergence was found within the family level (mean K2P distance=17.42%) and least within the species level (mean K2P distance=2.92%). The COI marker used was able to distinguish between species within the family Helicarionidae. Neighbor-joining tree based on the Kimura-2-parameter model of DNA substitution shows that *Ryssota* is not monophyletic. By employing DNA barcoding, we can complement current research in areas such as molecular phylogenetics and population genetics of this understudied taxon.

T4.P2

MOLECULAR TAXONOMY OF *VIANA REGINA* (MORELET, 1849) IN CUBA (GASTROPODA, NERITIMORPHA, HELICINIDAE)

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Cuba has a rich terrestrial malacofauna with > 1300 species of which about 95% are endemic. One of the emblematic species is *Viana regina* (Morelet, 1849), which is an endemic taxon in the region of Pinar del Rio. Currently, the species is divided in three subspecies with relatively well-defined distribution areas, viz. *V. r. regina* (Sierra de Viñales to Soroa), *V. r. laevigata* (Pfeiffer, 1865) (Sierra de los Organos) and *V. r. subunguiculata* (Poey, 1859) (Sierra de Guane to Sierra de Quemado). The three taxa differ only in a few subtle and highly variable conchological features, including shell color patterns and the form of the peristomal lip. Some authors have even suggested that the variation in these characters may reflect ecophenotypic, rather than subspecific, differentiation. As such, the significance of these supposedly taxon-specific differences and the concomitant taxonomic interpretation of the three subspecies need corroboration. Therefore we analyzed nucleotide sequence variation of three mtDNA (COI, 16S rRNA, Cyt b) and

two nuclear (ITS-1, ITS-2) gene fragments in nine *V. regina* populations (165 specimens), representing the three subspecies. These sequence data were used for phylogenetic reconstruction and DNA barcoding, showing that the three subspecies are consistently differentiated under a phylogenetic (lineage) species concept. The three taxa also seem to show a strong geographic structuring. The implications of these results will be discussed in the light of future conservation plans for *V. regina*.

T4.P3

NEW INSIGHTS ON THE PHYLOGENETIC POSITION OF THE HELICID SPECIES *CYLINDRUS OBTUSUS* BASED ON NUCLEAR AND MITOCHONDRIAL DNA MARKER SEQUENCES

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Cylindrus obtusus is an endemic of the eastern Alps. Besides many interesting peculiarities in biology, ecology and anatomy, its systematic position seems enigmatic and has been discussed controversially in the past. Its genital anatomy, highly consistent with the genus *Arianta*, has led to placing the species within the family Helicidae, subfamily Ariantinae. However, *C. obtusus* shows a conspicuous aberrant shell form within this group – all other representatives display globular or more or less depressed shells – and it has a geographically and ecologically rather restricted distribution. This raises questions about the age of the species, its evolutionary history and its relationships within Ariantinae. Here we tested the presumed sister group relationship of *Arianta* and *Cylindrus* using phylogenetic methods, including additional genera of Ariantinae and of some other subfamilies of Helicidae. Five molecular markers were used: partial sequences of three mitochondrial genes, *cytochrome oxidase subunit 1, 12S rRNA* and *16S rRNA*, and two nuclear genes for *histone 3* and *histone 4*. Phylogenetic trees calculated using Bayesian methods show that the closest relative of *C. obtusus* is indeed the genus *Arianta*, with about 20% p distance between the two taxa. Furthermore, the analyses provided insights regarding phylogenetic relationships within Ariantinae. As no fossils of *C. obtusus* have been found, except some rare and probably young findings within the extant distribution range in the Eastern Alps, no reliable dating of the age of the split between *Cylindrus* and *Arianta* is available. Our findings underline the relevance of genital anatomical characters for taxonomic issues, opening the question as to why the shell morphology in this species is so different from its closest relatives, and whether its restricted distribution, habitat preferences and ecological requirements, along with its evolutionary history, can explain this phenotypic difference.

T4.P4

PHYLOGEOGRAPHY AND SUBSPECIES CLASSIFICATION OF *CLAUSILIA DUBIA* DRAPARNAUD 1805 IN EAST AUSTRIA (GASTROPODA: PULMONATA: CLAUSILIIDAE)

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Clausilids are one of the most species-rich groups among land snails. In Austria they are very abundant in the alpine region inhabiting different habitats. In this study we investigate *Clausilia dubia* Draparnaud 1805, a species which displays a broad variability in its morphology, and hence has been subdivided into several subspecies. This classification was reassessed by morphological analyses (various shell characters) and for the first time by molecular analyses (partial sequences of the mitochondrial COI gene). In Austria 17 subspecies of *C. dubia* have been described, 13 of them occur in the investigated area of the Northern Calcareous Alps of eastern Austria. The individual distribution areas of these subspecies often overlap and some subspecies occur even syntopically.

The aim of our study was to evaluate whether the described subspecies are genetically and/or morphologically differentiated. Moreover, we wanted to find out whether the morphological and the genetic results are in accordance. The determination of the subspecies proved to be difficult, but there are some subtle character combinations, which allowed to distinguish them. For an easier classification the subspecies were merged into four morphogroups. However, neither with the morphometric, nor with the molecular results a separation of any of the described subspecies or morphogroups was supported. Hence, the validity of the described subspecies appears doubtful.

T4.P5

PHYLOGENETIC RELATIONSHIPS AND DISTRIBUTION OF THE ENIGMATIC SEMISLUG *AILLYA* (GASTROPODA: AILLYIDAE)

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Aillya is an enigmatic African semislug, which was originally classified in the American Amphibuliminae (Orthalicoidea) by Odhner. Baker established a separate family for this group and included it together with the Succineidae and Athoracophoridae in the suborder Heterurethra. Minichev & Slavoshevskaja subdivided the Heterurethra even into three separate orders and introduced the name Aillyida for the Aillyidae. In contrast, Pilsbry, Solem, Tillier and van Mol supposed that *Aillya* is most closely related

to some limacoid groups, i.e. Helicarionidae or Urocyclidae. Molecular phylogenetic analyses based on ITS2 and partial 28S rDNA sequences proved that all these hypotheses were wrong. Rather, Aillyidae turned out to belong to the Achatinoidea. Together with the Ferussaciidae (and perhaps the Micractaeonidae), they form the sister group of the paraphyletic Subulinidae, in which Achatinidae and Thyrophorellidae are nested. *Aillya* was known so far only from Western Africa (Cameroon, Nigeria, Bioko Island). However, we could show that it is much more widespread and extends eastwards to Uganda.

T4.P6

DISTRIBUTION OF THE PORTUGUESE ENDEMIC HYGROMIID *CANDIDULA COUDENSIS* HOLYOAK & HOLYOAK, 2010

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Candidula coudensis Holyoak & Holyoak, 2010 is among the most recent described land snails from mainland Portugal. This recent description does not derive from a clarification of a set of species that were previously under the same name. Rather, it is a total novelty with a very restrict distribution that somehow was not included in ancient and modern sampling efforts. It has a conspicuous, rather distinctive, appearance, and could only be misidentified as *C. setubalensis* which occurs 150 km to the south.

In the paper of its original description, *C. coudensis* is believed to inhabit an area of less than 1 sq km, near Vale da Couda, a limestone encroachment predominantly occupied by dwarf scrublands, olive groves and other crops surrounded by limestone walls, and rare patches of Portuguese oaks. Based on that information we undertook a survey plan in order to determine the actual range of this species. We defined a 2×2 sq km grid over 60 sq km encompassing Vale da Couda, where the search of specimens was done from January to May 2013. The results from our systematic survey contributed to increase considerably the known range of the species. Nevertheless it is still one of the Iberian Hygromiids with a shorter distribution range.

T4.P7

DO COSMOPOLITANS SPECIATE? ANATOMICAL DIVERSITY OF *MYOSOTELLA* IN AZORES

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The ellobiid halophilic genus *Myosotella* Monterosato, 1906, is very diverse morphologically. However, owing to the wide range of intrapopulational conchological variation, its 40+ nominal species have been synonymized into one, *Myosotella myosotis* (Draparnaud, 1801). An Eastern European/Mediterranean species, it is spread throughout the world, having been recorded in the Macaronesia, South Africa, Bermuda, Eastern and Western North America, Western South America, New Zealand, Australia. This worldwide distribution has been explained by anthropogenic causes, considering the development and habitat requirements of the taxon. *Myosotella myosotis* lives from the supra-tidal to an almost terrestrial habitat, in marshes and cobble beaches, withstands brackish water as well as salt water, survives well in moist habitats and resists to immersion in salt water for several days; the eggs are laid in gelatinous masses attached to the substrate (rock or pieces of wood), the veliger stage is completed inside the egg and the juveniles crawl directly to the substrate. Therefore, deck equipment and ballast of past centuries sailing ships are currently accepted as the most plausible explanation for its worldwide distribution.

Recent anatomical research in *Myosotella* from the Azores, namely the internal morphology of the penial complex, has revealed striking differences from European specimens as well as among the various island groups of the archipelago. Specimens from Portugal (from Algarve to Aveiro) show very little variation in penial morphology, in contrast with the situation in the Azores. Whereas in the Eastern Group (São Miguel and Santa Maria) the anatomy is tentatively identified with that of the European *Myosotella myosotis*, those in the Central Group support the revival of the endemic *Myosotella bicolor* (Morelet, 1860); the islands of the Western Group (Flores and Corvo) harbor each a new, endemic taxon.

Such high level of endemicity in a supposedly cosmopolitan taxon calls for reassessment of the taxonomic status of *Myosotella* throughout the world, and the contrasting homogeneity of the specimens from the Portuguese coast hints at the possibility of a center of dispersion other than the traditional origin from European/Mediterranean coasts.

(Research supported by the SYNTHESYS Project http://www.synthesys.info/ which is financed by European Community Research Infrastructure Action under the FP7 "Capacities" Program).

T4.P8

FIRST DATA ON THE GENITAL ANATOMY OF THE GENUS *JEANNERETIA* (STYLOMMATOPHORA, HELICOIDEA: CEPOLIDAE), AN ENDEMIC TAXON FROM WESTERN CUBA

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The genus *Jeanneretia* Pfeiffer, 1877 is endemic in western Cuba (Pinar del Rio). It comprizes two subgenera, *Jeanneretia* and *Guladentia* Clench & Aguayo, 1951, with nine nominal species (and several subspecies). However, all these taxa were described on conchological features only, so that the taxonomy of this genus needs to be consolidated. Therefore, we provide here the first anatomical data of several *Jeanneretia* species of both subgenera.

The subgenus *Jeanneretia* s.s. has a long, slender penis and a cylindrical epiphallus with a weak retractor. The distal tip of the epiphallus splits into a long flagellum and the vas deferens. The vagina is short and gives rise to the oviduct and the pedunculus of the bursa copulatrix, the latter being longer than the spermoviduct, but shorter than the flagellum. The dart apparatus consists of a dart sac, an elongated gland inserted apically on the dart sac, and two long, slender, accessory glands with a tubular internal structure.

The genitalia of the subgenus *Guladentia* differ from those of *Jeanneretia* s.s. by: (1) the short flagellum and pedunculus of the bursa copulatrix, (2) at the basis of the dart apparatus there is a single, broad, bilobed, accessory gland with an alveolar internal structure, and (3) the spermoviduct + albumen gland are longer than any other genital structure.

These data are further compared with the genital anatomy of other Cepolid genera, such as *Eurycampta* Von Martens, 1860 and *Coryda* Albers, 1850.

T4.P9

REPRODUCTIVE STRATEGIES OF A TERRESTRIAL SNAIL ALONG AN ALTITUDINAL GRADIENT

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This study reports how the reproductive cycle of an endemic land snail, *Oxychilus* (*Drouetia*) *minor* (Riedel 1964), is shaped by abiotic factors over an altitudinal gradient of 800 m, in Pico mountain (Pico Island, Azores). Our results suggest that, at low altitude (200 m), individuals are active and mature from October/November to March, and they exhibit aestivation in the remaining months, as a consequence of soil dryness. Thus, at low altitude, gonadal maturation is considered to be primarily influenced by photoperiod, rainfall and temperature. On the other hand, at high altitude (1000 m), individuals are mature from March to July/August and they seem to have minimal gametogenic conditions to reproduce throughout the remaining months of the year. At this altitude, soil moisture is never a limiting factor therefore gonadal maturation is mainly shaped by photoperiod and temperature. In conclusion, besides quoting aestivation in the Azorean malacofauna for the first time, this study suggests that snails may develop physiological adaptations related to reproduction in accordance to the environmental conditions of their habitats.

T4.P10

REPRODUCTIVE BIOLOGY AND POPULATION DYNAMICS IN *CLAUSILIA BIDENTATA* AND *RUTHENICA FILOGRANA* (CLAUSILIIDAE) – OVIPARITY VS. OVOVIVIPARY

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Clausilia bidentata (Ström 1765) and *Ruthenica filograna* (Rossmassler 1836) are two clausiliid species co-occurring in well preserved deciduous forests of central Europe. Despite living under virtually the same habitat conditions they show different reproductive modes: oviparity (*C. bidentata*) vs ovovivipary (*R. filograna*). We compare their breeding phenology

(including anatomical and histological changes in reproductive organs), population dynamics and microhabitat preferences under natural or seminatural conditions.

There are no general differences in the structure of reproductive tracts between the species except for a periodic transformation of the oviduct's distal part in *R. filograna*. Its folds stretch thanks to muscle cells, so its lumen gets widened and form a kind of a brood bag where embryos develop before being born.

In *R. filograna*, previtellogenic oocytes and secodary spermatocytes are present right after the overwintering (February). Spermatids get numerous between June and September and mature oocytes are abundant in May, July and September. In *C. bidentata*, vitellogenic oocytes are numerous in April and October, while mature oocytes are prevailing in April. Spermatids are abundant in June and September.

The mean size of eggs (1.4mm x 1.1mm, *C. bidentata*) and embryos (1.5 x 0.8mm, *R. filograna*) as well as their number (2-4 vs 2-3) are similar. Under seminatural conditions in *C. bidentata* only about 50% of the snails lay eggs, whereas all adult *R. filograna* bear juveniles in spring and some of them repeat the reproduction in outumn. Survival of eggs and juveniles is higher in *C. bidentata*, so its population growth is similar to that of *R. filograna*.

Under natural conditions abundance in populations of *R. filograna* is higher, but their distribution is clustered and limited to patches of specific litter. *C. bidentata* is more eurytopic, with more even distribution and lower abundance.

The research was supported by MNiSW grant no. N-N303-568-838.

T4.P11

SHELL MORPHOLOGY AND REPRODUCTIVE ANATOMY OF THE GENERA *BENSONIES, KHASIELLA, OXYTESTA* AND *MACROCHLAMYS* (PULMONATA: ARIOPHANTIDAE: MACROCHLAMYDINAE) FROM NEPAL

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With more than 165 species within 10 genera the Macrochlamydinae Godwin-Austen, 1888 are the largest Ariophantidae subfamily within the Indian subcontinent.Three genera, viz. *Bensonies* H.B. Baker, 1938*, Khasiella* Godwin-Austen, 1899 and *Oxytesta* Zilch, 1956, are confined to the Himalayan range, while *Macrochlamys* Gray, 1847 is distributed throughout S and SE Asia. A variety of shell characteristics (imperforate vs perforate/umbilicated, smooth vs granulated/plicate) and other external features (simple vs tripartite foot, presence vs absence of a caudal horn over the mucous pore, presence vs absence of shell lobes) are currently interpreted as distinct genus-level characters. Yet, several features of the reproductive anatomy, particularly the coiled penial caecum, are similar in many species of the four genera. Therefore the taxonomic delimitation and phylogenetic relationships of these genera are not well-established. We illustrate this issue by highlighting similarities and differences in the shell and penial structure of representative species of Macrochlamydinae from Nepal.

T4.P12

COMPARISON OF PLANT AND SNAIL DIVERSITY PATTERNS IN THE WHITE CARPATHIAN MTS. (CZECH REPUBLIC) ACROSS FOREST AND GRASSLAND HABITATS

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There are similar ecological requirements for land snail and plant species as they are both strongly dependent on site conditions, often resulting in similar patterns of species composition changes along environmental gradients. The White Carpathian Mts. belong to the best explored areas of the Czech Republic for both taxa. This provides a unique opportunity to compare patterns of their species diversity and composition throughout the whole area and habitat variation. A total of 1238 plant and 101 snail species, recorded in 45 grid cells of 2.8 x 3.1 km^2 in size, were used for the analysis. Except patterns of the whole array, the aim was also to investigate the responses of forest and grassland assemblages separately and to determine relative roles of niche- on neutral-based processes on the compositional changes. We found that the entire species richness of plants and snails did not respond to the same variables, including a sharply different response to the representation of human habitats. While species richness of plants correlated with human habitats positively, the opposite was true for snails. This was caused mainly by a decline of forest snail species towards more human impacted areas as many snails are highly sensible to human-made degradation of woodland ecosystems and deforestation, of course. In contrast, we found that grassland species richness of both snails and plants responded the same variables, i.e. number of habitat types and longitude. Using the variance partitioning approach, we found notably higher importance of neutral-based processes for plant species data, in contrast to snails, driven mainly by environmental conditions. This pattern was obvious especially in grasslands, most likely as a result of the Holocene development of these communities and a long-term survival of some relict steppe plants, in contrast to snails.

T4.P13

DIVERSITY OF ONCHIDIIDAE (GASTROPODA: PULMONATA) FROM NEW SOUTH WALES, AUSTRALIA

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The taxonomy of the Onchidiidae is so chaotic that only very few species can reliably be identified. In order to revise the taxonomy of the Onchidiidae, our lab has been collecting new, fresh material from the Indo-West Pacific. In particular, we specifically try to go back to type localities so that it is easier to compare our new collections with the original descriptions and type materials. The undergraduate research presented here focuses on the diversity of onchidiid slugs from Sydney (New South Wales, Australia), which is the type locality for three species names (*Paraoncidium chameleon*, *Onchidella reticulata*, and *Onchidium daemelli*). Combined molecular (COI sequences) and morphological data, as well as natural history (habitats where slugs are found),

all suggest that there are five species of onchidiids in Sydney. Differences between all five species are presented. Nomenclature (especially new synonymies) is discussed, as well as species distribution beyond New South Wales and even Australia. Delineating species, however, seems to be the easy part. Indeed, names apply to three of those five species (*Onchidina australis*, *Onchidium daemelli*, *Onchidella patelloide*), but, at this point, the two other species have to be left unidentified at the species level (as *Peronia* sp. and *Onchidium* sp.). Additional work is needed to try to find if some names already exist for those two species. If they have not been named in the past, then new names will be created.

T4.P14

ACOCHLIDIAN SEA SLUGS ON SHORE LEAVE – ANOTHER INVASION OF THE LAND

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Invasion of the land has been a considerable challenge for most aquatic taxa due particularly to gravity and desiccation stress in the air. Thanks to the hard shell protecting and supporting the soft body, gastropods are among the most successful animals in this habitat shift from the sea to the land, with supposedly over ten independent invasions. Apparently, shell-less groups are more prone to desiccation and have had difficulties in the acquisition of suitable anatomical and physiological characteristics for the invasion. Land slugs therefore have usually been thought as descendants of land snails, which had gradually lost their shells in order to inhabit moist, protective spaces provided by rock fissures, pockets under stones and earthworm tunnel tracks.

Here we report an unambiguous example of terrestrial invasion by a lineage of aquatic slugs of the order Acochlidia on Ulong Island in the Republic of Palau, western Pacific. The Acochlidia are generally regarded as aquatic heterobranch slugs including minute marine species in the interstitial waters of coastal sands worldwide and otherwise a couple of large-sized species living benthically in coastal rivers on western Pacific islands. The recent description of two amphibious species of *Aiteng* (Aitengidae) from a mangrove forest in Thailand and the upper intertidal of coastal caves in Japan substantially extended the morphological and ecological diversity of the Acochlidia. In the present study, specimens were collected from leaf litter in a tropical rain forest at elevations of 20-30 m several hundred meters away from the sea, where associated gastropods are all typical land snails. Through an integrative approach including molecular phylogeny and 3D-reconstruction of internal organs, we conclude that the terrestrial slug from Palau represents another new species of the genus *Aiteng*. Our study indicates a habitat shift of ancestrally aquatic Acochlidia to a completely terrestrial life style with the invasion of the land from the upper littoral zone in the Cenozoic. This is the first land slug outside Eupulmonata.

T5

WHO ARE THE 'ACULIFERA'?

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The chitons (Polyplacophora) and vermiform molluscs (Solenogastres and Caudofoveata) have been focal to questions of pan-molluscan phylogeny. These groups are united by their spicular armature, which is the basis for the name Aculifera ('needle-bearing') of a putative clade uniting these classes. These animals have a reputation as taxonomically 'difficult' but are the source of much excellent work on development, phylogeny, anatomy, and ecology. This symposium honours the memory of one important advocate of 'aculiferans', Prof. Chris Schander (1960–2012). Subjects will include biology of all the included classes, as well as directly address the phylogenetic truth of the clade Aculifera.

T5.O1

SPECIES DIVERSITY OF APLACOPHORAN MOLLUSCS (SOLENOGASTRES, CAUDOFOVEATA) IN THE NORTHERN EUROPEAN ATLANTIC

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Current knowledge of global species diversity of aplacophoran mollusks (Solenogastres or Neomeniomorpha, Caudofoveata or Chaetodermomorpha) reflects only a small fraction of the real diversity. Even in geographic areas with a relatively long history of aplacophoran research, such as the Northern European Atlantic, there are frequently new species encountered. A current project investigates the diversity and distribution of aplacophoran species in Norwegian waters and adjacent areas (Faroer Islands, South-Eastern Iceland). About 800 lots of specimens were sorted and identified. Within the more than 50 species encountered, there were 25 species of Solenogastres new to science. The new species come from both the relatively well-known coastal areas (fjords) as well as the deep Norwegian Sea. The talk presents examples for distribution data and points out taxonomic peculiarities. Implications of the new findings on global species diversity estimates are discussed.

T5.O2

NEW METHODS PROVIDE ANSWERS TO OLD QUESTIONS-PHYLOGENETICS AND SYSTEMATICS OF THE CAUDOFOVEATA (=CHAETODERMOMORPHA)

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The shell-less, worm-shaped Caudofoveata (=Chaetodermomorpha) is by far the least known group of molluscs. These small, benthic marine animals can be difficult to sample, and possess few defining characters. Phylogenetic relationships within the taxon are unclear, and have long been a matter of debate. Up until now the evolutionary relationships of the group have never been investigated in a modern phylogenetic analysis, neither based on morphological nor molecular data. We here use molecular phylogenetics to resolve the relationships between and within the families of Caudofoveata. Phylogenetic analyses were performed using mitochondrial (COI, 16S) and nuclear genes (18S, 28S and H3) from specimens from 30 species in all described families to construct a worldwide phylogeny. Maximum likelihood analyses were performed in RAxML and Bayesian inference analyses in MrBayes. Contrary to traditional views, the family Prochaetodermatidae is the first branching taxon. Within this family, the grouping of species and genera is consistent with current taxonomic hypotheses. Monophyly of Chaetodermatidae is highly supported, while the family Limifossoridae is not recovered as monophyletic, but split into several clades. Within Chaetodermatidae, molecular data do not agree with the current classification based on morphological characters. In our analyses, *Falcidens* and *Chaetoderma* are not recovered as monophyletic. The only character distinguishing the currently recognized genera is the morphology of the radula. Comparative examination of radula morphology revealed that the "generic" differences at least in some cases may be related to ontogeny: in *Chaetoderma nitidulum*, the nominal species for the family Chaetodermatidae, the radula changes gradually from a *Falcidens*-type radula in small specimens to a *Chaetoderma*-type radula in larger specimens. Consequently, some of the currently recognized *Falcidens* species might in fact be juvenile *Chaetoderma*. Taxonomic classification of Chaetodermatidae is in need of revision, taking into account that other characters than radula morphology need to be used for genus delimitation in this family.

T5.O3

THE BRAZILIAN CAUDOFOVEATA: A GREAT APLACOPHORAN BIODIVERSITY BEGINNING TO BE DISCOVERED

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The Brazilian Caudofoveata (Aplacophora) are almost completely unknown, there being only scattered information about some deep-water species. This scenario is now changing, as a large amount of samples collected by the "HABITATS Project – Campos Basin Environmental Heterogeneity by CENPES/PETROBRAS", revealed 2354 specimens of Caudofoveata, obtained from 30 to 2000 meters depth off Rio de Janeiro, Southeastern Brazil. These animals were examined by light and scanning electron microscopy, with a special attention being paid to the structure of the sclerites and radula; they were compared with voucher specimens from other collections. Thirteen morphotypes were already recognized, the most common of these being the Chaetodermatidae Theel, 1875. A long tailed unidentified species of *Falcidens* Salvini-Plawen, 1968, is the most abundant (872 specimens from 53 to 1010 meters), and three other species of this same genus are also present: an unidentified, probably new species with a cylindrical body, from 100 to 975 meters; and the short tailed *F. targatus* Salvini-Plawen, 1992, from the continental shelf (originally described from 73 m off Uruguay), and *F. acutargatus* Salvini-Plawen, 1992, from the continental slope (originally described from 974 m of the Caribbean Sea). Apart from these, there is at least one more species of Chaetodermatidae, probably from the genus *Chaetoderma* Lovén, 1844. Prochaetodermatidae Salvini-Plawen, 1975, are represented by four species and Limifossoridae Salvini-Plawen, 1970, occurs with one small unidentified species and one long-bodied new *Psilodens* Salvini-Plawen, 1977. As there are no geographic or oceanographic barriers north to the Rio de Janeiro, some of these species must be also found along the remaining Brazilian coast. Similarly, some species (or genera and families) may be continuously distributed along the Uruguayan and Argentinean waters.

Financial Support: CENPES/PETROBRAS, FAPESP Proc. 2011/50297-4[1] and 2011/07629-6[2], SAE/UNICAMP[3].

T5.O4

THE FAUNA OF CAUDOFOVEATA: STATE OF THE ART

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Caudofoveata is a relatively small subclass of Aplacophora which occurs in all oceans except for the Antarctic and in all seas, except the Black and Caspian. At the moment, the global caudofoveate fauna consists of 145 species belonging to 14 genera. More than a half of the species are known only from original descriptions.

Nevertheless, there is a certain peculiarity in the distribution of caudofoveates, unlike other classes and subclasses of molluscs. The species diversity of caudofoveates in the Atlantic and the Pacific is relatively low: 55 vs. 63, respectively, and there is not a single species inhabiting both oceans. The number of species in the Arctic and in the Indian Ocean is the same – 14, but again there are no common species for the Indian and Pacific oceans and for the Arctic and Pacific. At the same time, there is one species common for the Indian and Atlantic oceans, while the Arctic and the Atlantic have 5 common species. At present, only two amphi-Pacific and five amphi-Atlantic species are recorded, which may evidence either the relict nature of the Caudofoveata with its quite unique distribution, or the considerable incompleteness of our knowledge of the caudofoveate diversity.

I am inclined towards the second explanation, particularly based on the experience of working with the Gulf of Mexico material. This well documented material resulted from many years of collection did not reveal a single species of caudofoveates, whereas subsequently it allowed to describe 7 new species of the family Prochaetodermatidae only.

Based on personal experience of working on material collected by modern techniques it can be suggested that our current view of caudofoveates concern not more than 20% of their actual diversity, and thus any speculations about regularities of their distribution in the World Ocean are premature.

T5.O5

UNIQUE EVENTS IN CHITONID REPRODUCTION

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Gametogenesis in chitonids is highly unusual giving rise to eggs with elaborate spiny hulls and sperm with saber-like nuclear extensions and tiny acrosomes. Recent study of oogenesis in a variety of chitonid families, has revealed unique mechanisms of egg hull formation. 3D reconstruction of serial sections of oogenesis in the chitonid *Acanthochiton garnoti,* confirmed that the egg hull is formed by microapocrine secretions, not by vesicles from the Golgi body. This novel process, observed for the first time in Mollusca, bi-passes the endomembrane system and releases compounds formed in the cytoplasm directly from the cell surface, via budding of 'microaposomes'. Fertilization is no less unusual, as chitonid sperm digest a minute pore in the egg hull that allows injection of DNA but appears to block entry of sperm organelles. Serial sections of fertilized eggs of *Mopalia muscosa* confirmed that a membrane bag, abandoned on the egg surface, contained the sperm mitochondria and centrioles. In virtually all other Metazoa the entire sperm enters the egg, and sperm mitochondria are digested by an elaborate system of detection and enzyme destruction. Normally one sperm centriole moves the two pronuclei together to form the zygote nucleus and later initiates cleavage of the embryo. Thus, in the absence of these sperm organelles in the fertilized egg, the developmental program of the chitonid embryo must be unique.

T5.O6

SEEING THE WORLD THROUGH NEW EYES: A NOVEL SENSORY ORGAN IN BASAL CHITONS (LEPIDOPLEURIDA)

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Chitons (Polyplacophora) are basal molluscs with a simple nervous system without cephalisation or apparently any anterior sensory organs. We report the first discrete anterior sensory structure in chitons, identified throughout the Lepidopleurida, the more plesiomorphic of the two orders of chitons. The "Schwabe organ" is clearly visible on living animals as streaks of brown or purplish pigment on the roof of the pallial cavity lateral to the mouth lappets. The pigment does not persist in most preserved specimens, which has presented a substantial challenge for descriptive work. As a result of new efforts to thoroughly describe the ultrastructure of the Schwabe organ via histology and electron microscopy, we can now confirm the presence of dense innervation of the epithelium in this area and its direct connection to the lateral nerve cord. Bundles of nerve fibres running through the epithelium are also frequently surrounded by the pigment granules which characterise the region. Basal cells, which project to the surface of the epithelium, and cells bearing a large number of ciliary structures, may be indicative of the function of the Schwabe organ. However, its role in chiton behaviour remains to be investigated and its primary stimulus is still unknown. The Schwabe organ is present in all genera within Lepidopleurida (and is absent from Chitonida) and represents a novel anatomical synapomorphy of the clade. Further study of this sensory organ may further illuminate the early evolution and radiation of Lepidopleurida and its relationships to other clades of molluscs.

T5.O7

FUNCTIONAL MORPHOLOGY AND MOLECULAR EVOLUTION OF CHITON 'SHELL' EYES

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Image-forming eyes have evolved multiple times in invertebrates. Here, we ask: 1) what are the functional consequences associated with the separate steps of eye evolution and 2) what are the changes in genotype associated with the transitions between these steps? To address these two questions, we are working with chitons (Phylum Mollusca; Class Polyplacophora), chosen because they have unique sensory structures embedded in their shell plates ("aesthetes") that vary from the ancestral condition of non-pigmented,

light-sensitive cells (“photoreceptors”), to pigmented cell clusters (“eyespots”), to what may be the most recently evolved lens-bearing eyes of any animal (“eyes”). Chitons also display multiple light-influenced behaviors that are simple, stereotyped, and easily-manipulated. Thus, chitons may reveal how new light-interacting structures (*i.e.* photoreceptors, pigment cells, and lenses) drive new light-influenced behaviors (*i.e.* light-detection, directional photoreception, and spatial vision). We are also using transcriptome sequencing to comp are gene expression between chitons with non-pigmented aesthetes, eyespots, and eyes. Through behavioral trials and morphological examination, we find that the chiton *Acanthopleura granulata* forms images using birefringent ‘shell’ lenses made of solid aragonite. Chitons that lack lenses do not demonstrate spatial vision but, intriguingly, are more sensitive to small changes in illumination than chitons with eyes. Through transcriptome sequencing, we find that the aesthetes of chitons – including those from species with non-pigmented photoreceptors, eyespots, and eyes – generally express a wide range of vision-related genes that include G-proteins, arrestins, and several types of opsin. Finally, using immunohistochemistry we find that the non-pigmented photoreceptors, but not the eyes, of *A. granulata* express an r-type opsin similar to those expressed by the cephalic eyes of many invertebrates. We hypothesize that *A. granulata* has multiple photo-systems that operate via different phototransduction pathways and mediate different light-influenced behaviors.

T5.O8

COMPARATIVE ASPECTS OF SOLENOGASTER MYOGENESIS AND THEIR IMPLICATIONS FOR MOLLUSCAN SYSTEMATICS

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Although monophyly of Mollusca is widely accepted, the relationships within the phylum remain unresolved. Some recent molecular-based phylogenies support the Aculifera hypothesis, whereby the “aplacophoran” taxa Solenogastres (=Neomeniomorpha) and Caudofoveata (=Chaetodermomorpha) together with the Polyplacophora (chitons) form a monophyletic assemblage, as sistergroup to the Conchifera, which comprise Monoplacophora, Bivalvia, Scaphopoda, Gastropoda and Cephalopoda. This is in contrast to some classical morphological phylogenies, which suggest a paraphyletic `Aculifera´, placing the Solenogastres as first offshoot of molluscan phylogeny. Furthermore, various studies have suggested that the Polyplacophora cluster with the Conchifera to form the Testaria clade.

We analyzed the ontogeny of the solenogaster *Wirenia argentea* to elucidate the evolutionary origin of Solenogastres. Aside from a well-developed ring musculature, our results show a simultaneous appearance of seven paired dorso-ventral muscles. Furthermore, we found several muscle systems that were formerly considered as confined to the polyplacophorans, including an enrolling muscle, a ventro-lateral muscle and a rectus muscle. We interpret these muscles as homologous and consider them as part of the bodyplan of the last common ancestor of Solenogastres and Polyplacophora. We also discovered a hitherto unknown muscle, which we term “ventro-median muscle”, in both solenogaster and

polyplacophoran larvae. Most of the shared larval characters are transitory elements during myogenesis of *Wirenia* that are not present in adult specimens.

The new findings support a close relationship of Solenogastres and Polyplacophora and, in the light of the recent phylogenomic studies, support the Aculifera hypothesis.

T5.O9

NEUROGENESIS IN SOLENOGASTRES (NEOMENIOMORPHA)

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The Solenogastres (Neomeniomorpha) are often thought to occupy a crucial position in the molluscan phylogenetic tree. Morphological similarities between adult solenogasters and the entoproct creeping larva have led to the conclusion that the Solenogastres are the earliest extant offshoot within Mollusca, and that Entoprocta and Mollusca are sister groups. Molecular studies, however, contradict both hypotheses. This disagreement hampers the reconstruction of the last common ancestor of molluscs and even the old question of segmented or unsegmented ancestry remains unresolved.

In order to contribute to this issue, we investigated the development of the nervous system in two species of Solenogastres, *Wirenia argentea* and *Gymnomenia pellucida*, using immunocytochemistry in conjunction with confocal laser scanning microscopy, as well as transmission electron microscopy. We investigated whether there are any ontogenetic remnants of annelid-like segmentation, e. g. formation of neural components in an anterior to posterior progression or a posterior growth zone, and whether the apical organ of the solenogaster larva is of the complex Entoprocta-Polyplacophora-type, which is one of the proposed synapomorphies of Entoprocta and Mollusca.

We did not find any signs of segmentation during neurogenesis in neither of the species investigated. Instead, neurogenesis starts from an apical as well as an abapical formation center and the two lateral nerve cords develop earlier than the ventral pair. Furthermore, a fifth longitudinal neurite bundle is formed along the ventral midline of the animal and persists through metamorphosis. A complex apical organ of the Entoprocta-Polyplacophora-type was not found in any of the two species.

Our data argue against a metameric origin of molluscs. Further studies on other molluscan groups are necessary to assess whether the anatomy of the apical organ of Solenogastres is the result of secondary simplification or represents the basal molluscan condition.

T5.O10

ACULIFERA AND THE EVOLUTION OF MOLLUSCA

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Recent molecular phylogenetic analyses support the traditional idea that Mollusca consists of two monophyletic lineages, the Aculifera and the Conchifera, but the

morphology of the last common ancestor of either of the two groups as well as the entire phylum remains unresolved. The discovery of fossils with shared polyplacophoran and aplacophoran characters may indicate that the ur-aculiferan may have looked like something in between an aplacophoran and a polyplacophoran, but morphological or developmental evidence from recent taxa have so far failed to either support or refute such a scenario. Recent data from our lab on the development of the neomeniomorph (solenogaster) *Wirenia argentea*, however, show that the larval musculature in this species bears numerous synapomorphies with the polyplacophorans, indicating that at least this group of aplacophorans stems from an ancestor with a polyplacophoran-like morphology. In this talk I will summarize current fossil, morphological and developmental landmark data and will discuss their bearings on molluscan evolution in the light of the Aculifera-Conchifera hypothesis.

T5.O11

SYMPOSIUM: WHO ARE THE *ACULIFERA*? THE TESTARIA CONCEPT (PLACOPHORA + CONCHIFERA)

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The phylogenetic relationships among the aculiferan groups Solenogastres (Neomeniomorpha), Caudofoveata (Chaetodermomorpha) and (Poly-)Placophora as well as the sistergroup to the Conchifera are still under discussion. Recent molecular analyses support monophyletic Aculifera as the conchiferan sistertaxon (Aculifera concept). Alternatively, morphological characters clearly favour Placophora as sistergroup to Conchifera (Testaria concept). We emphasize the plesiomorphic nature of the morphological similarities among the aculiferan taxa and in relation to the Conchifera. In contrast, the clade Testaria (Placophora + Conchifera) is based on several synapomorphies including the radula complex, the specific regionalization of the midgut, the dorso-ventral musculature, and the excretory organs. We outline the gradual differentiation from aplacophoran to polyplacophoran to testarian levels, also by integrating ontogenetic and palaeontological data. The molecular trees differ conspicuously in data and outgroup choice, and show high support for conflicting aculiferan and conchiferan branches. Resolving these discrepancies by improving outgroup representation, rooting of the Mollusca, and refining phylogenomic analysis tools may well reveal support for the Testaria concept.

T5.O12

TOWARDS A MOLECULAR PHYLOGENY OF CHITONS (POLYPLACOPHORA) USING COMPLETE MITOCHONDRIAL GENOMES

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Polyplacophorans are an early offshoot of mollusks with known fossils dating back to Upper Cambrian. Chitons have been considerably studied at or below the family

level, but very few studies have addressed the evolutionary relationships at higher taxonomical levels. As a consequence, a general framework for the phylogenetic affinities of polyplacophorans has been missing. Traditionally, taxonomical classifications of chitons have been based primarily on valve (shell plate) characters, in some cases even relying completely on them. Recent morphological and molecular characters have provided important insights into chiton evolution, challenging conventional phylogenetic hypotheses. We used high throughput sequencing methods (shotgun subcloning and Illumina) to obtain new mitochondrial genome sequences for selected major lineages of chitons, considerably expanding previously available data. The phylogenetic analyses of mitochondrial genome data corroborate with high support the monophyly of main taxonomic groupings into orders Lepidopleurida and Chitonida, and within Chitonida into suborders Chitonina and Acanthochitonina. The genus *Callochiton*, whose phylogenetic position remained highly disputed, is recovered basal within Chitonida with high support. In addition, we challenge the traditional definition of certain families as (e.g., Mopaliidae or Acanthochitonidae), and argue that recovered alternative relationships (which are strongly supported) make sense of additional morphologic characters and biogeographic patterns. Overall, we present a robust phylogenetic hypothesis for the class Polyplacophora as a reliable framework to understand evolutionary patterns and processes in this group, and urge for a critical revision of the higher-level taxonomic classification.

T5.O13

PRELIMINARY MOLECULAR PHYLOGENY OF APLACOPHORA

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The shell-less, worm-like aplacophoran molluscs have been central to discussions of early molluscan evolution. Recent molecular investigations strongly supported placement of the two groups, Solenogastres (=Neomeniomorpha) and Caudofoveata (=Chaetodermomorpha), in a monophyletic clade, Aplacophora sister to Polyplacophora (chitons). This clade, called Aculifera, comprises the sister taxon of all other molluscs and thus is important to understanding the early evolution of Mollusca. Within Aculifera, some work has addressed evolutionary relationships within Polyplacophora, but little is known about evolutionary relationships within Aplacophora. Therefore, the phylogenetic framework needed to understand the evolution of key characters for Aplacophora, Aculifera, and even Mollusca as a whole has been lacking. Here, we employed a phylogenomic approach to obtain the phylogenetic backbone for the aplacophoran molluscs. Specifically, we sequenced Illumina transcriptomes from twelve aplacophorans (plus one chiton outgroup) to greatly expand on the paucity of available genomic data for the group. Our results provide further support for aplacophoran monophyly and a sister taxon relationship of Aplacophora and Polyplacophora (Aculifera). Within Caudofoveata, Prochaetodermatidae was placed basal to a clade comprised of Limifossoridae + Chaetodermatidae, a result at odds with the commonly held hypothesis placing the putatively plesiomorphic Limifossoridae as the basal-most chaetoderm family. Within the much more diverse Solenogastres, we find that

Cavibelonia, the traditional order defined by hollow, acicular sclerites and a thick cuticle, is not monophyletic. Our results place *Alexandromenia* (Amphimeniidae) basal to the remainder of Neomeniomorpha with strong support in all analyses. The remainder of "Cavibelonia" (represented by the families Proneomeniidae, Simrothiellidae, and Pruvotinidae) is rendered paraphyletic by the order Neomeniamorpha (represented by two species of *Neomenia*) although support for the exact placement of Neomeniamorpha varied among analyses. Lastly, the order Pholidoskepia, which is characterized by sclerites as thin scales, was recovered monophyletic in all analyses. This work represents the first molecular phylogeny of Aplacophora, which has substantially altered understanding of the evolutionary history of this interesting but often overlooked group. Molecular phylogenetics practically turns upside-down previous hypotheses of phylogenetic relationships in both Neomeniomorpha (a cavibelonian taxon as the first branch within the clade) and Chaetodermomorpha (Prochaetodermatidae as the first branch within the clade). Especially in Neomeniomorpha, our results are consistent with a shift from support for the Testaria-hypothesis (small-sized pholidoskepian neomeniomorphs display the most ancestral morphology within Mollusca) to the Aculifera-hypothesis (ancestral molluscs were relatively large-sized, polyplacophoran-like animals).

T5.O14

USING MOLECULAR PHYLOGENETICS TO TEST AFFINITIES OF FOSSIL ACULIFERAN MOLLUSCS AND RECONSTRUCT THEIR CHARACTER EVOLUTION

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The nature and evolution of the aplacophorans and chitons have received much interest as they have been considered to represent a group with many plesiomorphic characteristics for the molluscs. Especially the aplacophorans have attracted much focus due to their lack of many typical molluscan organs, which has led some to portray them as close to the ancestral morphology of the molluscs.

The fossil record, on the other hand, suggest a much later and somewhat perplexing evolution of the group. While bona fide conchiferan molluscs are known from the Earliest Cambrian, not a single unequivocal aplacophoran or chiton is known from this time period. Chiton-like forms are recovered in the latest Cambrian. Aplacophorans are only represented by forms that are much younger and have an appearance like a chiton, with 7 or 8 shell plates and what appears to be a reduced foot. The fossil record is much more in accordance with a little appreciated hypothesis, which has been proposed mainly by Amelie Scheltema that the aplacophorans are secondarily reduced forms, perhaps via progenesis and do not represent an ancestral bodyplan.

Using molecular phylogenetics and divergence estimation I have tested this hypothesis. I have recovered a monophyletic Aculifera, which has now been found in three independent analyses, thus proving to be the most robust relationship among molluscan classes to date. Divergence estimates, using external calibrations from bivalves, gastropods, brachiopods and arthropods recovered a divergence between the aplacophorans and chitons in the Early Ordovician (480 to 470 Ma), which post dates the oldest chiton-like forms from the Late Cambrian (~495 Ma).

Molecular clocks also show that Multiplacophorans are an extinct offshoot from the chiton stem lineage which evolved certain crown group characteristics convergently to the crown group in addition to a bizarre skeleton of 17 shell plates girdled by large spines.

T5.O15

ON THE BASAL RELATIONSHIPS OF MOLLUSCS

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Among the most fascinating problems in animal systematics is the phylogeny of the molluscan classes, and especially the relationships among its vermiform, spicule-bearing and, and multi-gilled forms. Here I will discuss recent advances into the relationships of the two aplacophoran groups and chitons, monoplacophorans and the other molluscan classes, using evidence from target-sequencing approaches, next-generation phylogenomic data, anatomical information and the fossil record and discuss a possible roadmap for generating a robust phylogeny of the members of the phylum Mollusca.

T5.O16

WHO ARE THE "ACULIFERA"?

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The chitons (Polyplacophora) and vermiform molluscs (Solenogastres and Caudofoveata) have been focal to questions of pan-molluscan phylogeny. The three groups are ostensibly united by the spicular armature that is the basis for the name Aculifera ('needle-bearing') of a putative clade uniting these classes. A very few species from these groups have been called upon to serve as key players in high profile scientific debate on pan-Molluscan phylogeny in the last few years, yet the animals in general remain poorly understood and scientifically under-represented. These animals have a reputation as taxonomically 'difficult' but are the source of much excellent work on development, phylogeny, anatomy, and ecology. Indeed, a theme repeatedly emerges of hidden biodiversity at all levels. Among animals that are often dismissed as morphologically homogeneous, they in fact vary in ecology, modes of reproduction, sensory anatomy, and metabolic physiology, even among closely-related species. Given the frequency of independent vermiform body plans throughout Metazoa, and repeated evolution of shell-less-ness in most molluscan classes, a monophyletic origin of 'Aplacophora' probably seems one of the least parsimonious concepts in molluscan evolution, yet it has substantial support. Different datasets, whether molecular, anatomical, or palaeontological, evaluated

in isolation can support radically different interpretations for the relationships between 'aculiferan' members. However, in the next decades the field will quickly approach some consensus on the phylogeny within each class, and this will in turn inform exemplar selection for reconstructing deeper relationships. In the meantime, understanding the basic biology of the animals, and the range of variation within and between species, is fundamentally important to reliably reconstructing their recent evolutionary history.

This symposium honours the memory of one important advocate of clever and inspired work on chitons and aplacophorans, Prof. Chris Schander (1960–2012).

T5.P1

MITOGENOMICS REVEALS PHYLOGENETIC RELATIONSHIPS WITHIN CAUDOFOVEATA (APLACOPHORA)

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The worm-shaped, shell-less aplacophoran molluscs Caudofoveata (=Chaetodermomorpha) and Solenogastres (=Neomeniomorpha) have recently received a great deal of attention as part of the proposed clade Aculifera, but relationships within aplacophoran taxa are still largely unknown. Thus, we employed complete mitochondrial genomes to resolve relationships with particular attention on Caudofoveata. Mitochondrial genomes have been sequenced for most of the mollusk classes, but data have been conspicuously lacking for aplacophorans. We sequenced and assembled the mitochondrial genomes of seven species of Caudofoveata and one species of Solenogastres, chiefly using the Illumina MiSeq platform. We supplemented these data with additional available sequences from GenBank. After genomic assembly with Ray, the mitochondrial genomes were annotated using the MITOS server. Phylogenetic analyses of mitochondrial protein-coding gene DNA and amino acid sequences were carried out using maximum likelihood in RAxML. These analyses strongly support the monophyly of the Caudofoveata. Within Caudofoveata, Chaetodermatidae was recovered as monophyletic, but Limifossoridae was not. Additionally, comparison of mitochondrial gene order revealed arrangements of protein coding genes and tRNAs diagnostic for Caudofoveata. Gene order may also be diagnostic for Chaetodermatidae and Limifossoridae.

T5.P2

CONTRIBUTION TO ABYSSAL ANGOLA BASIN SOLENOGASTRES (MOLLUSCA) WITH PRELIMINARY RECORDS OF TWO SPECIES OF THE ORDER PHOLIDOSKEPIA

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Despite the fact that the abyssal plains suppose more than 40 % of the sea bed, only 11.2 % of the 270 species of described Solenogastres come from these environments, and they all belong to the order Cavibelonia.

During the expedition DIVA 1 (Me 48/1), in the Angola abyssal basin at 5100-5450 m depth, 72 Solenogastres were recollected. The first completed investigations of 38 specimens supposed the description of 9 new species and 3 genera. Turning to this, the Angola abyssal basin is the best known one for these Molluscs. A more comprehensive study of this basin, and the other abyssal basins, will probably reveal the existence of a greater number of species of Solenogastres in all of them.

First records of the study of 7 new Solenogastres of the above mentioned collection are presented. 1 of which belongs to *Macellomenia* and the other 6 specimens belong to *Nematomenia*, both included in the order Pholidoskepia. It is the first information of the presence of this order to more than 3000 m of depth. In addition, the investigation of the sclerites of the mantle and of the internal anatomy indicates that they might be classified as two new species of Solenogastres.

T5.P3

CAUDOFOVEATA FROM WAKASA BAY, WESTERN SEA OF JAPAN

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Fauna of the Class Caudofoveata in the Northwest Pacific has been poorly known. In the Sea of Japan, only four species: one *Falcidens* and three *Chaetoderma* species, have been described from Peter the Great Bay, Russia, and one undesecribed *Scutopus* species has been reported from Konoura, northern coast of Honshu, Japan.

Specimens collected from western Wakasa Bay, western Sea of Japan (35º45'N, 135º20'E), at the depth of 100 m, were identified as two *Scutopus*, one *Falcidens*, and one

Chaetoderma species. After close examination of taxonomically important features and comparisons with congeneric species, they were considered to be undescribed species. The morphology of those four species were described and illustrated in detail.

T5.P4

FIRST DATA ON TWO SPECIES OF *PRUVOTINA* (MOLLUSCA, SOLENOGASTRES, PRUVOTINIIDAE) FROM THE DEEP SEA OF GALICIA (NW SPAIN)

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In the Galician coast 27 Solenogastres species are known, 6 of which belong to Pruvotiinidae. *Pruvotina artabra* Zamarro *et al*, 2012 is the only specie of the genera *Pruvotina,* it comes from coral and stone bottoms situated between 600 and 1000 m depth.

During the expedition "A Selva 2008", which took place in carbonated oceanic crust bottoms of the platform and continental bank of the NW of Galicia (Spain) between 150 and 2500 m of depth, an important collection of Solenogastres was gathered.

23 specimens of the above mentioned collection are studied. 18 of which were recollected at 1000 m depth in an abundant coral substratum, and 5 came from a nodule substratum of 600 m depth. The study of the mantle sclerites places these specimens into the Pruvotiniidae family. In addition the internal anatomy structures, obtained from the histological sections, situated them into the genera *Pruvotina.* The important anatomical differences between these species and the other known species of the genera indicate that they might be classified as two new species.

T5.P5

A NEW SPECIES OF CHAETODERMIDAE (APLACOPHORA, CHAETODERMOMORPHA) FROM RIO DE JANEIRO, BRAZIL, FROM A POSSIBLE NEW GENUS RELATED TO *FALCIDENS* SALVINI-PLAWEN, 1968

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Knowledge on the Brazilian aplacophorans is very restricted, but a high diversity of these animals is beginning to be discovered by a recently, large collection obtained by

the "HABITATS Project – Campos Basin Environmental Heterogeneity by CENPES/PETROBRAS" in Campos Basin, off Rio de Janeiro. One of the most common species (n=220) in the samples from the continental shelf and slope (99.6-975 m depths) was studied, aiming to describe it. Isolated sclerites were examined by the SEM and through the light microscope were observed by birrefringence. Whole specimens were sectioned to study the internal organs, mainly from the digestive system. The radula was also observed by histological sections and exhibits a structure typical from species of *Falcidens* Salvini-Plawen, 1968. However, this species is distinct from most species of this genus, as it has a cylindrical body (up to 3 mm in length), without a collar near the oral region, or a tail on the posterior end. Voucher specimens of *Falcidens limifossorides* Salvini-Plawen, 1992 and *F. halanychi* Schander, Scheltema & Ivanov, 2006 were analysed. They are the most similar to that species from Brazil, but differ in the general morphology of the body (which is much more stout in the latter) and in some details of the sclerites. The histological sections revealed that the intestine of the Brazilian species is communicated posteriorly to the digestive diverticulum, and not anteriorly to the stomach. *Because of these distinct aspects, it is suggested that the Brazilian species is new, and also probably forms* a new genus *with F. limifossorides* and *F. halanychi*.

Financial Support: CENPES/PETROBRAS, SAE/UNICAMP [1], FAPESP Proc. 2011/07629-6[2] and 2011/50297-4[3].

T5.P6

DO CHITONS HAVE A COMPASS?

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Biomineralised magnetite in chiton radulae has been suggested to confer a potential magnetic sensitivity, but to date this has not been rigorously tested. Here, behavioural experiments on several species of chitons show they may be able to detect the orientation of a magnetic field. *Leptochiton rugatus*, *Katharina tunicata, Mopalia kennerlyi* and *Mopalia muscosa* (n=24 for each species) were placed in individual dishes within a 4-coil Merritt vertical magnetic coil. Subjects were randomly exposed to both ambient magnetic field, and a field artificially rotated clockwise by 87°, each for a two hour period (with the initial orientation selected at random). From time-lapse images, we measured each animal's initial orientation, its orientation when it first contacted the wall of the dish, final orientation, and final bearing position within the dish. Animals were allowed to roam freely throughout the experiment, and in transiting the arena most contacted the vertical wall of their round dish; among these specimens, in all four species the directional bearing of first contact with the wall was significantly clustered under the ambient (natural) magnetic field (Rayleigh's Uniformity, $p \leq 0.05$). That is, although they began the experiment facing all directions they turned and progressed to the same mean contact orientation, north-northwest (308º–342º). However, at the end of all experiments, terminal orientation was randomly distributed within each species. Under a rotated magnetic field, there was no clear direction of travel (randomly distributed contact orientation), and terminal orientations were also random in all four species. There is no clear effect of magnetic field direction on chiton orientation, although subtle difference between species in their bearing and orientation under ambient and rotated fields may indicate differential ability to detect or use magnetic fields among species. Chitons apparently orientate in a non-random manner under a natural magnetic field until they reach a landmark (the wall of the dish), though the importance of this ability may be substantially less than anecdotal evidence suggests.

T5.P7

A WANDERING MEATLOAF, I: PACIFIC GIGANTISM AND METABOLIC SCALING IN *CRYPTOCHITON STELLERI*

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The northern Pacific chiton *Cryptochiton stelleri* (known colloquially as the 'wandering meatloaf') is the largest living chiton species, reaching 2 kg in mass and living for upwards of 40 years. It occurs in large aggregations and is anecdotally known to be a particularly active grazer of large leaf algae such as *Ulva.* Gigantism in invertebrates is typically associated with extremely low metabolic demand and low metabolic rates, and classical allometric scaling laws of metabolic rate to body mass would predict that *C. stelleri* would operate at a significantly lower relative metabolic level than other phylogenetically or ecologically similar chiton species. Specimens of *C. stelleri* representing a mass range of three orders of magnitude, from juvenile (~1g wet mass, ~1 yr old) to full grown adults (~1kg, ~30-40 yrs old) were acclimated to a temperature of 12°C and their metabolic rates determined, in the form of respiratory uptake of O_2, using closed chamber respirometry. *Cryptochiton stelleri* shows a higher metabolic rate than would be expected under classical models of scaling and gigantism. This apparently elevated metabolism explains how this species in particular maintains a highly active lifestyle, and is consistent with the proposed hypothesis that highly active consumers are the evolutionary driver for gigantism in North-east Pacific molluscs.

T5.P8

SHELL EYES: GOOD PHYLOGENETIC CHARACTERS IN *ACANTHOPLEURA* (MOLLUSCA: POLYPLACOPHORA)?

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Historically, the gross morphology of chiton valves has played a paramount role in the systematics of the Polyplacophora, with the development of the insertion plates forming the primary basis of taxonomic schemes at the higher classification levels. The possession of insertion teeth on the posterior valve is a character used in a dichotomous separation of taxon at the familial level; yet Acanthopleurinae contains species both with, and without, this feature. Ferreira's 1986 revision of *Acanthopleura* synonymised four well-established genera, but this has not been accepted in subsequent publications. To address the conundrum in Acanthopleurinae, a scanning electron microscope examination was undertaken of 67 microstructural and morphometric characteristics of the intermediate valve, including features of the tegmental micro architecture, the ocelli, the aesthetes and the eaves.

The results demonstrate agreement on 81% of characters between the geographically separated sub populations of *Acanthopleura gemmata*, confirming minimal intraspecific variation. *Acanthopleura loochooana* exhibits a close affinity with the three species previously assigned to *Squamopleura* (*A. araucariana, A. curtisiana and A. miles*), while *A. echinatus and A. niger*, the two species from the west coast of South America, concur on 66% of characters, many of which are not found in the majority of *Acanthopleura* species. Finally, *A. rehderi* shares more in common with outgroup, *Onithochiton quercinus*, than with any species in *Acanthopleura*.

It is concluded that *Squamopleura* and *Enoplochiton* should be resurrected, with the former genus comprising *S. miles, S. auarcariana, S. curtisiana* and *S .loochooana*, and the latter comprising *E. niger* and *E. echinatus*. Furthermore, it is clear that *A. rehderi* has been incorrectly assigned to the genus, showing closer affinity to *Onithochiton*. However, a more detailed comparison with other genera of the shell-eyed chitons is required to confirm its taxomonic status.

T5.P9

MORPHOLOGY OF MEDITERRANEAN *ACANTHOCHITONA* (POLYPLACOPHORA), INCLUDING THE DISCOVERY OF A NEW SPECIES AND AN ILLUSTRATED FIELD IDENTIFICATION KEY

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Without doubt, molecular techniques have revolutionized taxonomy. However, less and less attention is paid to profound morphological descriptions, although several authors have argued for an "integrative" approach of phenotypic and genotypic characters. For many purposes, DNA-barcoding alone is not feasible due to restrictions in facilities (remote areas, research vessels), money or when live specimens are needed (e.g. experiments). Finally, unambiguous identification based on morphology is essential also to correlate elder findings deposited in collections.

The purpose of the present study is not only to describe a new species of the polyplacophoran genus *Acanthochitona*, but also to provide an identification key that can be used by itself in the field, without any additional literature and knowledge about chitons.

On a field trip to Banyuls-sur-mer, France, in 2010 and earlier years, specimens of a formerly unknown species of *Acanthochitona* were collected inside the so called "Trottoir", a eulittoral encrustation of the coralligenous red alga *Lithophyllum tortuosum* (Esper) Foslie, 1900, or other shallow-water and highly oxygenized "coralligene" substrates. Specimens were morphologically examined and described using light and scanning electron microscopy (SEM). In comparison to the other species of *Acanthochitona* in the Mediterranean, the new species differs considerably in the preferred habitat, in color and in structures of the tegmentum, radula and girdle.

The subsequently developed illustrated key is based on macroscopic, external characteristics and is designed for quick identification of the *Acanthochitona* species of the Mediterranean in the field. It is also provided with an illustrated overview of *Acanthochitona* morphology and therefore can be used also by non-experts and even non-biologists.

The study emphasizes the importance of good morphological descriptions and provides an example how to provide material for morphological identification for the rest of scientific and non-scientific community.

T6

HOW DID THEY GET HERE?: (PALAEO)BIOGEOGRAPHY OF TERRESTRIAL AND MARINE MOLLUSCS

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Oceanic islands are a privileged place for holistic evolutionary and (palaeo) biogeographical studies aiming to get a good understanding of the evolutionary processes and mechanisms involved. To achieve this goal, the mere existence of fossils in volcanic oceanic islands provides invaluable data for the questions of when and which organisms invaded the islands, speciated or even used them as stepping-stones for further range expansion. This symposium aims to bring recent and fossil molluscan experts together, in order to improve the knowledge and to disseminate the latest results of the research on oceanic islands marine and terrestrial patterns and processes of dispersal, colonization and speciation.

T6.O1

PALEOECOLOGICAL AND PALEOENVIRONMENTAL STUDIES USING FOSSIL LAND SNAILS FROM OCEANIC ISLANDS

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Land snails are particularly diverse on oceanic islands because isolation promotes speciation and radiation processes. Consequently, snails are usually an abundant animal group on islands. Moreover, snail shells are frequently preserved in a variety of paleontological (loess, eolianites, paleosols, etc.) and archeological (shell middens, burials, dwelling, etc.) sites. In carbonate-rich islands, fossil land snails can be remarkably abundant and may be used to reconstruct detailed paleoenvironmental and paleoecological information, including past climate, vegetation, species interactions, geographical distributions and biodiversity. The stable isotope composition of land snail shells tracks atmospheric conditions during calcification and the signature of the consumed and assimilated plants. The body size of congeneric species may inform about species interaction. Comparisons of the geographical distribution between fossil and modern specimens of the same taxa depict changes in the local biogeography of mollusks. Variations in snail richness and diversity from fossil assemblages could potentially reflect temporal changes in the environment. The fossil record also functions as an ecological baseline prior to anthropogenic interference, and accordingly, may be used to deduce pristine ecosystems before humans as well as quantify the degree of present human impact. In this presentation, I illustrate how fossil land snails from oceanic islands are used to understand past ecosystems through two case studies from the Canary Islands and the Bahamas.

T6.O2

FAUNAL COMPOSITION AND ISOTOPIC SIGNALS OF MOLLUSC SHELLS INDICATE SEAGRASS MEADOWS IN THE MIOCENE OF INDONESIA

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Today's centre of maximum marine biodiversity is located in the Indo-Malayan region. A large variety of organisms including bivalves and several large gastropod families contribute to this high diversity. Understanding the development of this biodiversity hotspot through the Cenozoic could answer numerous questions about the responses of highly diverse faunal associations to small and large scale environmental changes.

When assessing marine biodiversity through time comparisons of taxon diversity are only meaningful when comparing faunas from the same habitat since species numbers might vary considerably between different ecological settings. Therefore, it is indispensable to reliably discriminate between different habitats in the fossil record.

A good example for the difficulties which may occur when identifying marine paleo-habitats is the challenge of recognizing seagrass vegetation. Due to the low preservation potential of marine angiosperms, indirect indicators, e.g. associated organisms with a higher potential for preservation, are commonly used to infer the presence of seagrass meadows in the geological past.

Because of their high fossilization potential and their abundance in marine habitats molluscs yield the possibility to be useful paleo-seagrass indicators. Here we assess the potential use of indicator taxa (*Smaragdia*) and the taxonomic and ecological composition of whole mollusc assemblages for their suitability to determine seagrass associated faunas in the Miocene of Indonesia. The faunas, after assignment to paleo-habitats ranging from seagrass meadows to coral carpets, are analyzed for their stable isotopic signals (oxygen and carbon). Results show consistently heavier δ^{13} C ratios in shells presumably from seagrass meadows leading to the conclusion that carbon isotopes yield an additional tool to confirm assemblage-based paleoenvironmental interpretations within regions and limited stratigraphic time intervals.

T6.O3

A REVIEW OF THE HETEROBRANCH FOSSIL RECORD AND ITS MEANING FOR PHYLOGENY

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Heterobranchia are one of the major clades of Gastropoda. Members of this group can be identified by a change in shell coiling direction during ontogeny. In species with

planktotrophic larval development, this change normally occurs during metamorphosis i.e., at the protoconch/teleoconch transition. Most species have a sinistral hyperstrophic larval shell attached to a dextral teleoconch. In some heterobranch groups, change in coiling direction occurs within the larval shell (prior metamorphosis). Changes in coiling direction within the teleoconch are not diagnostic for Heterobranchia. Heterostrophy is commonly obscured, especially in taxa with non-planktotrophic larval development or direct development.

Shell heterostrophy has been observed in ancient (Early Ordovician) macluritids but reversal of coiling is from dextral to sinistral and seems to occur within the teleoconch. The oldest evidence for larval heterostrophy has been reported form the Early Devonian. In the Late Palaeozoic, high-spired heterobranchs with flatly sinistral larval shells are globally distributed (Donaldinidae, Streptacididae). Some of them are very similar to extant forms such as Ebalidae and Murchisonellidae. The typical Late Palaeozoic forms became extinct at the end-Permian mass extinction event. In the earliest Triassic, the first architectibranchs (or opisthobranchs) appeared representing the family Tubiferidae. At least some putative Palaeozoic members of these groups are convergent caenogastropods with orthostrophic larval shells. It is very likely that coastal swamp dwelling archaeopulmonates arose from early archtitectibranchs in the Late Triassic or Jurassic and gave rise to fresh water and land pulmonates subsequently. The origin of Late Palaeozoic terrestrial gastropods is obscure. Architectonicoidea have a Late Permian minimum age and Mathildoidea are first known from the Middle Triassic. The latter have a major radiation in the Late Triassic and another radiation occurred in the Early/Middle Jurassic. The origin of Nerineoidea (highly diverse in the Middle Jurassic/ Late Cretaceous) is still obscure. New protoconch data and teleoconch morphology suggest Pyramidellidae, Mathildoidea or architectibranchs as close relatives or sister group.

T6.O4

INTERTIDAL SLUGS ON THE MOVE: EVOLUTIONARY BIOGEOGRAPHY AND DISPERSAL IN *ONCHIDELLA*

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Direct-developing intertidal slugs of the genus *Onchidella* inhabit numerous isolated landmasses despite lacking a planktonic larval phase. Although previously assigned to several allopatric species, our genetic data indicate that southern Atlanto-Pacific direct-developing individuals all belong to one widespread taxon, *O. marginata*. The broad distribution of this species implies efficient transoceanic dispersal, and can be accounted for by the ecological association of *O. marginata* with buoyant macroalgae. Being soft-bodied, fossil data is unavailable, so here we use genetic techniques to test the hypothesis that these populations are recently connected through macroalgal rafting. We analyse mtDNA sequence and AFLP fingerprint variation (700bp COI, 215 loci) in a sample set encompassing a broad geographic range. We find that this widespread direct-developing species shows strong signatures of recent dispersal between oceanically isolated populations, even those separated by thousands of kilometres of open ocean. In support of Atlanto-Pacific connectivity of *O. marginata* mediated by rafting, we find that populations as far apart as New Zealand subantarctic islands, Tierra del Fuego and the Falkland Islands are dominated by two closely-related mtDNA haplotypes. Most of the studied New Zealand subantarctic and South Island populations were undifferentiated in AFLP markers, indicative of ongoing gene flow between them. Local mtDNA diversity and site-to-site variation were higher in the northern than the southern localities, suggesting that the latter have suffered population reductions during glacial periods.

T6.O5

A GLOBAL BIOGEOGRAPHICAL ANALYSIS OF THE SHALLOW-WATER MARINE GASTROPOD FAUNA OF THE NORTH-ATLANTIC OCEAN AND THE MEDITERRANEAN SEA

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A database was assembled with all shallow-water marine gastropods from the North-Atlantic Ocean, encompassing a revised checklist from the Atlantic shores of Scandinavia, British Isles, mainland Portugal, the Macaronesian archipelagos (Azores, Madeira, Selvagens, Canary Islands and Cape Verde), Western North-Atlantic shores (Virginean, Carolinian and Nova Scotia Biogeographical Provinces, the Caribbean Sea and the Gulf of Mexico), Greenland, NW-Atlantic African shores, and the Mediterranean Sea. This provisional database has over 4450 species.

The biogeographical relationships will be discussed, with a detailed analysis of the endemic element on each of the selected sites. Ideas regarding the role of centers of speciation and marine redistribution will be also presented.

T6.O6

THE PALAEO AND NEOBIOGEOGRAPHY OF THE MARINE MOLLUSCS OF THE AZORES FROM THE MIOCENE TO THE PRESENT: PROCESSES AND PATTERNS

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The geographical location of the Azores, midway between Europe and America, poses problems relative to their colonization and the biogeographic affinity of the biota presently living there. In the way of the Gulf Stream, originating off American shores, the Present Azorean biota, marine and terrestrial alike is predominantly European. To explain this distributional paradigm the present study investigates the Neogene fossil record of Santa Maria Island (Azores) in order to establish the biogeographical relationships of the late Miocene- to Recent littoral molluscan fauna of this archipelago. During this talk, the influence of the Pleistocene glacial-interglacial cycles will be discussed, with a special focus on the role of glacial terminations. Probable routes of dispersal to the Northeastern Atlantic archipelagos (Azores, Madeira and Canaries) will be also discussed, as well as the direct and indirect effects that the Pleistocene glaciations produced on the shallow water marine molluscs of these islands.

T6.O7

MOLLUSCAN MIGRATIONS IN THE MACARONESIA DURING INTERGLACIAL STAGES

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Studies on the distribution of fossil marine molluscs are usually focused on coastal species of interglacial stages during highstand conditions, due to their better preservation, and exposure of the deposits. The Last Interglacial Period (MIS 5, ~130 -75 ka) was characterized by higher than present temperatures and sea level, and marine deposits are commonly preserved worldwide above present sea level. These deposits are usually analyzed from a paleoclimatic point of view. Molluscs content provide information about the coastal paleoenvironments, and possible changes in the superficial ocean circulation around the world. In the Western Mediterranean, the presence of thermophilic species that have nowadays a tropical-subtropical Western African distribution, agree with the global higher temperatures described during this period. In order to analyze displacement of these species from African coasts, a review and comparison of the Mediterranean and Macaronesian paleontological content of MIS 5 and older interglacials is presented.

The paleontological data from Azores, Canary and Cape Verde archipelagos coincide with the higher temperatures recorded in the Mediterranean. A total of 52 warm-water species have been identified. The presence on that islands of some species that are absent in the Mediterranean, together with paleontological data from the African coasts, allows interpreting the existence of oceanographic or atmospheric thresholds controlling the migration of these warm species towards the Mediterranean during Last Interglacial. Some of these species appear in older interglacials deposits (MIS 11, 9 and 7) in Mediterranean and Canary Islands (e.g. *Strombus latus*). Hypothesis on environmental requirements and transport possibilities of these species are discussed.

Acknowledgments: Projects CGL2012-33430 and CGL201-23781, IGCP588, INQUA CMP Commission, GEOTOP Lab. Contrib., and UCM 910198-Group.

T6.P1

EXTENSIVE OCCURRENCE OF COLD-WATER MOLLUSCAN THANATOCENOSES ON THE SLOPE OF THE GULF OF CADIZ (SW IBERIAN PENINSULA)

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Remains of molluscs and corals were collected on the sea-bottom in the northern part of the Ibero-Moroccan Gulf, during an extensive sampling programme (INDEMARES CHICA) aimed to habitat characterization and designation of the offshore prospects for Natura 2000 marine protected areas. Samples were taken mostly in the 300-1000 m depth interval through dredging, trawling and box-coring. These contain a suite of species which nowadays live mostly north of the English Channel, together with other more widespread species.

Species now extinct in the area and unequivocally indicating a faunal shift are those currently living in shelf and/or upper slope areas of northern Europe and include the gastropods *Buccinum undatum*, *Neptunea antiqua*, *Colus gracilis*, and the bivalves *Chlamys islandica*, *Modiolus modiolus, Arctica islandica* and *Mya truncata*. Among these, *N. antiqua* seems to be the only one which never entered into the Mediterranean. The pteropod *Limacina retroversa*, nowadays restricted to water masses north of the English Channel but widespread in Mediterranean sediments of the Last Glacial Maximum, was also recorded. Most shells found in these thanatocoenosis nevertheless belong to species e.g. *Neptunea contraria*, *Pseudamussium peslutrae* and *Astarte sulcata* which, together with the deep-water corals *Lophelia pertusa* and *Madrepora oculata*, are still reported on the continental slope in the area but rare.

The abundant subfossil fauna contrasts with the paucity of the contemporaneous deep-sea fauna in the pathway of the Mediterranean Outflow Watermass (MOW). The impoverishment may be a consequence of exaggerated hydrodynamics, of the water quality but also of the shortage of recruitment from an impoverished Mediterranean source area. The abundance of subfossil remains in the present MOW pathway-could be explained if this outflow was reduced in intensity, but also by the existence of a richer bathyal fauna in the Mediterranean source area at the time of a colder climate.

T7

THERE'S SOMETHING ABOUT OPISTHOBRANCHIA

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Opisthobranch mollusks have received considerable attention during the past years by a growing and enthusiastic research community. The aim of this symposium is to bring together all those interested in the various aspects of opisthobranch biology and evolution, from systematics to phylogenetics, from development to behavior, symbiotic relationship and kleptobiology to general ecology.
We expect this symposium will be a discussion forum of the latest advances as well as a platform to establish strategies and collaborations to get projects together and exchange ideas to "address and solve" old and new questions.

T7.O1

PARALLEL CHANGES IN GENITAL MORPHOLOGY DELINEATE CRYPTIC DIVERSIFICATION OF PLANKTONIC NUDIBRANCHS (GLAUCIDAE: *GLAUCUS*)

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The relative roles of geographic and non-geographic barriers in the genesis of genetic isolation are highly debated in evolutionary biology, yet knowing how speciation occurs is essential to our understanding of biodiversity. In the open ocean, differentiating between the two is particularly difficult because of the high levels of gene flow found in pelagic communities. Here, we use molecular phylogenetics to test the hypothesis that geography is the primary isolating mechanism in a clade of pelagic nudibranchs, Glaucinae. Our results contradict allopatric expectations: the cosmopolitan *Glaucus atlanticus* is panmictic, whereas the Indo-Pacific *G. marginatus* contains two pairs of cryptic species with overlapping distributions. Within the *G. marginatus* species complex, a parallel reproductive change has occurred in each cryptic species pair: the loss of a bursa copulatrix. Available *G. marginatus* data are most consistent with non-geographic speciation events, but we cannot rule out the possibility of allopatric speciation, followed by iterative range extension and secondary overlap. Irrespective of ancestral range distributions, our results implicate a central role for reproductive character differentiation in glaucinin speciation – a novel result in a planktonic system.

T7.O2

HIDDEN DIVERSITY IN A REEF-DWELLING SEA SLUG, *PTERAEOLIDIA IANTHINA* (NUDIBRANCHIA, AEOLIDIDA), IN THE NORTHWESTERN PACIFIC

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Pteraeolidia ianthina (Angas, 1864) is an aeolid nudibranch (Gastropoda, Mollusca) common in shallow reefs in warm-temperate to tropical waters of the Indo-Pacific Ocean. This aeolid is usually distinguished by a single morphological character, namely bright blue (sometimes purple) bands on its oral tentacles, and it is considered to be a single species. However, high color variability has been reported in many parts of its distribution range. Therefore, we carried out population genetic analyses using molecular genetics techniques to resolve whether this aeolid is a multispecies assemblage or a single but highly variable species. Although this species is distributed widely throughout the Indo-Pacific area, this study focused on individuals in the northwestern Pacific area, as this region is of interest because it includes multiple climate zones from tropics to temperate and two ocean currents, the Kuroshio and North Equatorial Currents.

The population genetic structure of *P. ianthina* in the northwestern Pacific was investigated by analyzing the nuclear ribosomal RNA gene region, including 18S and 5.8S rRNA genes and the ITS1 region (559 bp). Among 400 individuals from 19 localities in the northwestern Pacific, three genetically distinct groups, which were separated by a minimum sequence difference of about 5% (*p*-distance) each, were detected. The marked genetic differentiation of these three groups even in localities where two or three groups co-occurred implied that they were independent species, although intergroup hybrid was observed in very low frequency. Within-population genetic variability was low in two species but high in one.

Eggs of the three species were obtained and their ways of early development clearly showed the species differences. With other ecological and anatomical traits differences observed, we will report the three cryptic species with in *P. ianthina*.

T7.O3

AEOLIDIA PAPILLOSA (LINNAEUS, 1761), SINGLE SPECIES OR A CRYPTIC SPECIES COMPLEX? A MORPHOLOGICAL AND MOLECULAR STUDY.

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Besides from being the type species of Aeolidiidae, *Aeolidia papillosa* has been reported from cold and/or temperate waters around the world, specially from the northern

hemisphere. The accepted geographical distribution of this species ranges from Norway (its type locality), to California, and includes Iceland, Greenland, the North Atlantic coast of USA, Alaska and the White Sea (Russia). In Europe this species is present in the Netherlands, the British Islands, the Atlantic coast of France and the Iberian Peninsula. Some records from west and eastern coasts of South America and northern Japan have also been reported. Nevertheless, the ongoing controversy about the validity of the *Aeolidia* species *A. serotina, A. papillosa* var. *pacifica, A. papillosa* var. *herculea* and *A. collaris* and the boundaries between them has prevented an accurate description of *A. papillosa'* morphological characteristics. Here we used morphological and molecular methods to test the distribution of *Aeolidia papillosa*. For this aim, we studied different specimens from the eastern Atlantic (Sweden, the Netherlands, France and northern of Spain), Artic (Russia), western Atlantic (Maine, Massachusetts) and Pacific coasts of North America (Alaska, the state of Washington, California and Chile). Maximum-likelihood and Bayesian analyses of partial DNA sequences of the mitochondrial cytochrome c oxidase subunit I and 16S rRNA genes and nuclear gene Histone-3 (H3) were used to produce phylogenetic trees. The presence of four cryptic species under the name of *A. papillosa* is revealed by our morphological and molecular studies.

T7.O4

TOWARDS A NEW AEOLID CLASSIFICATION: CONSEQUENCES OF THE FIRST MOLECULAR PHYLOGENY OF AEOLIDIDA (GASTROPODA, NUDIBRANCHIA)

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Aeolidida is the second largest group of nudibranchs after Doridina, but phylogenetic studies of this group are scarce. Several contributions are focused on some aeolid genera or a single family, most of them only from a morphological point of view. In addition, phylogenetic studies focused on higher taxa, such as Heterobranchia, also include some aeolid species. These studies usually support the monophyly of the aeolids and state the presence of cnidosacs and oral tentacles as their synapomorphies. Depending on the author, the number of families that constitutes Aeolidida varies, since the validity of some of them has been questioned. Indeed, several authors have highlighted the necessity of a comprehensive study of aeolid phylogeny. In this contribution we conducted a preliminary molecular phylogeny of Aeolidida. We included 177 representatives of the currently accepted families: 19 nominal species of Flabellinidae, one species of Fionidae, two species of Calmidae, four species of Eubranchidae, 36 species of Tergipedidae, 44 species of Aeolidiidae, 61 species of Facelinidae, two species of Babakinidae, one species

of Glaucidae, one species of Embletoniidae and three species of Piseinotecidae. Maximum-likelihood and Bayesian analyses of partial DNA sequences of the mitochondrial cytochrome c oxidase subunit I, 16S rRNA genes and nuclear gene Histone-3 (H3) were used to test the monophyly of Aeolidida as well as its different families. Excluding Embletoniidae, our results supported the monophyly of Aeolidida but point to necessary changes to the systematics of this taxon. Only Aeolidiidae and Babakinidae were monophyletic. Fionidae, Calmidae and Eubranchidae clustered within Tergipedidae, while Flabellinidae and Facelinidae, as traditionally constituted, formed polyphyletic lineages.
his family.

T7.O5

SECONDARY METABOLOMICS VERIFIES RADIATION IN AN ANTARCTIC MARINE INVERTEBRATE SPECIES FLOCK

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Antarctica's complex glacial history is postulated to have generated significant marine biological diversity, but is unclear why some taxa responded with diversification while others did not. During glacial cycles, grounded ice sheets extended far from the continent, massively disrupting the continental shelf and slope as habitable areas. However, some ice-free refuges must have existed, and would have reduced previously widespread population sizes, and provided allopatric barriers facilitating speciation. Previous work revealed a multitude of highly divergent mitochondrial lineages in the nudibranch sea slug *Doris kerguelenensis*, but because of the uniparental inheritance of mitochondria, it was unclear whether these lineages simply revealed stochastic sorting patterns of populations that rarely reach equilibrium between glacial cycles. Here we demonstrate that the mitochondrial groups also correlate with nuclear DNA and secondary metabolite profiles. These metabolites are not derived from the diet, but instead are synthesized de novo and are derived from encoded nuclear DNA. By extracting secondary metabolites from the same individuals we sequenced, we were able to directly link the secondary metabolome to a mitochondrial lineage. The correlation between the anti-predatory metabolites and the mitochondrial lineages suggest that these lineages represent cryptic species, and that together they represent the first marine invertebrate species flock that has been corroborated with multiple sources of nuclear data. It also suggests a synergistic role for selection and allopatry driving speciation in this system.

T7.O6

A COLORFUL QUESTION: THE NUDIBRANCH ´*FELIMIDA CLENCHI* SPECIES COMPLEX´ INVESTIGATED THROUGH MOLECULAR MARKERS

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The color pattern is a commonly used character in the taxonomy of nudibranchs. Among the Chromodorididae, 'species color groups' are usual and result in doubts concerning the number of species involved, also due to similarities in internal morphology. In the tropical Atlantic and Mediterranean Sea, the *Felimida clenchi* species complex includes three Atlantic species names: *Felimida clenchi* (Russell, 1935), *Felimida binza* (Marcus & Marcus, 1963) and *Felimida neona* (Marcus, 1955), and one eastern Atlantic/Mediterranean species name: *Felimida britoi* (Ortea & Pérez, 1983). The validity of these species and their geographic distribution has been a matter of ongoing debate. Using multi-locus markers for tree-based and other species delimitation approaches, in complement to morphological characters and field observations, we aim to identify the main lineages of this group and their relationships, based on specimens covering the complex geographic range, including new localities such as St. Helena islands. Our results support the monophyly of the '*Felimida clenchi*' complex. However, the traditional species concepts in this complex were not recovered in most cases, as morphotypes assigned to different species clustered together and color forms considered to be unique to certain species are present in separate clades. The inclusion of a higher number of specimens changed the topology of our preliminary tree, indicating that this feature is relevant when dealing with species delineation analysis. This study points for the need to reinterpret the value of color as an informative character in the taxonomy of chromatic nudibranchs.

T7.O7

THE SYSTEMATICS OF CEPHALASPIDEA REVISITED

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The Cephalaspidea is the second most diverse marine clade of the Euthyneura gastropods, after the Nudibranchia. They occur worldwide across all latitudes and depths. The definition of the group and the relationships between members has been hampered by the difficulty of establishing sound synapomorphies, but the advent of molecular phylogenetics in recent times has helped changed significantly this situation. Yet, because of reduced taxon sampling and few genetic markers employed in previous studies many questions about the sister relationships and monophyletic status of several families remained open.

In this study we included over 100 taxa covering 100% of the traditionally recognized valid families and about 50% of the genera. A molecular Bayesian phylogenetic hypothesis based on two mitochondrial and two nuclear gene markers (COI, 16S rRNA, 28S rRNA and Histone-3) is presented and discussed.

T7.O8

BROAD SAMPLING AND MOLECULAR PHYLOGENETICS REVEALS RAMPANT PARAPHYLY IN HAMINOEIDAE CEPHALASPIDS

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Haminoeidae is the most diverse family of the Cephalaspidea with 42 nominal recent genera described, accounting for approximately 50% of the generic diversity of cephalaspidean gastropods. Several of these genera have been loosely defined and their validity is questionable; about one third is known only from shells.

This work is the first attempt to test, in a broader molecular phylogenetic framework, the monophyly of the family Haminoeidae and of its genera and to investigate the evolutionary relationships within the family.

A multi-gene Bayesian phylogeny including mitochondrial and nuclear markers with about 100 samples revealed surprising high levels of paraphyly and the need for a redefinition of most genera. A new classification of the Haminoeidae is proposed.

T7.O9

NEW INSIGHTS INTO CEPHALAPIDEAN EVOLUTION: THE PHYLOGENY OF THE PHILINACEA (GASTROPODA, OPISTHOBRANCHIA).

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The only previous molecular phylogeny of Philinidae included species from a single clade within *Philine* and with limited outgroup sampling. Recent shallow and deep-water surveys of Indo-Pacific waters in the Philippines provided material for additional study of the diversity and phylogeny of the Philinacea. Anatomical and molecular studies reveal the presence of six additional undescribed taxa. Morphological characters, including anatomical details of the shell, radular morphology, gizzard plates and male and hermaphroditic reproductive systems are entirely congruent with the molecular differences found. Four of these taxa are members of the *Philine aperta* clade, while two taxa are members of a more basal lineage. This study reinforces view that the diversity of the Indo-Pacific Philinacea still remains incompletely sampled. Both morphological and molecular data support the phylogenetic position of these taxa. The more basal members have small gizzard plates or entirely lack them and have a simple penis, while species in the *Philine aperta* clade have plates with pores or slits and have a complex penis and prostate. In sampling broader outgroup relationships, some members of Philinidae cluster with species of Aglajidae, suggesting that Philinidae as traditionally constructed does not constitute a clade, but represents a paraphyletic assembledge. These relationships need to be further studied with more extensive taxon sampling of philinaceans, but are suggestive that further systematic revision is required to develop a classification consistent with the phylogeny of the Philinacea.

T7.O10

A GLIMPSE INTO EARLY HETEROBRANCH EVOLUTION - MICROANATOMY OF MURCHISONELLIDAE

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The Heterobranchia – a taxon containing roughly 50 percent of gastropod diversity – have presumably descended from minute marine snails. Little is known about the various lineages of small-bodied “basal” heterobranchs that show “prosobranch” affinities, but their study is relevant to understanding the evolution of the group per se.

The high-spired Murchisonellidae are associated with sea grass in coastal waters worldwide, but except for shell data, almost nothing is known about their biology and anatomy. Their minute size makes study with traditional methods difficult.

Molecular data about the family lately yielded surprising results: murchisonellids are not closely related to the externally similar and diverse Pyramidellidae, but should be placed among "basal" Heterobranchia. Moreover, their direct sister group is probably the enigmatic Rhodopemorpha, a group of minute, aberrant slugs found in the intertidal or interstitially in sand habitats and that was previously classified among opisthobranchs.

We present detailed microanatomical data on all major organ systems of a species of *Koloonella* Laseron, 1959 from eastern Australia, based on 3D reconstruction of semithin histological sections. The first such study of a high-spired snail, it reveals that the genus is indeed not pyramidellid as previously assumed. It is instead a fourth genus among Murchisonellidae, and shows the unique "jaw" apparatus described for the family among other "basal heterobranch" characters. Potential characters shared with the highly divergent Rhodopemorpha are evaluated, and systematic relationships and evolution are discussed.

T7.O11

THE ENIGMA FROM THE DEEP – INTEGRATIVE STUDY OF A REMARKABLE HETEROBRANCH SEA SLUG FROM OFF MOZAMBIQUE

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During the MAINBAZA cruise in April 2009, two small specimens of unknown and enigmatic sea slugs were collected from 260 - 440 m depth in the Mozambique Channel off South Mozambique. At first glance, the specimens could not be unambiguously assigned to any of the major heterobranch groups.

To assess their affinities, we examined these specimens using an integrative approach. One specimen was embedded in Epon and histological semi-thin serial sections of 1.5 μm were prepared. A computer-based three-dimensional reconstruction of all major organ systems was performed using AMIRA software. Externally, specimens are bilaterally symmetrical with the head-foot posteriorly covered by a rounded notum on top of the viscera. The head bears pairs of well-developed labial tentacles and rhinophores. Pigmented eyes are situated dorsolaterally behind the rhinophores. The broad foot bears sickle-shaped propodial tentacles and has a free tail which tapers to a pointed tip. The epidermis is invested with a proliferation of diverse gland cells. There are no remnants of a shell, mantle cavity or gill. The central nervous system is prepharyngeal with separate cerebral and pleural ganglia and four distinct ganglia on the euthyneurous visceral nerve cord, plus a putative osphradial ganglion. The excretory system is located dorsally and consists of a ramified, thin-walled vessel system. The hermaphroditic genital system appears to be monaulic, with a partially external sperm groove leading to a cephalic copulatory organ. First molecular phylogenetic results will help to infer the origin and relationships of this highly mysterious deep sea slug.

T7.O12

PHYLOGENY OF SACOGLOSSA: HOW KLEPTOPLASTY AND LARVAL TYPE INFLUENCE RATES OF MOLECULAR EVOLUTION AND SPECIATION IN HERBIVOROUS SEA SLUGS

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Theory holds that rates of evolution and diversification can be tied to key characters promoting niche expansion, but we have little understanding of how traits affecting resource use drive speciation in marine taxa. Shifts from migratory to non-dispersive larvae have also been suggested to influence macroevolutionary patterns in marine animals, but phylogenetic studies of diverse taxa have failed to support this hypothesis. Sacoglossa is a clade of specialized herbivores, some exhibiting kleptoplasty, the retention of functional algal chloroplasts. Many shifts in algal host and larval type have occurred across the Sacoglossa, which is thus an ideal taxon for comparative tests of trait-dependent evolutionary processes. I will present a four-gene phylogeny of 200 sacoglossan species, and within this phylogenetic framework will evaluate the influence of kleptoplasty, host shifts, and transitions in larval development on rates of evolution. Ancestral character state reconstructions and comparative model-fitting tests reveal that kleptoplasty accelerates the pace of molecular evolution, and is associated with high rates of host shifting. Kleptoplasty is supported as a key character that allowed Plakobranchoidea to radiate onto a range of novel hosts, possibly by reducing feeding rates on toxic algae during niche expansion. Mutation rates also increased in the kleptoplastic clade, potentially as a consequence of mutagenic radicals released during photosynthesis, or of genetic hitchhiking during selective sweeps associated with speciation. Contrary to predictions based on the fossil record, origins of non-feeding larvae are not associated with increased speciation, but do accelerate rates of sequence evolution, likely due to lower effective population sizes and/or stronger effects of local selection for lecithotrophic species. The results indicate that traits affecting resource use are tightly coupled to diversification, as predicted by models of ecological speciation, but not traits associated with dispersal; however, both types of traits influence mutation rates of apparently neutral DNA sequences.

T7.O13

PLAKOBRANCHUS OCELLATUS (SACOGLOSSA) CONTINUOUSLY ACQUIRES KLEPTOPLASTS AND NUTRITION FROM MULTIPLE ALGAL SPECIES IN NATURE

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The sea slug *Plakobranchus ocellatus* (Sacoglossa, Gastropoda) retains photosynthetically active chloroplasts from ingested algae (kleptoplasts) in its digestive gland cells for up to 10 months. Although its feeding behavior has not been observed in natural habitats, two hypotheses have been proposed: 1) adult *P. ocellatus* behaves as a photoautotroph without replenishing the kleptoplasts; or 2) it behaves as a mixotroph (photoautotroph and algivore) and replenishes kleptoplasts continually or periodically.

To address this question, we examined the source algae for kleptoplasts and temporal changes in kleptoplast composition and nutritional contribution. By characterizing the temporal diversity of *P. ocellatus* kleptoplasts using *rbcL* sequences, we found that *P. ocellatus* harvests kleptoplasts from at least 8 different siphonous green algal species, that kleptoplasts from more than one species are present in each individual sea slug, and that the kleptoplast composition differs temporally. These results suggest that wild *P. ocellatus* often feed on multiple species of siphonous algae from which they continually obtain fresh chloroplasts. By estimating the trophic position of wild and starved *P. ocellatus* using the stable nitrogen isotopic composition of amino acids, we showed that despite the abundance of kleptoplasts, their photosynthates do not contribute greatly to the nutrition of wild *P. ocellatus*, but that kleptoplast photosynthates form a significant source of nutrition for starved sea slugs. The herbivorous nature of wild *P. ocellatus* is consistent with insights from molecular analyses indicating that kleptoplasts are frequently replenished from ingested algae, leading to the conclusion that natural populations of *P. ocellatus* do not rely on photosynthesis but mainly on the digestion of ingested algae.

T7.O14

FUNCTIONAL CHLOROPLASTS IN SACOGLOSSA: A NON-PLAKOBRANCHID LONG-TERM RETENTION FORM – *COSTASIELLA OCELLIFERA*

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Costasiella ocellifera is the only kleptoplastic species that is not a member of the Plakobranchoidea, and whose photosynthetic capability was first noticed by Clark and colleagues (1981). Phylogenetic relationship of *Costasiella* within Limapontioidea, as well as limapontioidean groups with all other sacoglossan taxa, is not resolved. According to recent phylogenetic analyses, sequestration of chloroplasts with subsequent maintenance over a longer period of time has evolved at least twice.

Photosynthetic ability of the sequestered plastids within *C. ocellifera* during starvation is hardly studied and, so far, never confirmed by in situ PAM measurements. Furthermore, whether photosynthesis truly contributes to the survival during starvation is not known for this species. Thus, we investigated *C. ocellifera* with regards to photosynthetic capability under starvation conditions in (i) complete darkness, (ii) in a day/night cycle and (iii) under light with a photosynthesis-blocking chemical, Monolinuron. Our experiments clearly show that *C. ocellifera* is a long-term-retention form, but that photosynthesis may not be important for surviving periods of starvation. We further raise the question, if kleptoplasts may function more as a nutrition depot rather than providing the slug with photosynthates.

T7.O15

PHOTOPROTECTION MECHANISMS IN SACOGLOSSAN SEA SLUGS

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Some sea slugs can maintain functional chloroplasts from their macroalgal food sources in the cells of their digestive diverticula. These “stolen” chloroplasts (kleptoplasts) continue to photosynthesize in the absence of an algal nucleus, in some cases for as long as one year. Within the Metazoa, this phenomenon seems to have only evolved among sacoglossan sea slugs. Known for over a century, the mechanisms of interaction between the foreign organelle and host animal cell are just now starting to be unravelled. In the study of photosynthetic Sacoglossa, it is important to understand their relationship with light and the mechanisms involved in the protection of kleptoplasts from exposure to excessive light (photoprotection mechanisms). We investigated the occurrence of an active xanthophyll cycle (XC) as a photoprotection mechanism in the sea slug *Elysia viridis* from the North coast of Portugal. Using a combination of HPLC techniques and PAM fluorometry, we showed that adult specimens of this species acquire kleptoplasts

exclusively from the macroalgae *Codium tomentosum* and lack the ability to photoprotect from excessive light using the xanthophyll cycle. In *E. viridis*, within 5 min of a light stress (920 μmol m^{-2} s^{-1}) the effective quantum yield of photosynthesis decreased to less than 7% of the maximum quantum yield (F_v/F_m). After 30 min of light stress, non-photochemical quenching of chlorophyll fluorescence (NPQ) reached 3.2. Although 63% of F_v/F_m was restored within 60 min in the dark, 88% of NPQ was still sustained in that period of time. Similar results were obtained for *C. tomentosum*. Since no XC activity was detected in both *E. viridis* and *C. tomentosum*, the whole NPQ is likely to result from damaged reaction centres. The state of knowledge on the behavioural and physiological mechanisms suggested to be involved in the photoprotection of kleptoplasts in sacoglossan sea slugs are critically reviewed.

T7.O16

A NEW SPECIES OF *COSTASIELLA* (OPISTHOBRANCHIA, SACOGLOSSA) FROM FLORIDA, NOT ASSOCIATED WITH *AVRAINVILLEA*

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Species of the sacoglossan genus *Costasiella* are usually found associated with the green alga *Avrainvillea*. However, at least two species in the Indo-West Pacific Region, *C. pallida* Jensen, 1985 and *C. coronata* Swennen, 2007, have been found in habitats where *Avrainvillea* does not occur. In 2008 several specimens of a pale green *Costasiella* were found by Ms. Anne DuPont and her dive friends. This species shows some similarity with the type species of *Costasiella*, *C. virescens* Pruvot-Fol, 1951 from the Mediterranean and eastern Atlantic Ocean, and also with *C. formicaria* (Baba, 1959) from Japan. In the present study the new species from Florida was compared to *C. formicaria, C. coronata* and *C. pallida*. All these species are not associated with *Avrainvillea* and they share several morphological characters: (1) Fleshy ridges along anterior head margins, surrounding the mouth, (2) no pharyngeal pouches attached to the pharynx (also seen in a few *Avrainvillea* associated species), (3) narrow, pointed, smooth radular teeth with short bases and rapidly increasing in length, (4) albumen gland in cerata (also seen in several *Avrainvillea* associated species). The present species agrees the most with *C. virescens*. Both have distinct pedal tentacles, elongate tall pericardium, and a narrow tail, which is not ceras-like. The Florida specimens have much denser brown pigment on the dorsal body surface, but no or little pigment on the cerata. It has simple cylindrical rhinophores, though in living specimens they appear flattened. In most specimens there is a dark longitudinal line on the posterior surface of the rhinophores and also dark stripes are located on the anterior surface of the head. Morphologically the *Costasiella* species not associated with *Avrainvillea* form a clade separated from the *Avrainvillea* associated species.

T7.O17

CULTURING SEA SLUGS: WHY THEY MATTER?

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The interest on sea slugs' production has steadily increased in the last decades mainly driven by their potential use as model organisms. In particular, their use in neurobiological and pharmacological research prompted the development of suitable culture protocols to allow their mass production under controlled conditions.

Sea hares are one of the most well studied groups of sea slugs mostly due to their simple neuronal architecture, allowing research on behavior and physiological processes.

Nudibranchs are commonly targeted by bioprospecting efforts towards the discovery of new marine drugs. These organisms produce secondary metabolites "stolen" from their invertebrate preys, while some are also able to synthesize unique toxic compounds.

A growing interest in "solar-powered" sacoglossan slugs photobiology has also emerged in the last decade, as these puzzling organisms are able to "steal" chloroplasts from their algal prey and retain them functional in their animal tissues (e.g. *Elysia* spp.). The lack of a reliable supply of cultured organisms still impairs some experimental works that would certainly help to clarify the mechanisms controlling this remarkable symbiosis.

The culture of sea slugs has also started to be addressed to supply target species for the marine aquarium trade. Besides an obvious aesthetical interest, these organisms can also have a functional role in controlling aquarium pests (e.g., *Berghia verrucicornis* is used to control the glass anemone *Aiptasia* spp.) or nuisance algae (e.g., *Elysia crispata*).

Standardized methods for culturing most sea slugs are still missing, with the lack of knowledge on suitable larval diets and settlement cues triggering metamorphosis of competent larvae being two of the main bottlenecks. Additionally, the stenophagous feeding regime displayed by broodstock and developing juveniles of several species commonly requires the collection and/or culture of their prey (e.g. sponges, sea anemones, corals...); this need commonly impairs their long-term husbandry and/or large-scale grow-out.

T7.O18

REDESCRIPTION OF *PLEUROBRANCHAEA INCONSPICUA* (PLEUROBRANCHOIDEA: NUDIPLEURA) FROM BRAZIL, WITH A PRELIMINARY EVALUATION OF THE MORPHOLOGICAL CHARACTERS USED IN THE TAXONOMY OF *PLEUROBRANCHAEA*

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The classification of the family Pleurobranchaeidae has in many cases been based upon insufficiently described specimens, and the distinctions among species are considered difficult because the morphology of the classical hard structures, as radulae and jaws, can be used in most cases only for generic separation. Many authors considered the anatomy of the male apparatus as the most useful character. In the genus *Pleurobranchaea*, authors distinguish species by the shape of the cross section of the penial cuticle. In the present work, different portions of the penial cuticle of *Pleurobranchaea inconspicua* were analyzed and it was observed that its shape and size vary through the length of the penis. These characters seem not to be species-specific, since the penial cuticle of other species, as *Pleurobranchaea meckeli*, matches with *P. inconspicua* in some parts through the penial cuticle. A detailed anatomical study performed in *P. inconspicua* from Brazil allowed us to recognize that other characters, like the position of the aperture of the salivary duct, the position and presence/absent of extrinsic and intrinsic odontophoric muscles, nerves of the cerebro-pleural and pedal ganglia, shape of seminal receptacle, can be used to distinguish species. One of the preliminary results of this detailed study is the recognition of a species, possibly new to science, which was previously considered *Pleurobranchaea inconspicua*.

T7.O19

ADDRESSING THECOSOME PTEROPODS (GASTROPODA: EUOPISTHOBRANCHIA) SOFT BODIES IN 3D MICROANTOMICAL DETAIL

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Recently, thecosome pteropods have attracted special interest, as they may be among the marine organisms suffering most from proceeding acidification of the world ocean. Despite the general interest concerning environmental factors and their implications on these animals, the anatomy of their soft bodies has poorly been studied. Herein, we address the soft part morphology of *Creseis* and *Limacina* in histological and microanatomical detail. We present 3D models of all major

organ systems from reconstructing serial semi-thin sections using the software Amira, and supplement and partly correct earlier descriptions. For the first time we explore details of the thecosome central nervous systems comparatively, and discuss the evolution of thecosome body plans in the light of recent reorganizations of euopisthobranch systematics.

T7.O20

NUDIPLEURA OF MOZAMBIQUE

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There are indications of a second peak of biodiversity located in the Western Indian Ocean particularly between Madagascar and Mozambique. Despite of this, the diversity of nudipleuran gastropods (Opisthobranchia: Nudibranchia and Pleurobranchoidea) in this region is very poorly understood. In fact, prior to this study, no one has conducted an assessment of Nudipleura in Mozambique. The few Nudipleura records from Mozambique were from occasional observations; mainly from divers or researchers doing rapid biodiversity assessments. The purpose of this study is to assess the diversity of Nudipleura in Mozambique in order to create a baseline for future studies. The information provided through this intensive assessment is a prerequisite to solving more complex questions, such as biogeography and phylogenetic issues. Data has been collected monthly since January 2011 and still in process. Notes on ecology and distribution are being taken. A combination of techniques has been used, including SCUBA diving, snorkelling, analysis of substrate and small artificial reefs. So far 170 nudipleuran species (10 Pleurobranchomorpha and 160 Nudibranchia) were found. From those around 80% are new recordings for the country and potentially 36 species are new for science. The number of families recorded was 29, the most representative family was Chromodorididae (52) followed by Polyceridae (11).

T7.O21

ADDING A MISSING PIECE TO THE PUZZLE: “OPISTHOBRANCHS” FROM PERU

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The Peruvian sea slug fauna was very poorly investigated. In a recent review we have presented a revised checklist of Peruvian “opisthobranchs” (i.e. Acteonoidea, Nudipleura, Euopisthobranchia and the panpulmonate Acochlidia and Sacoglossa).

Older records have been compiled, critically assessed and compared with our findings from recent surveys along the entire Peruvian coast. Herein we report on opisthobranch species that were already known from Chile or elsewhere, and also provide some new morphological, biological and distributional data on species thus far only known from Peru. Challenges are discussed and an outlook on current and future work is given.

T7.O22

INDEPENDENT EVOLUTION OF SWIMMING BEHAVIORS IN NUDIBRANCHS INFERRED FROM NEURAL MECHANISMS

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Of the 2000-3000 species of Nudibranchia, only about 60 have been reported to swim. There are two predominant forms of swimming: left-right (LR) body flexions and dorsal-ventral (DV) body flexions. Both types of swimming are distributed across the phylogeny of Nudibranchia and its sister group Pleurobranchomorpha. This distribution makes the ancestry and evolution of swimming behaviors within the Nudibranchia unclear. Comparing the neural mechanisms underlying swimming may inform a discussion about the evolution of those behaviors.

We examined the neural mechanisms underlying LR swimming in three species within the nudibranch subclade, Cladobranchia: *Melibe leonina*, *Dendronotus iris*, and the Aeolid *Flabellina iodinea*. Although *Melibe* and *Dendronotus* have homologous neurons, there were significant differences in the neural mechanisms for LR swimming in these species. Preliminary results in *Flabellina*, showed a mixture of the neural characteristics seen in *Melibe* and *Dendronotus*. Thus, the behavior was not predictive of the neural mechanism for LR swimming.

We also examined DV swimming in two, more distantly related, species: *Tritonia diomedea* (Cladobranchia) and *Pleurobranchaea californica* (Pleurobranchomorpha). These species have homologous neurons performing similar functions. Furthermore, both also exhibited serotonergic neuromodulation, which was necessary for swimming but not found in the non-swimming species, *Hermissenda crassicornis*. In this case the behavior was predictive of the neural mechanisms but the phylogeny was not.

When we compared the two categorically distinct behaviors, we found that the homologue of one of the neurons that was rhythmically active in *Melibe* and *Flabellina* was not rhythmically active in *Tritonia*. Similarly, neurons that were rhythmically active in DV swimmers were not rhythmically active in LR swimmers. However, they appeared to play other roles in modulating LR swimming. In summary, although homologous neurons could be recognized across species, they had distinct functions that were poorly correlated with phylogeny or behavior suggesting independent evolution of the behaviors.

T7.P1

TERGIPES TERGIPES (FÖRSKAL, 1775) (GASTROPODA, NUDIBRANCHIA), TRULY AMPHIATLANTIC? A MOLECULAR APPROACH

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Nearly 13% of "opisthobranch" gastropods in the Atlantic Ocean are regarded as amphi-Atlantic. This assumption, which has been broadly based on morpho-anatomical similarities, has rarely been tested within a molecular phylogenetic framework. During the last decade, molecular methods have frequently shown that cosmopolitan or widely distributed "species" consist of taxonomic complexes of multiple linages.

One of the most interesting aspects of the specimens of the nudibranchs assigned to *Tergipes tergipes* is that, this species would have an amphiatlantic distribution. Since its original description, this species has been widely reported from both coasts of North Atlantic, the Mediterranean Sea (including the Adriatic Sea), the Black Sea and once from Brazil. However, the conspecificity of eastern and western populations has been subject to question. Here we used molecular methods to test whether eastern and western populations belong to the same species. We used the criteria of divergence and reciprocal monophyly, supported by concordant genealogically independent genetic markers, to define species. Partial sequences of COI, 16S and H3 were obtained from 15 specimens from Italy, the Netherlands, United and Kingdom and the western Atlantic of Maine. Bayesian analyses were conducted to produce phylogenetic trees. Our results support the hypothesis of an amphiatlantic distribution of this species.

T7.P2

GOING FURTHER ON NEMBROTHINAE – DESCRIPTION OF FOUR NEW SPECIES AND REDESCRIPTION OF *TAMBJA DIVAE*

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Traditionally, the subfamily Nembrothinae Burn, 1967 has been comprised by the genera *Nembrotha* Bergh, 1877, *Roboastra* Bergh, 1877 and *Tambja* Burn, 1962. Lack of detailed information and the existence of several undescribed species led some of us to carry a broad study on the taxonomy and phylogeny of the subfamily Nembrothinae in the recent years. As a result of these studies, 12 species were described: three *Roboastra*, seven *Tambja* and two *Nembrotha*. In addition, some specific names were synonymized and *Roboastra arika* Burn, 1967 and *Nembrotha caerulea* Eliot, 1904 considered as *nomen dubium*. Recent field trips to different regions of the world (Brazil and Vanuatu) have

provided material of some undescribed nembrothid species. In this contribution we report the rediscovery and redescribe *Tambja divae* (Marcus, 1958), a species previously known only from the original description, and describe four additional new Nembrothinae species.

T7.P3

REDESCRIPTION OF THE NUDIBRANCH *POLYCERA ALABE* (GASTROPODA, POLYCERIDAE)

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Polycera alabe Collier and Farmer, 1964 was described from two specimens; the holotype collected in Baja California and a serial section of the entire paratype mounted on eleven slides collected in the Gulf of California. This description includes quite good information of the external morphology but few details of the internal anatomy. The description of the internal anatomy includes the radular formula and the shape of the teeth of the holotype. The description of the reproductive system is missing although it is mentioned that the penis is armed. Data on the salivary glands, labial cuticle or any other internal features are not provided. In the past few years several specimens with a very similar colour pattern and external features to *P. alabe* have appeared in several field guides and web pages which has resulted in considerable confusion regarding this species. In order to clarify the identity of *Polycera alabe* Collier and Farmer, 1964, and to be able to compare with very similar species a complete and detailed redescription of the species is needed. In this contribution *P. alabe* is redescribed based on the revision of the holotype, the paratype and five more specimens from the type locality. Specimens previously identified as *P. alabe* from the Galapagos Islands and Costa Rica very likely correspond to two new cryptic species. The material examined for this study was deposited in the Department of Invertebrate Zoology and Geology of the California Academy of Sciences, San Francisco (CASIZ) and the Museo de Zoología de la Universidad de Costa Rica (MZUCR).

T7.P4

REDESCRIPTION OF AN UNCOMMON MEDITERRANEAN CHROMODORIDIDAE: *FELIMIDA ELEGANTULA* (PHILIPPI, 1844)

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According to the recent reassessment of the Chromodorididae Bergh, 1891 classification, all the Atlantic and Mediterranean species previously attributed to the genus *Chromodoris*

Alder & Hancock, 1855 should be reallocated in the re-erected genus *Felimida* Ev. Marcus 1971.

In this contribution we present the redescription of *Felimida elegantula* (Philippi, 1844). The original description (as *Doris elegantula*) was based on a single specimen from Palermo, Italy, in 1839, and lacks detailed morphological description. Herein, the external as well as the main internal anatomical structures were studied and characterized. The reproductive system is described for the first time. *Felimida elegantula* is a very uncommon chromodoridid and has been reported few times in localities of the Mediterranean Sea (Villafranche-sur-Mer, France; northern area of Malta; Sicile, Tirrenian Sea, Secche della Meloria and Palermo, Italy) and some of them are not properly published (Illa Malgrats, Balearic Islands, Spain). Preliminary phylogenetic analysis based on the mithocondrial gene COI confirms that *F. elegantula* belongs to the genus *Felimida*, being closely related to other Mediterranean species with dorsal spotted pattern, such as *F. luteopunctata* (Gantès, 1962) and *F. luteorosea* (Rapp, 1827).

T7.P5

THE PRESENCE OF THE MEDITERRANEAN NUDIBRANCH *CRATENA PEREGRINA* IN THE BRAZILIAN COAST - EVALUATION USING A MITOCHONDRIAL AND A NUCLEAR MOLECULAR MARKER

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The aeolid *Cratena peregrina* is one of the most common and typical nudibranchs from the Mediterranean Sea. The specific coloration of this species is believed to be characteristic and based mostly on this taxonomic character, *Cratena peregrina* has been recorded from different localities, not only in the Mediterranean Sea but, more recently, also in South Africa, India and tropical western Atlantic waters. In this work, Brazilian specimens of supposedly *C. peregrina* are included in a molecular analysis (maximum likelihood) with specimens of *C. peregrina* from different regions of the Mediterranean Sea. The COI and H3 trees both separate Brazilian and Mediterranean specimens into well-supported, reciprocally monophyletic clades. Brazilian specimens are very divergent to the Mediterranean ones, representing a different, probably new, cryptic species of *Cratena*. Our results once again emphasize that similarity regarding external morphology and body color pattern does not necessarily imply conspecificity in nudibranchs. ´Species´ with wide or disjoint geographical distribution should be studied more carefully, as cryptic species may be involved in many cases.

T7.P6

PLAY IF YOU DARE! FIND THE COLOUR DIFFERENCES AMONG THE SPECIES OF THE *ANTEAEOLIDIELLA INDICA* COMPLEX

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Traditionally, two different specimens have been considered as members of the same species when they share the same or a similar external appearance. However, it is currently accepted that some species may exhibit a broad range of colouring, this variability being supported by molecular studies. The colouration of the aeolidiid species *Anteaeolidiella indica* (Bergh, 1888) has been accepted as very variable. Therefore the specific names introduced over the years for the different colour forms of "*A. indica*" (early as *Aeolidiella*) were regarded as junior synonyms. The recent molecular phylogeny of Aeolidiidae showed that *Anteaeolidiella indica* is a species complex composed of at least seven distinct species. The names of *Anteaeolidiella cacaotica, A. saldanhensis, A. takanosimensis* and *A. lurana* were resurrected and two undescribed species from the Indo-Pacific were evident. In the present contribution, we demonstrate that these multiple linages detected by molecular methods are also supported by significant colour differences. Based on these colour patterns, we also show some putative new species found in different web pages.

T7.P7

A NEW PIECE IN THE PUZZLE FOR THE RIVERINE SLUGS OF THE ACOCHLIDIIDAE (PANPULMONATA: ACOCHLIDIA)

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The slugs of the family Acochlidiidae are an outlier among otherwise marine, meiofaunal and therefore minute members of the Acochlidia: by comparison, they are giant (in centimeter-range), with adults living exclusively in coastal rivers and creeks of tropical islands in the Indo-West Pacific. Historically, the family is the longest known among the order, but only recently research has shown that Acochlidiidae are a derived clade that evolved an amphidromic lifestyle with a specialized larval stage and that adults predate on the calcareous egg-capsules of freshwater snails of the Neritidae.

Currently there are two known morphologically distinct taxa among acochlidiids: one lineage with the slender, uniformly reddish colored *Strubellia* (2 described species) which resembles the Pseudunelidae (the marine sister group of the Acochlidiidae), and a second lineage with seemingly more derived, flattened and pigmented, brown or greenish *Acochlidium* (3 sp.) and *Palliohedyle* (2 sp.).

A 2010 survey of freshwater gastropods on the Moluccan island of Amboina, Indonesia, discovered two specimens of a hitherto unknown acochlidiid that shows intermediate characters. Externally, it resembles a blue-green *Strubellia*, and 3-dimensional reconstruction based on semithin histological sections shows that digestive and excretory systems largely resemble that in *Strubellia.* Scanning electron microscopy and histology, however, shows that the species has evolved the complicated trap-like copulatory organ which resembles that of *Acochlidium.* A molecular phylogeny of acochlidiids using multilocus markers confirms that the species is indeed sister to a clade including *Acochlidium* and *Palliohedyle*. This suggests that a complex copulatory organ evolved earlier than the *Acochlidium*-like morphotype.

T7.P8

3D MICROANATOMY OF *ERCOLANIA* N.SP. (GASTROPODA, PANPULMONATA): A SACOGLOSSAN DWARF FEEDING ON THE SEAGRASS *HALOPHILA OVALIS*

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With few exceptions, Sacoglossans are tiny suctorial herbivores feeding on cell sap of algae. The family Limapontiidae comprises some extremely minute species, most of them members of the genus *Ercolania*. To date, the anatomy of these aberrant species has been poorly explored. We herein present a detailed study on the anatomy of *Ercolania* n.sp., not exceeding a body length of 2 mm. High quality morphological data was generated by 3D reconstruction using AMIRA software based on histological sections, all major organ systems are described. While most sacoglossans feed on siphonalean algae, this species has specialized to feed on the seegrass *Halophila ovalis*. Implications on morphological evolution towards and within the genus are discussed.

T7.P9

SLUG SPICULES: ADDING INSIGHTS FROM HISTOLOGY AND TRANSCRIPTOME ANALYSES TO THE ALREADY COMPLEX PICTURE OF BIOMINERALIZATION IN GASTROPODA

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Molluscan shells are remarkable in their variety of forms and shapes, and appropriately receive the attention of biomineralization research. Beside shells, other biomineralization products occur among gastropods, although yet of unclear evolutionary origins. Among heterobranch gastropods, intra- or extracellular calcareous deposits are especially prominent in lineages of meiofaunal and nudibranch slugs, a morphotype that evolved independently several times. It remains unclear, though, whether these calcareous deposits are homologous to the shell, or whether they develop independently and convergently.

We compare data on the ultrastructure of spicules and the histology of spicule-bearing cells of different (mainly meiofaunal) slug lineages (Acochlidia, Rhodopemorpha, Sacoglossa). Spicules are highly variable in size and shape but all occur intracellularly and are each formed by a single cell. To further investigate the genetic background of biomineralization in slugs, we generated and *de novo* assembled two adult transcriptomes for different species of Acochlidia, sequencing paired end (150bp) reads using the Illumina Genome Analyzer II. The transcriptomes were screened for a compiled list of proteins previously described as being involved in biomineralization (i.e., shell deposition) in Mollusca. Based on our data, we report the expression of the 'shell-forming' genes *nacrein* and *perlustrin* in shell-less slugs as well as other proteins directly or indirectly related to the shell deposition.

The distribution of spicules in the investigated taxa, and their intracellular nature and composition, do not support a homology with heterobranch shells and rather present independently evolved products for biomineralization. To date, the lack of a broad comparative dataset on the genetic processes of shell deposition hinders sound interpretation of our transcriptomic data. Nevertheless, some putatively plesiomorphic 'shell-forming' genes – e.g., those involved in the formation of the larval shell – might be retained and reactivated later in the evolutionary history for the formation of spicules.

T07.P10

DIVERSITY OF CEPHALASPIDEA GASTROPODS IN NORWAY

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The Cephalaspidea is one of the main lineages of the traditional Opisthobranchia sea slugs. Unlike most other opisthobranchs they are characterized by the presence of a spiraled external shell with few shell-less groups and groups with vestigial internal shells also present. Previous knowledge about these molluscs in Norway resulted mainly from investigations in three geographical regions of the country: the Artic zone, the Oslofjord, and in a smaller scale the Bergen area on the SW coast. Recent works report up to a total of 34 species in the country, but nevertheless, the complex taxonomy of the Cephalaspidea resulting from poor species descriptions often based on shells alone, makes the identification of many of the European taxa problematic. Therefore, a project was set up aiming to review the systematics of the Cephalaspidea in Norway based on the study of national and international museum collections, newly collected specimens, and type material, and combining the study of shells, morphology (radulae, gizzard plates and the male reproductive system) and DNA characters in a molecular phylogenetic framework.

Thirty-eight species ascribed to 12 genera and six families (Diaphanidae, Retusidae, Philinidae, Philinoglossidae, Cylichnidae, Scaphandridae) were recognized. The validity of five of those remains to be confirmed and two result from recent descriptions.

T7.P11

FOLLOWING SEA SLUGS: RESULTS OF A RECENT OPISTHOBRANCH EXPEDITION IN THE NORTHEASTERN AND SOUTHEASTERN BRAZILIAN COASTS

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The coast of Brazil is an interesting area for the study of opisthobranchs. Not only because it comprises diverse coastal ecosystems across tropical and warm-temperate waters, but also due the fact that most tropical western Atlantic species have their type-locality in this country. As part of a project on the biodiversity of Atlantic opisthobranchs, an expedition was carried out on different localities in the northeastern (Alagoas) and southeastern (São Paulo) Brazilian coastlines. The two regions are around 2000 km far apart from each other. Through intertidal and SCUBA diving sampling, a total of 84 species were found, 53 in Alagoas and 40 in São Paulo region. At least six species are undescribed and four are new records from Brazil. Fifteen species were found in their type-localities, some for the first time after their original description. Specimens of these were photographed individually, being important for comparative studies to material from other regions. Despite the existence of a recent paper on the opisthobranch fauna of Alagoas, 17 species were for the first time collected in the area. The warm waters of Alagoas also resulted in a high number of herbivorous groups, such as sacoglossans and aplysiids. The results indicate that Brazil still hides an unknown opisthobranch fauna, not only in poorly studied regions, like the northeastern coast, but also in the less explored subtidal zone and islands, from where interesting species were for the first time found.

T7.P12

VACUOLAR CELLS SEEM TO BE A SPECIAL TRAIT OF THE ESOPHAGUS AND CROP OF CARNIVOROUS CEPHALASPIDEANS (EUOPISTHOBRANCHIA)

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Cells with a very large vacuole surrounded by a very thin layer of cytoplasm were observed in the connective tissue of the crop or esophagus of the cephalaspideans *Philinopsis depicta*, *Aglaja tricolorata* and *Philine quadripartita*. These vacuolar cells can be abundant close to the epithelium, but they were never seen in direct contact with the lumen of the digestive tract. In *P. depicta* and *P. quadripartita* just small amounts of dispersed flocculent material were observed by transmission electron microscopy (TEM) within the electron-lucent vacuole. Nevertheless, in *A. tricolorata* the central vacuole and the vesicles in the peripheral cytoplasm contained electron-dense loops. The flat nucleus is located at the periphery of the cell and cell membrane invaginations are common.

Using the pyroantimonate method for TEM, calcium was detected in the vacuole and vesicles of vacuolar cells. With this technique, electron-dense deposits are formed in structures that contain calcium, even if present in very low quantity. Control sections were treated with an EGTA solution, which removes the electron-dense deposits containing calcium. Additionally, the presence of calcium was investigated with an electron microprobe equipped with WDS detectors. The X-ray intensity maps confirmed the presence of low amounts of calcium in the electron-dense pyroantimonate the deposits. Calcium detection in the vacuolar cells supports a relationship with the calcium cells of the connective tissue of pulmonate gastropods. These cells could provide ions for buffering the pH of body fluids. So far, similar cells were not found in the digestive tract of herbivorous cephalaspideans. Thus, the presence of vacuolar cells might be an apomorphy of the esophagus and crop developed in carnivorous cephalaspideans.

T7.P13

WHAT HAPPENS, WHEN CNIDOCYSTS ARE SEQUESTERED IN AEOLIDS? NEW RESULTS ON SEQUESTRATION AND SUBSEQUENT MATURATION IN CNIDOSACS

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Sequestration of cnidocysts from their prey with subsequent use in defence is known from few metazoan phyla. Especially members of the taxon Aeolidoidea (Nudibranchia,

Gastropoda) are well known for this. One of the still unanswered questions is why cnidocysts do not explode while feeding on the cnidarian, and why these same unexploded cnidocysts can be transported along the digestive tract into the specialized morphological structures, the cnidosacs, to finally be armed for putative defence against predators.

The most plausible explanation for this phenomenon would be to have a certain amount of immature and therefore non-functional cnidocysts in the food. Published studies on cnidarians suggested the cnidocysts to mature by acidification/ enrichment of protons in the cnidocyst's capsule. After this hypothesis only immature cnidocysts are transported into the cnidosac and then have to be made functional by accumulation of protons. In this study we present results on the fate of cnidocysts in the digestive tract. With a fluorescence staining method we tested the hypothesis of acidification as a factor for maturation. With a special marker (Ageladine A) we could show that kleptocnides indeed change their pH value after incorporation into the aeolidoidean cnidosac.

T7.P14

DIET PREFERENCES OF AGLAJIDAE SEA SLUGS

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Research about dietary specialization indicates that carnivory is the main trophic strategy in Aglajidae. Aglajids are well known active predators, feeding on several items like small crustaceans and opisthobranchs sometimes of the same species, which they swallow by suction. In the present study, a review of the knowledge of the dietary preferences of Aglajidae species is presented, together with new data resulting from novel investigations. The trophic level of aglajid genera is evaluated by analyzing gut contents of species from various niches and biogeographical regions. Gut contents were identified by light and scanning electron microscopy. This project is funded through a doctoral grant to the first author by the Consejo Nacional de Ciencia y Tecnología (CONACYT- México), fellowship BAZS/188890/2010, and hosted by the University of Bergen (UiB-Norway).

T7.P15

MATING AGGREGATIONS IN INTERTIDAL NUDIBRANCHS *(DENDRODORIS HERYTRA* AND *D. LIMBATA)*

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Certain nudibranch populations from the intertidal zone are known to aggregate during the onset of reproduction. The few reports available show that the sudden appearance and disappearance of these populations are associated with short shoreward migration movements to spawn.

Here we provide solid evidence of yearly-based mating aggregations of two intertidal nudibranch species *Dendrodoris herytra* and *D. limbata* survey in Sado´s estuary (Portugal). More specifically, during our three-year survey, we observed that the nudibranchs started to be exposed, during low tides (<0.8 m), to air exposure in March (1 individuals/km^2 for both species). The peak of densities (60 individuals/km^2 for both species) was always registered in April. Concomitantly, we registered the appearance of several egg masses that support the reproductive purpose of such behavior. Every year, these aggregations ended around June with densities of 4 to 12 individuals/km^2 in *Dendrodoris limbata* and *D. herytra*, respectively. Both species were absent from the intertidal zone for the rest of the year (July-February). We argue that aggregations of these non-gregarious organisms favor mating encounter and increase their reproductive output (i.e. number of viable egg masses).

T7.P16

THE ENEMY INSIDE YOUR SEA SLUG – ENDOPARASITES OF THE FAMILY SPLANCHNOTROPHIDAE (COPEPODA)

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The Splanchnotrophidae are a copepod family living endoparasitically in nudibranch and sacoglossan hosts, but little was known on biological interactions and evolution. Our morphology-based phylogenetic hypothesis suggests that all copepod sea slug endoparasites belong to a clade (*Briarella* plus Splanchnotrophidae); copepod invasion of sea slug hosts thus occurred just once. Ancestral hosts could be dorid nudibranchs of the family Chromodoridae, with several parasite lineages switching to other nudibranch host taxa. Sacoglossans were infested at least twice independently. This is surprising considering the large phylogenetic distance of nudibranchs and panpulmonate sacoglossans, with their last common ancestor dating back to the early Mesozoic at least. Our first results from sequence analyses are largely compatible with morphology-based topologies. Molecular species delimitation using COI trees and ABGD analyses confirm the morphology-based taxonomy of *Ismaila* species. In central Chile there is a flock of parasite species that possibly diverged sympatrically via switching and specializing to a certain host species. Our findings of genetically similar but morphologically distinct *Ismaila* individuals in distant host taxa might be suggestive for recent adaptation and ongoing speciation. In contrast to current taxonomy, some European splanchnotrophids rather than infesting different host species and even families or classical nudibranch suborders, may be cryptic species complexes specialized to certain hosts also.

Our 3D models of splanchnotrophid microanatomy induce some conclusions on parasite functions and interactions with their host. For example, the sac-like digestive tract of *Ismaila aliena* lacking any intestine or anus supports our earlier assumption on a hemolymph-uptake rather than eponymous tissue-feeding at least in certain splanchnotrophids. The combination of modern software-based imaging techniques, molecular sequence analyses and evolutionary reconstructions is powerful and eventually will lead to a deeper understanding of sea slug hosts and their most significant parasites in a functional and evolutionary framework.

T7.P17

FIRST RECORD OF THE ECTOPARASITE *DORIDICOLA* AFF. *AGILIS* (COPEPODA: CYCLOPOIDA) FROM DIFFERENT SPECIES OF THE GENUS *HYPSELODORIS* IN ATLANTIC WATERS (NW SPAIN)

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Scuba diving photography carried out since 2007 in the coastal region off Northwest Iberian Peninsula (from Aveiro 40º37'N, to Aguete 42º20'N) allowed the identification of the cyclopoid copepod *Doridicola* aff. *agilis,* as an ectoparasite of the nudibranch *Hypselodoris*. Overall, 98 specimens of the genus *Hypselodoris* were observed, of which 77 were *H. cantabrica*, 14 *H. villafranca* and 7 *H. tricolor*.

Prevalence of 18% were found for *H. cantabrica* (14 infected hosts from 77 observed specimens), with a mean intensity of 2 parasites per host. On the other hand, prevalence of 14% were recorded either for *H. villafranca* (2 infected hosts from 14 observed specimens) and *H. tricolor* (1 infected host from 7 observed specimens), both having a mean intensity of 1 ectoparasite per specimen.

The rhynchomolgid *Doridicola* aff. *agilis* has been recorded so far from at least 20 genera of nudibranch, one genus of aplysiomorphs, as well as in the cephalopod *Todarodes sagitattus.* However, it is the first time that this species has been cited from the nudibranch genus *Hypselodoris.* The only exception ever recorded for this genus was the ectoparasitic copepod *Doridicola larani*, associated with the chromodorid nudibranch *Hypselodoris obscura* described from Moreton Bay, southern Queensland (Pacific Ocean). Further genetic and morphological analysis is needed in order to identify the copepod species accurately.

T8

GAINS AND LOSSES OF FRESHWATER BIVALVES AND THEIR CONSEQUENCES FOR ECOSYSTEMS

(sponsored by Instituto Português de Malacologia – IPM)

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Fresh waters are experiencing declines in biodiversity far greater than those in terrestrial and marine ecosystems. If the loss of species continues at current rates, the opportunities to conserve much of the remaining biodiversity in freshwater will soon vanish. Freshwater bivalves are considered one of the most threatened faunistic groups in the world and should be taken into account in freshwater ecosystems conservation actions. Although many bivalve species are disappearing, others (e.g. *Corbicula fluminea*, *Dreissena polymorpha* and *Limnoperna fortunei*) have been introduced in rivers and lakes causing major ecological and economic impacts. Nevertheless, regional variation in the knowledge of the actual diversity of bivalves, their ecology and impact factors may imperil our ability to understand changes and take adequate actions. Under these assumptions (i.e. loss and gain of species), the present symposium aims to discuss 1) the biology and conservation of native freshwater bivalves, 2) the impacts of introduced bivalve species to ecosystems and 3) advances in other topics, such as taxonomy, genetics and physiology, essential for any ecological study and conservation action.

T8.O1

CONSERVATION STATUS OF FRESHWATER MUSSELS IN EUROPE: STATE OF THE ART, PERSPECTIVES AND FUTURE CHALLENGES

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Freshwater bivalves of the Unionoidea provide important ecosystem functions, yet many of their populations are in decline. In the present work, we comprehensively review the status of all of the currently described species in Europe, addressing their phylogenetic and taxonomic relations, their distribution and conservation status, as well as their habitat preferences and main threats in order to suggest prospective conservation action. Information on the current status of Unionoids in Europe is very unevenly distributed with rather detailed information available for flagship species such as the freshwater pearl mussel (*Margaritifera margaritifera*) and little or no information available on other species. Similarly, in certain regions such as the British Isles, the Iberian Peninsula and central Europe, information is more consistent than in other parts of Europe. In order to make conservation more effective in the future, we suggest a more standardized international approach to surveying European freshwater bivalves that need to encompass more ecological and genetic data.

T8.O2

CONSERVATION OF THE ENDANGERED FRESHWATER HABITATS UNDER HIGH ANTHROPOGENIC PRESSURE AROUND SAINT-PETERSBURG

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Recent studies revealed 5 populations of pearl mussel and 2 populations thick-shelled mussel in the rivers at the borderline of Saint-Petersburg city and adjacent settlements. Most of them are small, but reproduction was noticed in almost all of them.

The survival of these populations is surprising because Saint-Petersburg is a very large city. More than 5000000 people permanently live there. In most European countries pearl mussels and thick-shelled mussels are often disappearing even in much less populated areas.

This is not the only example of survival of endangered species close to Saint-Petersburg. Some mammals are especially remarkable in this respect. Bear, lynx, wolf, flying squirrel, some rare bats also have been recorded in small numbers, sometimes even within an administrative borderline of the city. These "umbrella species" are tightly connected with a habitat containing dense arboreal vegetation and big variety of plants. Such habitats persisted around Saint-Petersburg partly because it is relatively young city. It was established in 1703 in empty place. Some areas around it are still not developed intensively and are covered by natural arboreal vegetation, which is used rather extensively than intensively or not used at all.

Conservation of natural vegetation at the river banks and drainage area is the main reason of survival of the rare bivalves.

Two neighbour Russian territories – Pskov and Novgorod - demonstrate the opposite situation: now human population is smaller there, but it existed over the period of more than 1000 years. Long land use resulted in shallowing of rivers and extinction of rare bivalves.

T8.O3

ECOLOGY AND CURRENT STATUS OF THE FRESHWATER PEARL MUSSELS *MARGARITIFERA DAHURICA* (MIDDENDORFF, 1850) AND *MARGARITIFERA LAEVIS* (HAAS, 1910) (BIVALVIA: UNIONOIDEA) IN THE FAR EAST OF RUSSIA

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The current population status of the two Far Eastern species *Margaritifera dahurica* (Middendorff, 1850) and *M. laevis* (Haas, 1910) were studied in rivers from Sakhalin Island, Primorsky District, Kunashir Island and the Kamchatka Peninsula. Species of the pearl mussels was determined by molecular-genetic analysis sequencing the cytochrome oxidase subunit I (*COI*) mitochondrial gene.

We appreciated the current population status of *M. dahurica* in rivers Ilistaya, Ussuri (basin of the Amur River) and Komarovka River (basin of Razdolnaja River).The density of pearl mussel 0.004 - 3.3 ind./m^2. The length of the shells of the mollusks was 25.4-164.0 mm.

The populations of *M. laevis* were studied in rivers from Sakhalin Island (Lyutoga, Adamka, Armudanka, Tym, Voskresenovka), in the rivers from Kunashir Island (Sennaja, Golovnina, Ricarda, Serebryanka) and from Kamchatka Peninsula (Nachilova River). The density of *M. laevis* from the Lyutoga River 1.4 - 25.7 ind./m^2. The size range of living specimens was 30.4 - 123.5 mm. In the rivers Tym, Adamka and Armudanka the density of the pearl mussel varied from 0.01 ind./m^2 to 0.2 ind./m^2. In the Voskresenovka River we recorded a population of *M. laevis* with a density more than 600 ind./m^2, and the samples contained mostly young mussels. The size range of living specimens was 25.1 - 127.4 mm. The population density of *M. laevis* from Nachilova River was 0.19 ind./m^2. The size range of living specimens was 34.8-64.37 mm.

The status of populations can be characterized as satisfactory with a good level of reproduction.

Research supported by: RFBR grant no. 12-04-00594-a, 11-04-98815, grant of the Russian Ministry of Science and Education, President of Russia Grant MK-2455.2013.4.

T8.O4

UNIONID ASSEMBLAGE RESPONSE TO A TAR SANDS OIL SPILL IN THE KALAMAZOO RIVER, MICHIGAN USA

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Unionids are bioindicators of water quality because of their filter feeding capacity and sensitivity to pollution. In July 2010 Enbridge pipeline 6B ruptured and spilled over 3 million liters of diluted bitumen oil into Talmadge Creek, a Kalamazoo River tributary near

Marshall, Michigan USA; this oil flowed into the Kalamazoo River. The oil was contained at Morrow Lake, which is over 45 km downstream of the original spill into Talmadge Creek. During the summer of 2012 our study looked at the unionid assemblages at sites upstream (n=5), in the oil spill reach (n=4), and downstream (n=3) of where the oil was contained. We used timed, transect, and quadrat surveys to determine the assemblage, size classes, gravidity and shell deposits at all sites. ANOVA were used to analyze assemblage, abundances, sizes, and shell counts. Tukey-Kramer post-hoc tests were used to analyze where the significant differences occurred among the sites. We will present Nonmetric Multidimensional Scaling (NMDS) analysis of the unionid assemblage data as well as Multiresponse Permutation Procedure (MRPP) analysis to show any statistical significant differences among the sites. Overall, fewer live species of unionids were found in the spill region compared to the upstream and downstream regions. When standardized by area surveyed more shells were found in the spill region compared to the upstream and downstream regions with less evidence of reproduction in the spill region. Size classes, that generally represent age, showed results consistent with Ortmann's Law and the River Continuum Concept. We will discuss the complexities of using unionid data to assess responses to oil spills and present suggestions for future scenarios.

T8.O5

SUITABILITY OF DIFFERENT *MARGARITIFERA* STOCKS FOR BIOINDICATION STUDIES

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The freshwater pearl mussel (*Margaritifera margaritifera*) is a highly specialized and sensitive freshwater bivalve, whose survival in the juvenile phase is indicative of high quality habitats. This contribution investigates the use of juvenile freshwater pearl mussels as bioindicators, considering the interactions between mussel stock and study stream temperature regimes. A standardized cross experiment was carried out investigating juvenile mussel growth and survival of four different pearl mussel stocks originating from the Rhine, Danube and Elbe drainages, representing distinct genetic conservation units. The juvenile mussels were exposed in their four native streams and an additional stream in the Danube drainage. Per study stream, five standard mesh cages were installed. Each cage contained an equal number of juveniles per stock in separate chambers. Growth and survival rates of juvenile mussels were checked after three and nine months of exposure.

Mussel stocks generally differed in survival and growth rates. After three months, survival ranged between 14 and 51% for the different mussel stocks. Average survival rates differed strongly between study streams with 20% in the Wolfsteiner Ohe and 46% in the Giessenbach (both in the Danube system). After three months the highest growth rates were detected in the Wolfsteiner Ohe with 181%, the lowest in the Giessenbach with 166%. The strong influence of mussel stock and study stream makes a consideration of these factors obligatory for the interpretation of bioindication studies using juvenile freshwater pearl mussels. Testing of alternatives to native streams may increase growth and survival in captive breeding programs until impaired native streams are restored.

T8.O6

DREISSENA IMPACTS ON UNIONIDAE: A SYNTHESIS OF TRENDS IN NORTH AMERICA AND EUROPE AND RECENT FINDINGS FROM THE LOWER GREAT LAKES

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The continued invasion of zebra mussels (*Dreissena polymorpha*) and quagga mussels (*Dreissena rostriformis bugensis*) in North America and Europe has threatened the survival of native unionid mussels. We used data from multiple waterbodies in Europe and North America at different stages of *Dreissena* invasion to test the relationships between the number and weight of attached zebra mussels per unionid host, densities of dreissenids in a waterbody, and time since invasion. We found an overall trend for increase of attached dreissenid weight with unionid host's size during the first stage of invasion, however, this adverse impact reduces beyond 10 years after the invasion. We also learned that while impacts of zebra mussels on unionids are well described, there is little comparable data for quagga mussels. Considering that zebra mussels have been almost completely replaced by quagga mussels in most of the Great Lakes, and the fact that quagga mussels have weaker attachment strength, we hypothesized that the adverse impact of dreissenids on unionids is now less than in the early stages of the invasion. We conducted extensive surveys of unionids in lakes Erie, St. Clair and Ontario in 2011-2012, and recorded the number, weight, and species of dreissenids attached to unionids shells. Confirming our hypothesis, most of the unionids found were free of dreissenids, and infested unionids had fewer attached dreissenid mussels than in the early 1990s. Despite the quagga mussels' lake-wide dominance, zebra mussels were more often found on unionids, and their number and weight per host unionid were higher than those of quagga mussels.

T8.O7

IMPACTS OF *DREISSENA* FOULING ON THE PHYSIOLOGICAL CONDITION OF NATIVE AND NON-NATIVE BIVALVES: INTERSPECIFIC AND TEMPORAL VARIATIONS

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The impact of *Dreissena* fouling on unionids has been scarcely studied in Europe despite the fact that in some ecosystems (e.g. Lake Balaton, Hungary) infestations of several

hundreds to a thousand individuals per unionid have been observed. At present, the zebra mussel *D. polymorpha* is still a dominant species in Lake Balaton, and in last decade three other non-native bivalve species were introduced potentially increasing the pressure on native unionid survival. We examined whether the fouling of dreissenids (zebra and quagga (*D. bugensis*) mussels; although this last species is still found in low density) has harmful impacts on native (*Anodonta anatina*, *Unio pictorum* and *Unio tumidus*) and non-native (*Corbicula fluminea* and *Sinanodonta woodiana*) bivalves and whether there are any interspecific and temporal variations in fouling intensity and physiological condition (determined by a standard condition index and glycogen content). A significant deleterious impact of *Dreissena* fouling was detected on the physiological condition of native unionids in July (more pronounced in *A. anatina*) and September (more pronounced in both *Unio* species), when the infestation rate was high. For non-native species, *Sinanodonta woodiana* had the largest energy reserves, but a significant negative impact was detected on its physiological status under a high level of dressenid infestation; for *C. fluminea*, no significant impact on the physiological condition was detected. Overall, this study confirms that *Dreissena* may threaten unionid species including the invasive *S. woodiana*, although high interspecific and temporal variations were observed. This situation should be taken in account in future ecological and conservational assessments because species respond differently to *Dreissena* fouling and effects seem to be more pronounced in late summer/early autumn.

T8.O8

CORBICULA FLUMINEA IMPACT IN LAKE MAGGIORE (ITALY): FEEDING PLASTICITY AND DIETARY OVERLAP WITH NATIVE MUSSELS

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Feeding plasticity of *Corbicula fluminea* is possibly of major importance for successfully competing indigenous bivalves in Lake Maggiore (Italy), thus promoting overdomination of the alien species in the area. After its first detection in 2010, our studies on spatial and temporal dynamics of abundance, biomass and population structure revealed that the newcomer spreads to over 1/3 of the lake littoral, reaching·10^{3}ind·m^{-2} in three years. A comparison with historical data evidenced a strong decline of the most abundant native mussel species (*Unio mancus*), whose actual density is reduced of about 75% after *Corbicul*a establishment. Although native mussel depletion cannot be unequivocally attributed to the impact of *Corbicula*, change in bivalve species dominance is expected to impact ecosystem structure and functioning. Understanding the ecological role of invasive/native species is essential for predicting how the ecosystem might be altered after the invasion. To this aim, we compared daily filtration rates and food spectra of the two competitors- *U. mancus* and *C. fluminea*. Filtration rates were measured by the clearance method under different experimental conditions and over the whole diurnal cycle. Dietary sources and trophic niche overlap were determined by C, N stable isotope analyses of soft tissues of organisms collected along the season and at different developmental stages. Preliminary results suggest that success of *Corbicula* is also related to its ability to shift diet preferences along the seasons. *Corbicula* seems to stand already as a keystone littoral species in Lake Maggiore, likely being a strong competitor for space and food to native mussels (i.e. *Unio mancus*).

T8.O9

INFLUENCE OF WATER TEMPERATURE AND TURBIDITY ON SPAWNING OF THE THREATENED FRESHWATER PEARL MUSSEL *MARGARITIFERA MARGARITIFERA*

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Abiotic disturbances cause decline and extinction of threatened species. The present study investigated how gravid mussels of *Margaritifera margaritifera* were impacted by such disturbances. It was a lower proportion of gravid mussels in streams with than in streams without recruitment at an early spawning date, but changed to the opposite at a late spawning date. High water temperature early in the season in streams without recruitment was probably the reason to why the mussels were gravid earlier in these streams. The combination of high turbidity and water temperatures may be the reason to a reduced growth of the gravid mussels in streams without recent recruitment. There was a positive effect of adult mussel density on the proportions of gravid mussels. Early gravidity is likely to cause an early larval release from the mussels, and larval release from the host fish during winter in streams without recent recruitment, which is a time of bad growth conditions for the juvenile mussels. Clear-cut and global warming are factors that are likely to cause increased sedimentation and water temperatures in streams. One restoration measure that may reduce the sediment input *and* water temperatures is intact vegetation surrounding the streams. It is urgent that such measures start soon as it may take a long time until such rehabilitation measures have an effect in streams. Meanwhile, redistribution of adult mussels from sparse to dense populations is one option that may be worth testing to increase the numbers of gravid mussels.

T8.O10

INTERACTIONS BETWEEN FRESHWATER MUSSELS AND THEIR HOST FISHES: IMPLICATIONS FOR CONSERVATION

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Unionid freshwater mussels need to attach to a host fish for completion of their life cycle. This contribution highlights how conservation of both mussels and their fish hosts can benefit from an understanding of this interaction. Standardized laboratory infections of different fish species and genetic lineages with glochidia larvae of the European freshwater pearl mussel (*Margaritifera margaritifera*) and the thick-shelled river mussel (*Unio crassus*) revealed (i) substantial intra- and interspecific variation

in host suitability, (ii) different development times on different host species, (iii) temperature thresholds of successful glochidia development, and (iv) optimum infestation densities of hosts with glochidia for stocking of glochidia-infested fishes and for captive mussel breeding. As evident from increased mortality and decreased swimming performance at high glochidial infection densities, the interaction between mussels and their host fishes is clearly of parasitic nature. Data on host suitability, availability and use from the wild suggest that different fisheries management strategies are needed to better conserve both endangered mussel and fish populations. This is particularly true for the fish hosts of *Unio crassus* which have often been considered undesired fish species.

T8.O11

THE EFFECTS OF FRESHWATER MUSSEL GLOCHIDIA ON FISH HOST BEHAVIOUR: CONSEQUENCES FOR UPSTREAM PHORESIS

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Unionid bivalves are vitally dependent on their fish hosts during parasitic phase but the relationship is considered to be primarily phoretic. This study uses a host-parasitic relationship between duck mussel (*Anodonta anatina*) and chub (*Squalius cephalus*) as a model system to investigate parasite-induced alterations of host behaviour in freshwater bivalves. The study addresses whether the fish infected and uninfected with *A. anatina* glochidia display distinct behavioural patterns (overall activity, rate of spreading - upstream dispersal, instream habitat preferences) with possible consequences for upstream phoresis. One laboratory and two field experiments in a central European river were conducted to address these issues using passive integrated transponder (PIT) systems and radio-telemetry. Infected fish were found to be generally less active in the laboratory and less successful in upstream dispersal from isolated stretches in the field. Moreover, radio-telemetry revealed habitat shifts of the infected fish further from the riverbank. These results suggest that glochidia-mediated fish behavioural changes likely do not support the spread of glochidia over long distances but rather cause reductions in fish activity and slight habitat shifts, which might be beneficial for the survival of host and the associated mussel larvae. Our study demonstrates the importance of parasite-induced alterations of host behaviour for unionid bivalves.

Study was supported by the Czech Science Foundation (13-05872S) and ESF/MŠMT (CZ.1.07/2.3.00/30.0040).

T8.O12

RESCUING FRESHWATER PEARL MUSSELS (*MARGARITIFERA MARGARITIFERA*) FROM EXTINCTION - A RACE AGAINST TIME: A CASE STUDY FROM NORTHERN IRELAND

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Research in the 1990s on the status and distribution of in the north of Ireland evidenced significant declines. Remaining populations were dominated by older individuals and showed little evidence of recruitment. These findings led to the establishment of Special Areas of Conservation and Species Action Plans (SACs; SAPs) to protect mussels. Estimates of when the youngest individuals in the populations would die suggested that FWPM would become extinct in Northern Ireland by 2080. More recent research, which used non-linear logistic regression to model extinction trajectories for mussel population in the UK and Ireland, predicted a slightly later extinction date (2100). In addition, molecular differences between mussel populations from different catchments have been identified. Such findings emphasise the urgent need for catchment-based protection and restoration of populations showing accelerating declines.

Key approaches to the restoration of endangered species include protection, habitat improvement and captive breeding, the method of last resort. Protection is provided under SACs but is unlikely itself to lead to natural recovery. This is because populations of pearl mussels in Northern Ireland face extinction in the short-term as reproduction and mussel habitat are compromised. Because river catchments are subject to complex interacting impacts such as siltation due to land drainage and run off from agriculture and forestry, habitat improvement will take many years and is unlikely to occur before the predicted date of extinction. A successful captive breeding involving collaboration between Ballinderry Fish Hatchery and Queen's University, Belfast resulted in reintroduction of mussels at two sites in the Ballinderry catchment.

Future work will involve catchment restoration, captive breeding and the establishment of sanctuary sites where populations composed of isolated individuals from the river and juveniles from the captive breeding programme will be established – a novel approach which potentially has wider application in Europe.

T8.O13

SUCCESSFUL CAPTIVE REARING OF *MARGARITIFERA MARGARITIFERA*: DO WE KNOW ENOUGH?

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The freshwater pearl mussel *Margaritifera margaritifera* is an endangered species protected in Europe by the Habitats Directive and Bern Convention. Attempts to restore threatened populations using captive rearing programs have increased during the last

couple of decades, with variable success. In the frame of the Life+ project "ECOTONE – Management of riparian habitats towards the conservation of endangered invertebrates (LIFE10 NAT/PT/000073)", a population located at the river Paiva in Portugal was targeted for restoration, including Habitat improvement and a captive rearing program. The methods used where based in previous studies, but gravid females were only collected when glochidia were considered mature and used immediately to infest the fish. Commercially acquired trouts aged 0+ were used and kept in flow through systems during winter. Temperature was not manipulated during the parasitic and excistment periods. No evidence of significant glochidia loss during the parasitic stage was detected, resulting in high juvenile drop-off per fish. Excistment seemed to be triggered both by accumulated temperatures (Day-Degree concept) and temperature variations. Excistment was achieved without need of a previous 15ºC period. Juveniles were reared in diverse conditions (closed/open systems, presence/absence of substrate, food type) and survival and growth patterns compared. The results support the importance of well-established protocols as close to natural conditions as possible.

T8.O14

SALMONID FISH HATCHERIES OF THE WHITE SEA AS FRESHWATER PEARL MUSSEL (*MARGARITIFERA MARGARITIFERA* (L., 1758)) BREEDING STATIONS

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The freshwater pearl mussel *Margaritifera margaritifera* (L., 1758) is an endangered species in its entire distribution area: most populations are declining, disappearing and are overage. Only some populations in Europe, including the Northern part of Russia, have a natural capability for recovery.

Main reasons are degradation of natural ecosystems and depressing of populations of pearl mussel host fishes.

Abundance of salmonid populations in the rivers of the White Sea coast is being supported by fish hatcheries for a long time. However, their potential to support pearl mussel populations in good conditions has not deserved consideration neither from fish-breeders nor from malacologists. Fish hatcheries influence quantity and density of salmonid stock in the river. Fluctuation of these factors is significant for good or poor recruitment of pearl mussel population in this river. Arkhangelsk oblast has two salmonid fish hatcheries – Solzenskiy on the river Solza and Onegsky on the Andozero Lake (Onega river basin).

Viable population exists in the river Solza with Kazanka tributary upstream and downstream of fish hatchery. Pearl mussel population is degrading in the river Kozha. Both rivers are used by hatcheries for catching of breeders and release of young salmon and brown trout. Abundance of salmon population in Solza river is supported by young salmon releasing. Due to fish hatchery activities the young salmon abundance within spawning-nursery areas (NSA) is significantly higher of minimal level for pearl mussel recruitment (0.03-0.05 ind/m^2). Juvenile salmon (0+) gills examination revealed glochidia on the gills of young salmon from Solza fish hatchery.

The reason why the pearl mussel recruitment slackens in the Kozha is that abundance of salmon in the Onega drainage at the end of XX century has declined. The second reason is that releasing of one-year salmons (1+) by Onezhsky fish hatchery was started in 1967. As a result the abundance of young salmons within NSA is below the minimal level and pearl mussel recruitment has stopped.

Research supported by: President of Russia Grant МД-4164.2011.5, RFBR grants № 12-04-00594-а, № 11-04-98815-р_север_а, № 13-04-10107_к; Ural Branch of RAS grants № 12-П-5-1014, № 12-У-5-1022, № 12-М-45-2062, № 12-5-7-009; Federal Program "Kadry" № 8660, № 8774, № 14132211023.

T8.O15

CONSERVATION OF TWO EUROPEAN ENDANGERED FRESHWATER MUSSELS. A THREE YEARS BREEDING EXPERIMENT

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We present the results obtained since 2010 to 2013 rearing *Unio ravoisieri* Deshayes, 1847 and *U. mancus* Lamarck, 1819 under the "PROYECTO ESTANY" (LIFE + programme of the European Union: LIFE08 NAT/E/000078). These two species were included under the name *U. elongatulus* C. Pfeiffer, 1825, one of the two unionids covered by the Habitats Directive, the main European law for fauna protection. The experiences have being carried out in the breeding facilities designed at the Banyoles Lake in Girona (North East Spain), where the naiad populations are in serious decline. *Unio mancus* is also distributed throughout the Mediterranean rivers of Iberia and France and *U. ravoisieri* only lives in the mentioned lake and the neighbour Fluviá Basin; there are other populations in the rivers of Tunisia and Algeria.

The main innovation of the breeding facilities, a laboratory with indoor tanks and canals, and outdoor pools and canals, is the natural nourishment for the newborn naiad juveniles, which comes from the lake water and sediment. Although the three lake native fish species *Barbus meridionalis, Squalius laietanus* and *Salaria fluviatilis* are successful hosts for the naiads glochidia, barbels are more easily managed during the process. Near 100,000 healthy juveniles of *U. ravoisieri* and *U. mancus* born in 2011, 2012 and 2013 are currently reared and fatten in the different indoor and outdoor rearing systems. In April 2013 we have planted 500 two years old juveniles (sizes between 1.2-2 cm) in the lake, the future habitat of all the reared juveniles in the project.

T8.O16

HOW TO ESTABLISH A NEW POPULATION OF *UNIO CRASSUS*? A CASE STUDY IN THE BIAŁA RIVER

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The Biała river is a medium size river in the S-Poland. The lower part of the river is inhabited by large population of *Unio crassus* (ca 200 000 ind.), which was separated from other large population in its tributary, the Biesninka stream, due to water pollution and river dams. After removal of the dams, 16 “stepping stone” populations were set up in order to spread the distribution of the species to restore its historical distribution. We analyzed water chemistry, fish distribution and morphology of the river in order to find out, which factors are responsible for successful re-establishment of the species. It appears, that crucial role is played by local site morphology and local hydrology. The most successful (in terms of adults survival and young recruitment) are straight sections of the channel, with small areas of still water and fine sediment, protected from the influence of main water current, where both adult survival and young recruitment are the highest. Analysis of movements of individuals marked with radio-transmitters reveal, that in unfavorable conditions individuals disperse, which is likely to hamper mating and survival of adults and young recruitment.

T8.P1

PRESENCE AND IMPLICATIONS OF ORGANIC LAYERS IN FOSSIL AND EXTANT UNIONOIDA (MOLLUSCA, BIVALVIA)

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The presence of embedded thin organic layers in the nacreous layer in the shell of several species of Unionoida is widely considered to be a reaction to prevent shell dissolution. Their microstructural characteristics have also been used as taxonomic characters to separate the families Margaritiferidae and Unionidae. This paper focuses on the description and interpretation of these organic layers in samples of four extant species of European Unionidae coming from acid and alkaline waters, six extant species of Margaritiferidae, one Cretaceous Unionidae and two Cretaceous Margaritiferidae species. Our results demonstrate that organic layers characterise species of Unionoidea at least since the Cretaceous in specimens coming from both acidic and alkaline waters. Beyond this, their thickness is the only useful character to separate both families. In the Margaritiferidae they are present in *M. margaritifera, M. valdensis*, *M. idubedae, M. laosensis, M. laevis* and *M. monodonta,* and absent in *M. auricularia* and *M. marocana*. In Unionidae they appear in *Protopleurobema numantina*, *Potomida littoralis* and in some specimens of *Unio mancus, U. delphinus* and *U. tumidiformis*. We argue that organic layers played a fundamental role of shell protection in the bivalve evolution during the invasion of freshwater by the earliest Unionoida, today being an evolutionary adaptation which improves fitness to acidic water in some species.

T8.P2

CONSERVATION UNITS BASED ON MITOCHONDRIAL AND NUCLEAR DNA VARIATION AMONG THE THICK-SHELLED RIVER MUSSEL *UNIO CRASSUS* POPULATIONS IN POLAND

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The aim of this study was to delineate conservation units for the thick-shelled river mussel *Unio crassus* in Poland. The genetic relationships among 14 mussel populations were determined, using length variation at 10 polymorphic microsatellite loci and sequence variation in the *cox1* and *ND3-ND2* fragments (1833 bp) of the mitochondrial DNA. The analysis of the mtDNA sequences shows that *Unio crassus* in Polish rivers belong to two highly divergent haplotype groups (lineages) differing by mean divergence estimate of 3.4%. These two lineages have a largely allopatric distribution, implying two geographical population sets: northern and southern. The inferred genetic structure of *Unio crassus* in Poland was largely congruent between mitochondrial and nuclear markers, separating the sampled populations into almost non-overlapping groups. Because of the important differences between these clades, they may be defined as conservation units, which should be managed separately.

T8.P3

SPATIAL DISTRIBUTION AND ABUNDANCE OF UNIONIDAE MUSSELS IN EUTROPHIC FLOODPLAIN LAKE

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We studied the distribution of freshwater unionids in eutrophic floodplain lake, at 13 transects, across the depth gradient. The clam distribution within the waterbody is not random: in freshwater lakes, all species form a crowded stripe along the lake shore, showing highest densities at optimal depth of ca 0.5 m. The distribution of most numerous species change along the shore changes in case of *Anodonta anatina* and *Unio pictorum*, whereas the number of *A. cygnea* remains constant. Most numerous species show positive relation to silt layer. In generalized model of unionids, the number and the considered lake features confirmed the above relations and indicate a trade-off between water depth and distance from the bank, which might be responsible for the occurrence of the depth optimum.

T8.P4

MARGAL ULLA LIFE PROJECT: A REAL CHANCE FOR THE RESTORATION OF *MARGARITIFERA MARGARITIFERA* (L.) POPULATIONS IN GALICIA (SPAIN)

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Galicia is situated on the southwestern limit of *Margaritifera margaritifera* European range.

Though the current distribution map of this species shows a significant number of populations (approx. 55), most of them are fragmented, with low abundance and little or no recruitment.

The Ulla river is the second main basin of Galicia and presents historical populations of freshwater pearl mussel (FPM). This basin is a clear example of the environmental impacts the Galician rivers have endured over the last century, which have affected negatively the aquatic fauna, leading to endanger this naiad as a biological indicator of water quality .The aquatic impacts include acidification and pollution incidents such as slurry or industrial spills, degradation of the river bed substrate, from dredging and siltation, alteration of the riparian forest, river bank erosion and building of weirs and dams which create barriers to the movement of the host fish.

The Margal Ulla Life project (2010-2015) was designed to recover the populations of the FPM and the pyrenean desman, *Galemys pyrenaicus*, by improving the health of the river through the implementation of actions focused on the habitat and these species.

The main actions on *M. margaritifera* consist of improving the knowledge about its distribution in the basin, the population conservation status analysis, the identification of management units using ecological and genetic information, the development of captive rearing activities, and the reintroduction by stocking juvenile mussels and native infested salmonids.

If the project achieves the expected outcome, its model could be implemented in other Galician rivers, becoming a unique and true opportunity to the species in the Iberian Peninsula.

The Life project, the first results and the problems found regarding with the actions on *M. margaritifera* are presented.

T8.P5

GENETIC STUDY FOR REPRODUCTIVE SELECTION IN A LIFE CONSERVATION PROGRAM

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The freshwater pearl mussel *M. margaritifera* appears as one of the most critically threatened bivalve in Europe, particularly the southern peripheral populations in NW Iberian Peninsula, where low and very structured genetic variation was described. In this study, we report the microsatellite variability of *M. margaritifera* from the Ulla basin, a large Altlantic river in NW Spain, where a conservation plan for this species has been recently established (LIFE09 NAT/ES/000514).

A total of 429 pearl mussel specimens were collected in several transects of the Ulla basin. The samples were located along different hydrographic regions (sub-basins), where the individuals are distributed in the upper and medium courses, within the main river and its tributaries. Genotyping for 12 microsatellite loci revealed low intrapopulation genetic diversity within transect samples and within sub-basins. In addition, we detected high genetic differentiation among sub-basins.

According to these results, we selected two breeding groups (60 individuals each) for further captive breeding, representing a conservative proposal of management units based on the genetic divergence observed. One breeding group included the most genetically differentiated sub-basin (Arnego tributary); the other one embraced mussels from the remaining sub-basins of Ulla river. Both groups were translocated to be maintained ex-situ for supportive breeding, which will play a major role in the LIFE conservation program.

T8.P6

APPLICATION OF SPECIAL MEADOW MANAGEMENT WITHIN THE MEASURES OF ACTION PLAN FOR FRESHWATER PEARL MUSSEL (*MARGARITIFERA MARGARITIFERA*) IN THE CZECH REPUBLIC

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Freshwater pearl mussel (FWPM) is a critically endangered mollusc in the Czech Republic, currently occurring in the oligothrophic watercourses of southern and western Bohemia. On the basis of a recent genetic research (2011) we distinguish 3 conservation units with irregular population distribution at 5 main localities. Action Plan for

Margaritifera margaritifera in the Czech Republic (guaranteed by Nature Conservation Agency of the Czech Republic, NCA CR) has been adopted to improve the population status. For over thirty years, new findings, important practices and experience were gained which resulted in the New Action Plan, the strategic document for FWPM conservation for forthcoming decades.

Even though many environmental parameters have been enhanced for this stenoecious species in the last 20 years, several problems still persist such as land-use changes in riparian corridors resulting in possible lack of accessible nourishment for the youngest FWPM stages. In order to improve the juvenile food supply, special meadow management is applied alongside the tiny meandering streams bringing organogenic detritus into main watercourses. Mowing grass, composting with added calcium for a period of 3 years and returning on the treated sites is done annually.

In situ caging method using juvenile pearl mussels is applied for the evaluation of management outcomes. Three sites with special meadow management were tested in 2011 and 2012. Each set consisted of one pair of cages placed upstream and one pair of cages placed downstream from the treated site. All sheet cages (with 10 individuals of ~ 1mm size each) were exposed in sub-mountain Blanice and Zlatý potok river basins for a period of 3 months (June – August). Juvenile growth, survival rate, water temperature regime and detritus composition was monitored. Despite year-on-year variation, preliminary results indicate significant relationships between the quality of food supply and special meadow management.

T8.P7

RESTORATION OF *MARGARITIFERA MARGARITIFERA* AND *UNIO TUMIDIFORMIS* POPULATIONS IN ALDER LINED STREAMS

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The freshwater mussels *Margaritifera margaritifera* and *Unio tumidiformis* are two endangered Iberian species protected under the Habitats Directive. The river Paiva (Douro basin, northern Portugal) is a typical mountain salmonid stream, with permanent flowing, cold and oligotrophic water, while the river Torgal (Mira basin, south-western Portugal) is a temporary Mediterranean-type stream. Both are Alder lined for much of their extention, and this is a priority habitat for conservation according to the Habitats Directive. The river Paiva holds an aging population of *Margaritifera margaritifera* in its upper and middle reaches, replaced gradually downstream for unionid species such as *Anodonta anatina* and *Unio delphinus*, while a very localized community of unionids (*A. anatina, Potomida littoralis, U. delphinus* and *U. tumidiformis*) lives in a 750 m long reach of the river Torgal. The Life+ project "ECOTONE – Management of riparian habitats towards the conservation of endangered invertebrates (LIFE10 NAT/PT/000073)" aims to restore Alder habitats and channel integrity in these rivers and to improve the conditions for endangered invertebrate species living there, namely *M. margaritifera* and *U. tumidiformis*. Restoration measures include stabilizing banks, restoring riparian vegetation, creating permanent water zones in the river Torgal and reinforcing freshwater mussel populations by means of infested host fish release and captive reared juveniles' introduction.

T8.P8

HOST FISH LIMITATION, AN ADDITIONAL THREAT TO THE IMPERILLED NAIADS IN EUROPE: A CASE STUDY ON *UNIO DELPHINUS* AND *POTOMIDA LITTORALIS*

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Freshwater mussels or naiads (Bivalvia, Unionoida) are among the most critically threatened faunistic groups worldwide. This decline is mainly provoked by habitat loss and fragmentation, habitat degradation, introduction of invasive species, among other biotic and abiotic alterations. In fact, these bivalves have a complex reproductive behavior where their larvae (glochidia) parasitize and depend on specific fish species as hosts for metamorphosis and upstream dispersion. For this reason, conservation of freshwater mussels is intertwined with the respective host fish and is of outmost importance to establish which fish species are suitable for each bivalve species. In the present work we successfully reproduce and determined the host fish species for *Potomida littoralis* and *Unio delphinus* from the Douro basin, Portugal. Additionally, in the present communication a revision on the fish hosts of European naiad is also presented. Interestingly, almost all effective hosts are native fish species. Due to the increasing presence of invasive fish species and the construction of dams and barriers that reduce fish movements and dispersion, the conservation status of the already imperiled freshwater mussel fauna in Europe may suffer a great decline in near future.

T08.P9

ZOOGEOGRAPHY OF THE NAIAD MUSSELS IN SWEDEN

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The Swedish naiade fauna (Unionoida) consists of seven native species. In the late 1980's a revision of museum collection and an evaluation of literature data for mapping the species' distribution began. During the latest decades, the use of freshwater mussels in environmental monitoring and the search for populations of red-listed species has considerably increased the knowledge of the species' distribution and ecology.

The most common and abundant species is *Anodonta anatina* (Linnaeus), distributed throughout the country, absent only on higher altitudes in the Scandinavian mountain ridge in the west.

A wide distribution, from south to north, is also exhibited by *Margaritifera margaritifera* (Linnaeus). There are considerable distribution gaps in large areas in the southern and eastern parts of Sweden, especially in districts dominated by silt and clay. Totally approximately 550 watercourses harbor the species, but only half of them have viable populations. The general trend is decreasing and *M. margaritifera* is red-listed in category EN.

Unio pictorum (Linnaeus), *Unio tumidus* Philipsson, *Anodonta cygnea* (Linnaeus) and *Pseudanodonta complanata* (Rossmässler) are all more fastidious, predominantly southern/southeastern species with their northern border situated in middle of Sweden, in the so called "*limes norrlandicus*-zone" (or northern border of the oak), which constitutes an important bio-geographical transition zone between the N. Scandinavian (Boreal) and S. Scandinavian regions. All species are more common in the east, *U. tumidus* being the commonest species. *A. cygnea*, *P. complanata*, and especially *U. pictorum*, are rare in western Sweden (the two latter species red-listed as NT).

Unio crassus Philipsson is the rarest species, with a pronounced eastern/southeastern distribution. The distribution is split up in 4-5 subareas with large gaps between. The species has disappeared from peripheral localities in the north and west. It is red-listed in category EN.

The diversity of species is markedly higher in eastern Sweden, with a few river systems (rivers Helge å, Emån, Stångån, Svartån and Kilaån) harboring all seven species.

T9

MUDFLAT MOLLUSKS

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Intertidal mudflats are conspicuous features of coastal habitats, and often harbour high densities of molluscan macrofauna; yet they present unique challenges to researchers, not the least of which is the difficulty of access and movement on these unstable substrates. Nonetheless, the critical importance of mudflats to benthic production, the multiple trophic links to the pelagic ecosystem, and the importance of mudflats – and their molluscan fauna – to semi-terrestrial predators such as migratory shorebirds, has stimulated considerable ecological research on this habitat, and on mudflat mollusca in particular. This theme session proposes to present some of the current accomplishments and future directions for molluscan research on mudflats, from taxonomic to physiological, ecological and anthropogenic problems.

T9.O1

IMPACT OF REPEATING MASSIVE EARTHQUAKES ON INTERTIDAL MOLLUSCAN COMMUNITY IN JAPAN

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History repeats itself. In these 3500 years, massive earthquake like the Pacific coast of Tohoku Earthquake in 2011 have occurred at least seven times. Major earthquakes with big tsunami have occurred in five-hundred-year cycles along the Pacific coast of northern part of Japan. The 3.11 tsunami caused a lot of damage to the Tohoku region including marine life.

During the earthquake of 3.11, wave-like movement observed on the surface of the tidal flats in Yatsu, near Tokyo. Liquefaction occurred just after the earthquake before tsunami. We observed many fissures moving and a jet of water from liquefaction coming to the surface around the Yatsu tidal flats. Bivalves like *Mya arenaria oonogai* normally distributed in deep were dug out to surface with a jet of water in Gamo tidal flats, northern Japan. Some species of infaunal bivalves were also rushed by the tsunami in Matsukawa-ura Inlet, Fukushima. In this way, not only the tsunami but also the liquefaction brought quick damage in the coastal marine life. The infaunal bivalves dug from the tidal ground were not killed instantly. Some adult specimens of *Macoma contaculata* and *M. arenaria oonogai* had been survived on the tidal surface in Matsukawa-ura Inlet, Fukushima by the end of June 2011.

The earthquake caused sudden land subsidence of about 1m in maximum around the Oshika Peninsula, Miyagi where intertidal zone became subtidal zone. Spat of Pacific oyster *Crassostrea gigas* was observed to attach to new hard substances after summer. It may take at least several ten years to recover the co-seismic land subsidence. What creatures will advance to new environment and will disappear? We have to clarify not only short-term effect which may explain an initial recovery of intertidal and subtidal animals but also a long-term effect which may explain continuous changes in population with land subsidence.

T9.O2

ALLOMETRIC MODELLING IN THE MUDFLAT SPECIES *TAPES PHILIPPINARUM* AND *CERASTODERMA EDULE* USING THE COPULA APPROACH.

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Ecophysiological and population studies of molluscs often incorporate growth models; the allometric relation of weight to length is particularly important, and is usually modelled using the power law, followed by linear regression on log-transformed data, although other techniques have been used. These procedures are all confronted by one or more of the following problems: (1) the data often do not, in fact, follow a power law, especially in the fields of studies mentioned above, (2) back-transformation is controversial, and (3) most previous techniques suffer from the constraints of parametric regression, which are often either not verified correctly, or unintentionally violated. All these problems may be a source of bias for the subsequent applications, results, and conclusions.

We present the technique of copula–based regression, a relatively new approach initially used in the economic sciences, which does not require the supposition of pre-cast relations such as the power law, is scale-invariant, captures all dependence structures, and is not necessarily contingent upon predetermined data distributions. We demonstrate its use in a case study of the length-weight allometric relationship in two mudflat species of marine bivalve, *Cerastoderma edule* and *Tapes philippinarum*, on both a fishery-impacted site and a non-impacted site on the French Atlantic coast. Our results underscore the inappropriateness of the power law- linear regression approach when data do not follow the power law, and the advantages of the copula technique in modeling this type of allometric relationship. *We anticipate that copula-based regression will allow more accurate and reliable modeling of allometric relationships for studies of growth, fecundity, feeding, and energy allocation, not only in these mudflat molluscs, but in many other marine animals.*

T9.O3

POPULATION DYNAMICS AND LIFE-TABLES CONSTRUCTION OF THE SOFTSHELL CLAMS *MYA ARENARIA* L. ON AN INTERTIDAL SILTY-SAND FLAT IN THE WHITE SEA

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Long-term observations of the bivalve mollusc *Mya arenaria* bed structure were undertaken at four typical intertidal silty-sand beaches in the Kandalaksha Bay, the White Sea. In the studied soft-shell clam beds considerable inter-annual changes in abundance, size and age structure were observed. The variability in age structure was expressed mainly in significant changes in number of juveniles (specimens settled in the previous year, <1 years old). In such beds, individuals of only 1 or 2 generations dominated over a long period. The main reasons for the fluctuations of the bed structure appear to be

connected to inter-annual variation in recruitment rates. These variations are obviously caused, on the one hand, by the intensity of molluscs intraspecific interactions, and on the other (no less), by the conditions of juvenile survival in the first winter.
One of the studied *Mya arenaria* bed was observed since 1980. From 1989 to 2003 the bed comprised almost only the 1988generation. This generation was traced from 1989 to 2012 (i.e. over 24 years). Using the data on number of this generation in each observation the cohort life table was built. The age-specific mollusc mortality rate (M_t) was calculated as $M_t= (N_t - N_t +1) / N_t$, where N_t - the number of individuals surviving to age *t*. The mortality rate was found to change more than 10-fold (0.06 to 0.68 y-1) throughout the study period. No any regular changes in this index were observed. Periods of low mortality alternated with a much higher degree of elimination. Several reasons for the mortality growth during *Mya arenaria* life span could be preliminary proposed: a) elimination of non-viable individuals at the early stages of life cycle; b) increased intraspecific competition during periods of rapid mollusc growth; c) getting to the mid-level of life span; d) achieving maximum age.

T9.O4

THE EFFECT OF MACROFAUNA ON THE SUCCESS OF COCKLE (*CERASTODERMA EDULE*) POST-LARVAL COLONISATION

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Cockle (*Cerastoderma edule*) populations often have highly patchy distributions as seen in many other intertidal soft sediment invertebrates. High densities of filter feeders and/or bioturbators have been thought to reduce the success of larval settlement. However, current studies on the common cockle indicate that the post-settlement stage maybe more important for post-larvae interactions with macrofauna than larval settlement. Manipulative field experiments were conducted to investigate the effect of adult cockles and lugworms (*Arenicola marina*) on cockle colonisation success. Two field manipulation experiments which excluded the presence of adult cockles and lugworms separately, in two locations (Dee estuary and Traeth Melynog respectively), were established from the time of initial larval settlement to late summer in 2012. Each experiment consisted of six control, procedural control and exclusion plots, each 1 m^2 in area. From May to August an increasing trend of higher colonisation in plots where lugworms were excluded was observed. By August post-larvae density in the exclusion plots were significantly higher than in the control treatments, over double at 544 post-larvae per m^2. The field experiment excluding adult cockles produced the opposite trend, colonisations of *C. edule* post-larvae was lower in the adult cockle exclusion plots. The mechanisms controlling the trends seen in the field experiments are still unclear from the literature and preliminary laboratory experiments conducted by the authors and warrant further investigation. We conclude that the presence of adult cockles and lugworms influences the colonisation success of *C. edule* post-larvae. From the current results we suggest the density, distribution and population dynamics of macrofauna, such as those tested, may have significant implications on the success and spatial distribution of cockle recruitment.

T9.O5

DESCRIBING MORPHOLOGICAL FEATURES OF OOCYTES: AN ATTEMPT TO UNRAVEL REPRODUCTIVE ASPECTS OF TELLINIDAE AND PSAMMOBIIDAE SPECIES (BIVALVIA: TELLINOIDEA)

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In species of the bivalve superfamily Tellinoidea, gamete morphology studies are scarce, in spite of their ecological and economic importance to many human communities. Comparative investigations using Transmission Electron (TEM) and Light Microscopies (LM) have complemented anatomical descriptions, leading to improved elucidation of reproductive biology of bivalves. We have been suggesting that there are two clearly and well defined patterns of sperm morphologies among Tellinidae species. Tellininae produces modified spermatozoa whereas Macominae produces primitive spermatozoa. The helical nuclei overlapped in its base by mitochondria could be a synapomorphy of all genera examined until now belonging to the subfamily Tellininae, but interestingly also occurs in at least two Psammobiidae. The oocyte morphology of the species *Macoma constricta*, *Strigilla pisiformis* (Tellinidae) and *Sanguinolaria sanguinolenta* (Psammobiidae) was studied in the present work, aiming to describe features that could be useful for understanding the reproductive biology of Tellinoidea. Our data suggest that oocytes develop within acini that constitute the female gonad. Each acinus is involved by connective tissue with haemocoelic sinus and myoepithelial cells. The site of connection between the female gamete and the acinal wall is called stalk. Oogenesis in these bivalves seems to be classified into solitary type. LM of the gonad revealed oocytes at each developmental stage within the reproductive organ. This asynchrony indicates that the investigated species spawn gametes over many months or seasons. This strategy multiplies the possibility of gametes experiencing propitious conditions and allows for increased triumph of external fertilization. These preliminary results will be used to verify possible correlations between long nuclei and the thickness of large yolky eggs. Finally, we will compile sperm ultra-structure information, egg morphological descriptions, shell traits and DNA data trying to find evidences which confirm or deny the existence of proximity between Psammobiidae and Tellininae species.

Financial Support: FAPESP 2010/15486-8, 2009/07679-3 and PNPD/CAPES 1106/2010.

T9.O6

ULTRA-STRUCTURAL SPERM FEATURES AND MOLECULAR DATA OF *CARYOCORBULA CARIBAEA* (D'ORBIGNY, 1853), A SPECIES WITH EXTRAORDINARY CONCHOLOGICAL PLASTICITY

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Systematics of Corbulidae supported by anatomical and conchological studies remains confused and controversial due to the large phenotypic plasticity of the shells. Nowadays, associations of data have been proposed in order to scrutiny phylogenetic issues. Ultrastructural spermatozoon study and molecular analyses are performed to clarify and provide valuable taxonomic information. This work targeted individuals with conspicuous shell differences *a priori* belonging to two putative species. The spermatozoon was classified into primitive or *aquasperm* type, showing short and conical acrosomal vesicle, barrel shaped nucleus, midpiece composed of four spherical mitochondria and simple flagellum. The consistent similarity shared by spermatozoa produced by all studied specimens indicated that our sample corresponded to one coherent unit. Considering that individuals with relevant conchological variation were not distinguished by sperm ultrastructural traits, their mitochondrial gene 16S rDNA was partially sequenced and compared. DNA sequences associated with descriptions of sperm ultrastructure and shell attributes suggested that we were only dealing with *Caryocorbula caribaea*, despite the extraordinary conchological plasticity exhibited by the collected specimens. Based on the present work and the available literature about bivalves, it is possible to state that albeit discriminating investigations built on conchology and sperm morphology are valid and undoubtedly important, they are not always conclusive. Definitely, we confirmed that combined data analysis has been the most suitable tool to identify Corbulidae species.

Financial Support: PNPD/CAPES 1106/2010, FAPESP 2010/15486-8 and PIBIC/CNPq.

T9.O7

CREPIDULA'S ARROWS: STRUCTURE AND UNUSUAL TRANSMISSION MODE OF SLIPPER SHELL SPERMATOZOA

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To better understand the reproductive biology of the invasive slippershell *Crepidula fornicata*, we examined the spermatheca and spermatozoa of adult specimens collected in the intertidal using histology, scanning and transmission electron microscopy. The mature, filiform gamete presents the general organization of a caenogastropod spermatozoan, with a sharply-pointed acrosome, an elongated nucleus, an elongated midpiece containing the mitochondria arranged radially about the axoneme, and a long flagellum containing glycogen reserves arranged about the axoneme. Following copulation, the spermatozoa line the inner epithelium of the spermatheca. TEM micrographs show that the acrosomes are anchored within the cells of this epithelium, which degenerates, probably as a result of the lesions sustained. A new epithelial layer forms beneath the degenerating layer. These results are discussed in the context of *C. fornicata*'s reproductive biology, most notably sperm competition and survival.

T9.P1

MOLLUSCAN ASSEMBLAGES IN THE MUDDY BOTTOMS OF THE RÍA DE ALDÁN (GALICIA, NW IBERIAN PENINSULA)

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Molluscs are a group of great importance in muddy subtidal bottoms. Some species of bivalves are frequently among the most abundant ones in these communities, and gastropods, though less numerous, usually show a great diversity. The Ría de Aldán is a small embayment placed in the NW coast of the Iberian Peninsula, belonging to a group of tectonically-formed estuaries named Rías Baixas. Its inner part is characterized by muddy bottoms with high organic matter contents. Two sampling stations in that part of the embayment were studied from May 1998 to May 1999, and here we compare the molluscan fauna found in each of them. In each station, five replicate samples were taken monthly by means of a Van-Veen grab (0.056m^2) and then sieved through a 0.5mm mesh. Benthic fauna present in the samples was sorted, and all the molluscs were identified and counted. An additional sample was taken to determine sediment characteristics. Physico-chemical variables of water and sediment were also measured by means of a portable microprocessor.

A total of 11883 individuals were found, belonging to 135 different taxa (3 polyplacophorans, 81 gastropods, 50 bivalves and 1 scaphopod). The outermost station, which had a coarser and more heterogeneous sediment, accounted for a total of 6492 individuals from 97 different taxa, while the innermost one, which was muddier and more organically enriched, accounted for a total of 5391 individuals from 88 different taxa. The most abundant taxa were the bivalves *Kurtiella bidentata* (Montagu, 1803), *Chamelea striatula* (da Costa, 1778), *Thyasira flexuosa* (Montagu, 1803) and *Tellina fabula* Gmelin, 1791; and the gastropods *Cylichna cylindracea* (Pennant, 1777) and *Calyptraea chinensis* (Linneo, 1758).

T9.P2

TWO YEARS INVESTIGATION OF INTERTIDAL MOLLUSCAN COMMUNITY AFTER THE MASSIVE EARTHQUAKE AND TSUNAMI

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The phenomenon said to happen once in 1000 years occurred in Japan. Following the Pacific coast of Tohoku Earthquake on March 11th in 2011, massive land subsidence and tsunami struck in eastern Japan. The coastal ecosystem was damaged by them. The aim of this study is to understand changes in the distribution and abundance of intertidal mollusks in sandy shore after the earthquake. We examine the inhabitant of mollusks from May 2011 to April 2013 in Mangoku-ura Inlet and Sokanzan tidal flats that lies in the most inner part of Matsushima Bay in Miyagi Prefecture and Matsukawa-ura Inlet in Fukushima Prefecture.

Mangoku-ura Inlet was occurred land subsidence of 80 cm. Therefore intertidal zone became subtidal zone and part of the land became intertidal zone. Therefore, *Littorina brevicula* and *Batillaria cumingi* that can move themselves were found at shores that were land before the earthquake. Matsukawa-ura Inlet was attacked by tsunami reached over 9 m. Surface sand and most of the mollusks inhabited in there were temporarily rushed by the tsunami. And then *Macoma contaculata* and *Mya arenaria oonogai* that were distributed in deep were dug out to surface. In Sokanzan tidal flats, May 2011, juveniles and adults of mollusks were found at the same place. Also, much epifauna found at the surface.

The result suggests that sort of disturbance was different by place. Therefore, to assess the impact on macrobenthic community by sort of disturbance, we examined changes in species richness of macrobenthic animals before and after the earthquake. The result showed that species richness decreased significantly at Matsukawa-ura Inlet in comparison to other two sites. Although many mollusks were damaged by land subsidence and tsunami, plural recruitment of juvenile was observed after July 2011. However we proved some species of mollusks were unstable their populations after the earthquake.

T9.P3

COLONISATION PATTERNS OF COCKLE *CERASTODERMA EDULE* LINNAEUS (1758) POST-LARVAE

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The common cockle *Cerastoderma edule* is an important bivalve species of soft-sediment intertidal shore communities of north western Europe, and is a commercially exploited species. Cockle populations often have highly patchy distributions and the source of this spatial variability in distribution is currently considered to be generated through early post-settlement processes. The objective of this study was to record initial colonisation patterns and how it changes over time across the shore to inform possible processes creating patchiness. A staggered nested design was used from June 2010 to February 2012 at Traeth Melynog on Anglesey with 75 sample points distributed across 15 transects at exponentially increasing distances, from 0.7 to 133.3 m. All cockle post-larvae sampled were counted and their shell length measured. Settlement of post-larvae occurred in late May to early June and was restricted to the low shore with a peak density of 4,663 post-larvae m^2 at a mean shell length across all stations of 777 μm ± 43 (S.E.). After June, colonisation of the mid shore, and to a limited extent the high shore, took place resulting in a distribution similar to that of the adult cockles. The low intertidal shore was important for initial benthic colonisation of cockles in 2010 and 2011. This indicates that post-larval up shore redistribution may be significant for population structure and distribution. This has implications for the understanding of post-settlement mortality spatially on a shore through heterogeneous size and density distributions but also temporally as post-larvae redistribute either actively by bysso-pelagic migrations, or passively in scouring currents.

T10

CLIMATE CHANGE AND MOLLUSCAN ECOPHYSIOLOGY

(sponsored by American Malacological Society – AMS)

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Anthropogenic climate changes have altered the physical and chemical nature of the marine environment with impacts on the geographic distribution, physiological performance, and evolutionary trajectories of molluscs. These changes include sea-surface warming, ocean acidification and expanding hypoxia that may act independently or synergistically to alter physiological processes such as metabolism, calcification, acid-base balance, blood-oxygen transport, and growth among others. The scope and scale of physiological change that individuals undergo will fundamentally influence the ecological and evolutionary responses of populations and species, many of which are important components of marine ecosystems. This symposium will address the direct and indirect impacts of increased carbon dioxide and the mechanisms marine molluscs use to compensate for these changes, their natural evolved tolerances, and the energetic, ecological, and biogeographic consequences of compensation. While climate change will impact all marine organisms, molluscs are unique in many respects and this symposium will explore those characteristics. We have recruited and continue to invite speakers whose talks will address the effects of climate change, broadly defined, on molluscs at any time scale and at any level of biological organization, from molecules to ecosystems.

T10.O1

WARMING FORE-REEF SLOPES AND ITS EFFECT ON THE BIOLOGY AND DISTRIBUTION OF *NAUTILUS:* REPLAY OF ANCIENT GREENHOUSE MASS EXTINCTION HISTORY?

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Species of the living nautilids, belonging to the genera of *Nautilus* and *Allonautilus,* are distributed across and enormous range of the tropical Western Pacific and eastern Indian Oceans. They are found exclusively on fore reef slopes, usually at depths between 100 and 600m, although in two places, New Caledonia and Vanuatu, they can be found at near surface depths at night. We have been accumulating comparative population size data from both “fished” and “unfished” sites where Nautilus is known to occur to test the possibility that some species or populations may be threatened by overfishing, and the data strongly show that our sampled, fished population, from Bohol, Philippine Islands, is as much as two orders of magnitude rarer than from the Great Barrier Reef, Fiji, and Samoa. However, even samples from these latter unfished sites demonstrate lower populations than were present only two to three decades ago, and this observation cannot be ascribed to fishing alone. Oceanic warming may be driving predators to

greater depths, where they now interact with nautiluses at higher frequencies, and shell breakage data supports this hypothesis. If correct, we may be witnessing wholesale changes in fore -reef slope ecosystems caused by warming temperatures. New research on heat shock proteins are also now being used to better understand these possible changes.

T10.O2

VERTICAL MIGRATION ACROSS ENVIRONMENTAL GRADIENTS OF TEMPERATURE, OXYGEN AND CARBON DIOXIDE IN THE JUMBO SQUID, *DOSIDICUS GIGAS*, IMPLICATIONS FOR CHANGING CLIMATE

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The Eastern Pacific is characterized by sharp vertical gradients in temperature, oxygen and carbon dioxide. At intermediate depths (~300-800 m), oxygen levels are less than 1-2% of air saturation, temperatures are 10-20 °C cooler than overlying waters and high levels of carbon dioxide reduce the pH by about 0.6 units relative to the surface waters. These “oxygen minimum zones” are believed to be expanding worldwide due to natural and anthropogenic climate-change. The subsurface hypoxia found in extreme OMZs restricts most apex predators to the upper water column. The jumbo squid, *Dosidicus gigas*, is a top predator that migrates daily to hypoxic depths in the Eastern Pacific. Here we present an analysis of the environmental limits to metabolism and vertical distribution in *D. gigas*. We find that *D. gigas* maintains high metabolic activity in the upper water column while actively foraging at night. Metabolism is maintained, independent of the PO_2, down to a critical level (P_{crit}, 1.6 kPa at 10 °C) by a respiratory protein with a high affinity for oxygen and strong temperature and pH-sensitivity. Below the P_{crit}, *D. gigas* suppresses total metabolism by ~50%. Reduced ATP consumption serves to maintain energy charge, conserve fuel stores and minimize the accumulation of deleterious anaerobic metabolites. We provide evidence that transcriptional and translational arrest is a primary means of energy conservation. Metabolic suppression minimizes energy expenditure at depth, reducing the need for active foraging, which is otherwise light-limited.at depth. Moreover, the capacity for metabolic suppression provides habitat flexibility as oxygen minimum zones expand due to climate change. We show that increasing carbon dioxide levels in shallow waters may reduce blood-oxygen binding and limit activity levels, but that the effect of high CO2 levels at depth is negligible compared to the hypoxia-induced metabolic suppression.

T10.O3

LOWER HYPOXIA THRESHOLDS OF MOLLUSK EARLY LIFE STAGES LIVING IN A WARM ACIDIFIED OCEAN

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By the end of this century, carbon dioxide (CO_2) emissions are expected to decrease surface ocean pH by as much as 0.5 units and, at the same time, the ocean is expected to warm with an associated expansion of coastal and midwater hypoxia. Yet, the synergistic effects of ocean acidification and global warming on the hypoxia thresholds of marine biota are, to date, completely unexplored. Here we show that in contrast to the prediction of a universal temperature-dependence model, a cornerstone of the metabolic theory of ecology, the future warming scenario leads to lower energy expenditure rates in cuttlefish (*Sepia officinalis*) embryos. Thus, the metabolic depression strategy overrules Boltzmann kinetics. We also demonstrate that stressful abiotic conditions in today's ocean are already experienced within cuttlefish eggs. The record of oxygen tensions below critical pO_2 in embryos subjected to future warmer and hypercapnic scenarios indicates that such harsh conditions will be magnified in the years to come, especially in populations at the border of their thermal envelope. Such scenario promotes premature hatching and smaller post-hatching body sizes, thus challenging the survival and fitness of early life stages and shifting species' biogeographical range.

T10.O4

CAN COASTAL CALCIFIERS ADAPT TO A FUTURE, MORE ACIDIC OCEAN?

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Seasonally hypoxic coastal ecosystems are already acidified: respiratory processes go along with the production of carbon dioxide. Hypoxic systems frequently experience seawater pCO_2 values of >1,000 µatm already today. Future changes in pCO_2 due to equilibration of the ocean with anthropogenic CO_2 ('ocean acidification') are non-linear, leading to frequent occurrence of pCO_2 values >2,000 µatm, particularly in brackish habitats, such as the Baltic Sea (Melzner *et al*. 2013 Mar Biol online early). However, such coastal communities are often dominated by calcifying species, indicating that high fluctuations in pCO_2 can be compensated to some degree by mytilid mussels and some echinoderms. Here, I will discuss the impacts of high pCO_2 on acid-base regulation abilities in larval and adult stages of molluscs and echinoderms and will point at the potential unifying role of energy budget modulation for assessing vulnerability. I also will compare laboratory and field results and discuss the need

for more complex experimental approaches to estimate future vulnerability of species and communities to anticipated ocean change.

T10.O5

MOVING BEYOND MORTALITY: A METABOLIC FRAMEWORK FOR EXPLORING EFFECTS OF CLIMATE CHANGE ON INTERTIDAL MUSSEL BED ZONATION

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At the interface of the terrestrial and marine environments, intertidal ecosystems potentially serve as an early indicator of the impacts of climate change. Observations of shifts in zonation and changes in geographic patterns in bed-forming mussels have been reported worldwide, with subsequent impacts on infaunal diversity. Because local environmental conditions are often idiosyncratic, forecasting likely future effects of climate change on zonation can be challenging. Using well-developed coupled biophysical (heat budget) and energetic (Dynamic Energy Budget) modelling approaches, combined with a decade-long continuous record of intertidal mussel temperatures, we explore how changes in environmental conditions (wind speed, air temperature, water temperature and wave splash) are potentially translated into effects on mussel size, growth and reproductive output in mussel beds. We use a generic modelling approach that is applicable to mussels in the genus *Mytilus*, and perform a sensitivity analysis of parameters that are likely to vary between species, or as the result of local adaptation and acclimatization. Our results emphasize the interactive influence of multiple environmental drivers, and caution against the use of single metrics such as air temperature in forecasting where, when and with what magnitude environmental change impacts are likely to occur.

T10.O6

INTERTIDAL OYSTER AND MUSSEL BEDS IN A GLOBAL WARMING PERSPECTIVE. TRADE-OFFS AND MICROCLIMATIC DOWNSCALING

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Intertidal organisms on rocky shore have evolved morphological and physiological adaptations to environmental variability. Variation in temperature, in particular, has a

prominent effect in shaping this habitat since it largely influences individual organisms' performance and therefore, community composition. Species living in tropical regions have been hypothesized to be particularly sensitive to global warming because of their limited acclimation capacity and the fact that the range of environmental temperatures often approaches their predicted upper thermal limits. The present study challenges the generality of these projections by investigating the thermal performances of the tropical bivalve, *Isognomon nucleus* and the role of microclimatic engineer of the Mediterranean *Mytilaster minimus*.

I. nucleus was subjected to acute warming when re-immersed after the exposition to heat events of increased intensity when emersed. Extreme heat exposure did not induce detrimental effects in the bivalves. In contrast, metabolic performance thermal tolerance and average lethal temperatures were enhanced in individuals that endured the most severe conditions during aerial exposure. The benefits of the thermal response following acute heat event will be discussed showing the trade-off between thermal tolerance and energy assimilation efficiency.

In parallel we quantified the efficiency of mussel beds of *M. minimus* as ecosystem and microclimatic engineers. The rich biodiversity of infauna inhabiting these beds was sustained not only by the quantity and quality of the sediments entrapped by the mussel bed but also by the thermal heterogeneity of this bioma. These microclimate features represent a key-reading to infer on persistence of both mobile and sessile species which display a thermal niche narrower of the *M. minimus* one.

T10.O7

THERMOTOLERANCE OF ADULT GREEN-LIPPED MUSSELS (*PERNA CANALICULUS*): PATTERNS OF MORTALITY AND METABOLOMIC IDENTIFICATION OF KEY BIOMARKERS

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The green-lipped mussel (*Perna canaliculus*) is an economically and ecologically important marine species within New Zealand, yet its fate under future climate change conditions is unknown. To address this, we sought to characterise the thermotolerance capacity of *P. canaliculus* adults, and identify any metabolic biomarkers of thermal stress in this species. To achieve this, mussels were exposed to a 3 h acute temperature challenge using temperatures of 20 °C (Ambient), 25 °C, 29 °C, 31 °C, 33 °C, and 35 °C. Additionally, mussels were divided into two treatments, namely '*pre-stressed*' (1 h exposure to 29 °C, the day before thermotolerance experiment) and '*naïve*' (no pre-stress administered).

No mortality was observed in mussels exposed to 20, 25, 29, and 31 °C even after 30 days recovery. However, naïve mussels exposed to 33 and 35 °C exhibited 100% mortality 48 h post experiment; whereas pre-stressed mussels only exhibited mortality at 35°C. Gill tissues were harvested from mussels from both treatments and metabolite levels characterised via GC-MS. Analysis of 48 metabolites via ANOVA revealed a statistically significant interaction between *treatment* × *temperature* for succinic acid. This was evidenced by greater accumulation of succinic acid in naïve vs pre-stressed mussels at 33°C; and even greater succinic acid levels accumulating in both treatments at 35 °C. Therefore, our results reveal that mortality in thermally stressed *P. canaliculus* is abrupt and mortality seems assured once temperatures reach 35 °C. Accumulation of succinic acid tracked patterns of mortality thus has potential as a biomarker of thermal stress. Furthermore, with increased "heatwave" events predicted under climate change the persistence of this species in the intertidal zone of New Zealand remains uncertain.

T10.O8

THE INTERACTIVE EFFECTS OF OCEAN WARMING AND ACIDIFICATION ON PACIFIC OYSTER LARVAE

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Crassostrea gigas larvae were produced and cultured over the entire larval cycle until metamorphosis in four different conditions (control 20 °C pH 8.1; 24 °C pH 8; 20 °C pH 7.4; 24 °C pH 7.4) based on future IPCC scenarios to investigate the impacts of changes in temperature and pH on larval (shell) development. By using various molecular techniques such as gene fishing, cloning and degenerate PCR, four genes involved in biomineralisation processes during the development of *C. gigas* were identified. With quantitative real-time PCR the expression of *CGCaM, CGDent, CGPerl* and *CGMG4* were analysed and differences during development and between the different environmental conditions were compared. Using Fourier Transform Infrared spectroscopy and scanning electron microscopy, changes in mineral crystallinity and in shell microstructures during development and between the different conditions were analysed.

It was shown for the first time how the synergistic effects of ocean acidification and ocean warming affect biomineralisation processes in a commercially important bivalve species and the resulting implications on *C. gigas* development from a molecular to a mineralogical level. The study demonstrated that the effects of temperature and pH, alone and in combination, had overall negative effects on *C. gigas* development, based on decreased growth rates, increased mineral disorder and altered gene expression of skeletogenesis-related genes. Under the conditions of this experiment, low pH was a greater single stressor than high temperature, whereas the combination of these two factors produced greater changes in physiology and shell properties in *C. gigas* than each of the factors alone. It can be concluded that impaired shell growth including corrosions, malformations and increased mineral disorder are likely to jeopardise the survival of larvae and may lead to reductions in both natural and commercial oyster populations.

T10.O9

PHYSIOLOGY AND BIOGEOGRAPHY: THE RESPONSE OF EUROPEAN MUSSELS (*MYTILUS* SPP.) TO CLIMATE CHANGE

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To understand how ecological communities may respond to climate change we have adopted the approach of determining the response of major ecosystem constituents (i.e. ecosystem engineers) that determine community composition and function. We utilize two approaches, correlative and mechanistic, to understand the current and historical distributions of the marine mussels *Mytilus edulis* and *M. galloprovincialis* in Europe. Both are dominant space-occupying species that control biodiversity in many coastal ecosystems and are the basis of the largest aquaculture production in the world. Correlating species distribution records with sea surface temperature (SST) through Random Forest modeling indicates that winter temperatures around 9-10 °C limit the northern range of *M. galloprovincialis*. A mechanistic analysis of physiological energetic response to temperature of the two species indicates that *M. edulis* cannot sustain a positive energy balance for sustained periods when SST is greater than 23 °C, while *M. galloprovincialis* can maintain a positive energy balance at SST up to 30 °C. There is no difference in energetic response of the two species at cold temperatures (5-10 °C). The upper temperature threshold of positive energy balance in each species corresponds closely to the distribution of SST at their respective southern range limits in Europe. Alternatively, the northern range limit of *M. galloprovincialis* coincides with areas where winter SST is less than 9 °C, but there is no evidence of an energetic limit to this species at the cold end of its geographic range. Presently there is no mechanistic explanation for the difference between species in their northern range limits; however, as indicated by the Random Forest model, *M. galloprovincialis* appears to be limited by cold temperatures during winter, suggesting the hypothesis of failure in reproductive development. These approaches allow for the ability to forecast changes in the distributions of these two species in Europe as SST continues to increase.

T10.O10

OPEN AIR DINING: CIRCATIDAL FORAGING PATTERNS OF THE INTERTIDAL WHELK *NUCELLA OSTRINA* IN A COMPLEX THERMAL LANDSCAPE

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An important first step to predicting the effects of climate change is to characterize the microclimate in which the organism lives, a considerable challenge for small mobile organisms in complex thermal landscapes, such as the rocky intertidal zone. For the predatory whelk *Nucella ostrina*, foraging on its barnacle prey generally requires

movement higher on the shore, potentially increasing the risk of thermal stress. How do snails balance the reward of food with the risk of overheating? We used outdoor tidal mesocosms to examine foraging patterns of snails over 16 weeks, manipulating the timing of aerial exposure but not total emersion time. Snails exposed to daytime low tides followed a biweekly pattern, leaving refuges to feed for 2-4 days, then retreating for approximately 10 days. Peak foraging preceded the onset of spring tides, when aerial exposure occurred only during early morning hours; snails fed on days with reduced thermal risk. Snails experiencing only nighttime low tides foraged aperiodically. In the field, we placed *N. ostrina* on artificial concrete islands to choose between barnacle prey placed on western or eastern faces, or to shelter in a cool refuge. Snails again exhibited feeding peaks on days when aerial temperatures were reliably cool. Moreover, snails predictably shifted from western to eastern faces on days with afternoon low tides. These results suggest that *N. ostrina* alters its behavior to capitalize on relatively small-scale spatiotemporal differences in microclimate, a foraging pattern that consistently minimizes exposure to extreme aerial temperatures. In a climate scenario of increased aerial temperature, mobility may give this predator an advantage over its sessile prey. These results underscore the importance of characterizing the temporal patterns of microhabitat use when assessing the thermal exposure of mobile organisms.

T10.O11

ADAPTATION TO HEAT IN THE MEDITERRANEAN SNAIL SPECIES *XEROPICTA DERBENTINA*: STRATEGIES TO SURVIVE ELEVATED TEMPERATURES

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Dry and hot environments challenge the survival of terrestrial snails. In these animals, physiological and biochemical adaptations are of high importance to minimize overheating and desiccation. In seven populations of the Mediterranean snail species *Xeropicta derbentina* we investigated heat response strategies reflected by histological and biochemical response patterns after exposure to elevated temperature (25-48 °C) in the laboratory. Three response strategies could be observed which are characterized by different maxima of stress protein induction and different levels of cellular injury, which all rendered survival possible. In the digestive gland, calcium cells which are known to be involved in central metabolic processes, e.g. detoxification or osmoregulation, were shown to be more heat-resistant than other cell types of this organ. This phenomenon was associated with Hsp70 induction: with increasing stress protein levels, the integrity of calcium cells improved or, at least, did not decline in all investigated populations. Furthermore, we studied oxidative stress in individuals of one of these populations after exposure to the above mentioned temperature levels by measuring lipid peroxide formation in whole body homogenates by means of the ferrous-oxidation-xylenol-orange-method (FOX) assay. We observed an increase in lipid peroxides with rising temperature until 40 °C. At 43 °C, however, low levels of lipid peroxides were found resembling the control level at 25 °C. Compared to 43°C, increased lipid peroxide levels were found in snails exposed to 45 °C and 48 °C. It is discussed to which extent different lipid peroxide levels can be related either to increased antioxidant defense mechanisms (e.g. antioxidant enzymes like catalase, glutathione peroxidase or glutathione reductase) and / or decreased cellular injury.

T10.O12

OCEAN ACIDIFICATION AND WARMING ALTER ALLOMETRY OF METABOLISM IN CHITONS: ENVIRONMENTALLY-DRIVEN CHANGES TO METABOLIC SCALING INDICATE RESPONSES TO MULTIPLE STRESSORS ARE MEDIATED BY BODY SIZE

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Despite some superficial homogeneity and apparently simple lifestyles, chitons exhibit variation in both basal metabolic rates and allometric scaling, with differences linked to their natural history. Allometric scaling of metabolism with body mass has long been considered a fundamental mechanistic 'law' in organisms. However, there is ample evidence scaling relationships show significant variation within certain boundaries, associated with ecology and activity patterns. Recent models such as the Metabolic-Level Boundaries (MLB) hypothesis have proposed theoretical frameworks explaining this observed variation. If metabolic scaling is variable among species and plastic to extrinsic factors, it may be altered under conditions of environmental change such as warming and ocean acidification. To test these ideas, we acclimated full ontogenetic body-size ranges of three species of chitons from the NE Pacific (*Katharina tunicata, Tonicella lineata, Mopalia muscosa*) to altered seawater temperature and pH. To determine synergistic and antagonistic effects of these stressors on both basal metabolism and its allometry, three temperatures and two pH conditions were examined in a factorial design. Under normal pH, higher temperatures as expected caused metabolic rates to increase, but also the allometric scaling exponent b to decrease, a key prediction of the MLB hypothesis. The effect of ocean acidification was variable: in two species, metabolism was significantly depressed and the scaling exponent b significantly reduced under low pH at low temperatures, but this was not seen at higher temperatures. Our data show the effects of stressors on metabolism are not equal across the ontogenetic range of the species, and illustrate the limitations of comparing responses at a species standard mass and the importance of examining representative body size ranges in future studies. Chitons are likely robust to future changes in ocean conditions, however responses to these stressors may represent permanent additional energetic costs and cause trade-offs with other vital physiological processes.

T10.O13

INFERRING IMPACTS OF CLIMATE CHANGE ON MARINE POPULATIONS FROM MACARONESIA USING LIMPETS, A KEYSTONE INTERTIDAL ORGANISM, AS MODEL SPECIES

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Climate change is occurring at a rapid pace on a global scale. An analysis of high-resolution sea surface temperature (SST) data from the last 30 years showed that throughout the Azores there is a clear warming SST trend (0.39 +/- 0.041ºC per decade), with extremely hot days becoming significantly more frequent (9.11 +/- 3.71 days per decade) and extreme cold events less frequent (-14.49 +/- 4.90 days per decade). Climate change is affecting marine species in multiple ways including geographical distribution, abundance and biological processes such as reproduction and growth. Intertidal ecosystems in Macaronesia are extremely vulnerable due to their high degree of geographic isolation. Therefore, recovery of local populations by larval input from other locations after disturbance will be slow, if not impossible. In this project we are assessing the resilience potential of intertidal populations to climate change in the NE Atlantic, using commercially valuable and heavily exploited limpets (*Patella* spp.) as model species. Understanding the mechanisms underlying physiological responses to environmental factors, their limits and genetic basis, is vital to predict local extinction risk, its impact on the ecosystem and possible repercussions on fisheries activities. This study is being conducted on a large geographical scale, encompassing ten sites across Macaronesia and another 10 in mainland Europe. We are employing a combined approach of in situ experiments such as the deployment of environmental data loggers and common-garden trials with state-of-the-art molecular methodologies like RNA-Seq and DNA microarrays. Here we will be presenting the first results of this project, including the discovery of stress-related genetic markers from limpet transcriptomes and how these will be used to decipher tolerance thresholds to environmental factors such as temperature, desiccation and hypoxia.

T10.O14

ADAPTATION OF LAND SNAILS TO STRESSFUL CONDITIONS: FROM WHOLE ANIMAL TO CELLULAR MECHANISMS

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The ability of land snails to colonise terrestrial habitats is the result of their developing a range of behavioural and physiological adaptations for coping with problems of maintaining water, ionic and thermal balance to ensure their survival under specific microhabitat conditions. This is all the more difficult for land snails which inhabit arid and semi-arid zones, where conditions of high ambient temperature and low humidity prevail. One of these adaptations is their annual cycle of activity and aestivation that

correlates with seasonal changes in temperature, humidity and water availability. This presentation summarizes some 20 years of research on resistance to desiccation and heat in *ca*. 25% of the Israeli land snail fauna. In general, resistance to heat and aridity is correlated with distribution patterns and with abiotic environmental variation. The study comprised of intra-generic and intra-specific comparisons and micro-habitat and phylogeny-related differences. We also tested the effects of body size, ontogeny and the physiological set-points of the water regulatory mechanisms. Lately, we study the cellular mechanisms functioning under stress conditions and reflected in the pattern of expression of heat shock proteins (HSPs).

T10.P1

THE FUNCTIONAL TRAIT-BASED APPROACH TO INVESTIGATE LIFE HISTORY TRAITS IN MARINE INVERTEBRATES TO PREDICT EFFECTS OF GLOBAL CLIMATE CHANGE ON ECOSYSTEMS

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Due to the actions of Man, biodiversity is constantly shrinking in every known ecosystem worldwide. The loss begins with modifications of functional traits at the individual level, proximately involving an alteration in the amount of energy available for metabolism by individual organisms: with insufficient energy, metabolic machinery does not work efficiently and organisms are unable to reach their maximal fitness throughout their life span. Here, we present a simple conceptual framework recently developed in our Lab in collaboration with many world-wide Universities inside a network studying the effect of climate changes on marine ecosystems, which is based on functional trait-based bioenergetic principles. Through some case studies, we show that the importance of the amount of available energy at the individual level is able to explain how emergent and classical anthropogenic factors may drive biodiversity loss starting from the individual reproductive failure. Flows of energy and matter through habitats and organisms are indeed subject to the laws of energy conservation and this allows us to mechanistically trace them through individuals and from individuals to populations and communities. The combination of lab and field experimental procedures with a robust mechanistic theory helps us to predict how each species operates under different sets of conditions (and when it does not). We are eager to investigate and possibly predict effects of both local (chemical [e.g., pollution], physical [e.g., thermal or boating noise]) and global (increasing temperature and CO2) disturbance, from benthic sessile to mobile pelagic organisms and from shallower intertidal to deeper subtidal habitats. Lab people, from undergraduate students to post-docs, like to face similar issues with quantitative rigor and innovation.

T10.P2

EVIDENCE OF LONG-TERM CHANGES IN THE DISTRIBUTION OF KEY INTERTIDAL SPECIES

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Globally, changes are occurring in the biogeochemistry and ecology of the oceans, which may influence the physiology, phenology, and species distribution. Biological communities are reacting to climate change through changes in the abundance and phenology of the organisms and through the poleward shift in species distribution. Rocky shores are relatively simple ecosystems, which makes them an excellent model system for the understanding of the consequences of climate change. This study aims to examine the evidence of long-term changes on the distribution of key intertidal species in the Azores. Grey literature and unpublished data collected in the late 1980's by Stephen J. Hawkins and his colleagues in the island of São Miguel (Azores) was compared to data collected in 2012. Whilst most taxa sampled in 1988 were still present during 2012, there were changes in species composition. In general, there was an overall decrease in the abundance of organisms that was more pronounced in the sheltered studied area. In addition, there was generally a shift upwards of the vertical distribution of many taxa, which was more pronounced in the exposed area. These changes are temptatively interpreted as a consequence of increased temperatures and wave action (both predicted by climate change scenarios). This study suggests that the consequences of processes responsible for long-term changes recorded in species distribution can be mediated by wave action. In addition, there was evidence that processes operating at large temporal scales may indirectly influence the distribution of species via changes in the abundance of their competitors.

T10.P3

SYNERGISTIC EFFECTS OF OCEAN ACIDIFICATION AND WARMIN IN SQUID EARLY ONTOGENY: EVIDENCE FOR SEVERE BIOLOGICAL IMPAIRMENTS

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We investigated a set of biological responses to climate-change related variables during early ontogeny of the squid *Loligo vulgaris*. Embryo's survival rates ranged from 92%-

96% under the present-day temperatures (13 °C-17 °C) and pH (8.0) scenarios. Ocean acidification (pH 7.5) and warming (+2 °C) led to a significant drop in survival rates (47%, $p<0.05$). The embryonic period was shortened by increasing temperature in both pH treatments ($p<0.05$). Embryo growth rates increased significantly during warming under the present-day scenarios, but there was a significant trend reversal under future warming conditions ($p<0.05$). Besides pronounced premature hatching, a higher percentage of abnormalities was found in late embryos exposed to future summer warming and lower pH ($p<0.05$). Under the ocean acidification scenario, oxygen consumption rates decreased significantly in late embryos and newly hatched paralarvae. There was a significant enhancement of the heat shock response (HSP70/HSC70) with warming in both pH treatments and developmental stages. Embryonic Q10 values ranged between 1-1.5, which was indicative of metabolic suppression. Upper thermal tolerance limits were positively influenced by acclimation temperature, and such thresholds were significantly higher in late embryos than in hatchlings under present conditions ($p<0.05$). Upper thermal tolerance limits of the hatchlings were higher under hypercapnia in comparison to embryos. We conclude that stressful abiotic conditions inside egg capsules will be exacerbated under near-future ocean acidification and warming scenarios. Occurrence of prolonged embryogenesis (linked to metabolic arrest and premature hatching), along with lowered embryonic thermal tolerance limits is expected to negatively affect survival success of squid early life stages.

T10.P4

CHARACTERISTICS OF SHELL MICROSTRUCTURE OF PELAGIC AND BENTHIC MOLLUSKS FROM ANTARCTIC WATERS, AND OCEAN ACIDIFICATION

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In Southern Oceans, pteropod *Limacina helicina antarctica* forma *antarctica* occurs as one of the most abundant zooplankton and it is notable for its function as key mesozooplankton species. Pteropod species show large patch biomass and its high grazing rates roles as a significant contributor in carbon export fluxes. *Laternula elliptica* is widely distributed in Antarctic shallow coastal waters and known as one of the endemic and dominant benthic bivalve.

Fundamental studies on shell structure are necessary as a prelude to applied research directed at tackling the anticipated effects of increased greenhouse gas emissions and ocean acidification. We examined the shell microstructure of the Antarctic species, *Limacina helicina antarctica* forma *antarctica* and *Laternula elliptica* and discuss the shell characteristics of the mollusc species inhabiting Antarctic waters from the point of adaptation to the cold seawaters and from the point of ocean acidification.

The shells of Antarctic *L. helicina antarctica* forma *antarctica* were very thin, approximately 2–9 micro m for shells of 0.5–6 mm in diameter. Many axial ribbed growth lines were observed on the surface of the shell. Distinct axial ribs were observed on the outermost whorl, while weak or no rib-like structures were observed on the inner whorls in the larger shell. There was an inner crossed-lamellar and extremely thin outer prismatic

layer in small individuals, and a distinct thick inner prismatic layer was observed beneath the crossed-lamellar layer in large individuals.
Shell thickness of the benthic dominant bivalve *L. elliptica* was approximately 99-132 μm in the shell of shell length 19 mm. It was composed of two calcareous structures, homogeneous or granular structure in thick outer layer and nacreous in thin inner layer, respectively. Characteristics of shell structure are discussed comparing with the previous results and from the point of adaptation to the Antarctic waters.

T10.P5

HOW CAN PHYSIOLOGY IMPROVE SPECIES DISTRIBUTION MODELS IN MARINE ORGANISMS?

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Species distribution models (SDMs) are central in exploring changes in biodiversity. The reliability of predictions of SDMs has been questioned because models often lack a physiological underpinning and rely on assumptions that may be unrealistic under climate change. In this study we explore how information on the limits of thermal tolerance can improve our ability to predict the effects of climate change and get us closer to the fundamental niche of the species. Using cephalopods as a model group, we determined in the lab the window of critical temperatures for different life stages (embryos, hatchlings and adults) and study how this information can improve our predictions for range shifts under a climate change scenario. The resulting framework may pave the way towards a better modelling of marine species distributions under climate change.

T10.P6

SALINITY TOLERANCE AND SPATIAL DISTRIBUTION OF *ARCTICA ISLANDICA* L. (MOLLUSCA, BIVALVIA) IN THE WHITE SEA

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This study reports on an extraordinarily dense settlement (100 ind./m^2 ; 700 g/m^2) of the bivalve *Arctica islandica* L. in the upper subtidal zone (5 - 15 m depth) in the silty-sandy area near Matrenin Island (White Sea, Kandalakshsky Bay, Chupa inlet). The size-age structure of the settlement is stable at different depths: down to a depth of 10 m all bivalve age groups are present, mostly young individuals (< 20 mm); at 10 - 15 m, the abundance of older generations (> 30 mm) sharply increases. This heterogeneity in distribution corresponded to the salinity regime: below 10 m, values do not fall below 20 ‰, but in shallower water the values may drop to nearly 10 ‰. To assess the possible influence of this gradient on the structure of this population, experiments were conducted to define the lower limit of salinity tolerance. This involved analyzing non-acclimated *A. islandica* individuals in July-August 2010. Bivalves of three different size classes were collected and placed in six different containers with salinities ranging from 6.8 – 24.1 ‰. After 24 hours, the degree of burrowing (in % of individuals) was determined as an index of activity. The resulting lower limit of tolerance of the tested individuals (about 14 ‰) was significantly lower than those given in the literature (about 20 ‰). This explains the distribution of individuals across the full range of depths (5-15 m). Bivalve size is also a statistically significant factor in their activity. At a salinity of 18.3 ‰, the activity of *A. islandica* larger than 30 mm was significantly lower compared with specimens under 20 mm. This helps explain the observed concentration of large bivalves below 10 m, where salinity never falls below 20 ‰; young individuals are apparently less sensitive to low salinity.

T11

INVASIVE MOLLUSKS

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Rapa, Zebra, Spanish, Slippershell… these are just a few of the molluscan 'bad boys' – habitat invaders who wreak havoc, cost millions, and defy our ability to do anything about it. It is universally agreed that any hope for control or remediation depends on the fullest possible understanding of their underlying biological bases and ecology. In this session, we welcome papers which aim to do so, as well as those which tend toward forecasting and damage assessment/control.

T11.O1

THE SLUGS OF BRITAIN AND IRELAND: UNDETECTED AND CRYPTIC SPECIES INCREASE A WELL-STUDIED, ECONOMICALLY IMPORTANT FAUNA BY UP TO 29%

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The slugs of Britain and Ireland form a well-studied fauna of economic importance, including many widespread European species invasive elsewhere (e.g., at least half of the 36 known British slug species are established in North America). The first molecular genetic study of the fauna was carried out to investigate patterns of intraspecific and interspecific variation in mitochondrial DNA (16S and COI), morphology, and geography, and to verify the identity of specimens used in an identification guide. Contrasts with nuclear DNA (ITS-1) and morphology were investigated with reference to the evidence for interspecific hybridisation. Phylogenetic and divergence analyses supported the distinctness of at least 35 of the 36 known species (two species in *Arion* subgenus *Carinarion* are scarcely distinct). By the same criteria however, a further 6-10 previously undetected species (17-29% of the fauna) are also established in Britain and/or Ireland. Although overlooked, less than half of these are morphologically strictly cryptic and some appear previously undescribed. Most are probably accidentally introduced, and several are already widespread in Britain and Ireland (and thus perhaps elsewhere). At least two are likely to be plant pests. The relative degree of intraspecific variation appears to be a poor guide to the native status of species, with high and low variation occurring in both native and introduced taxa. 16S and ITS-1 data showed some evidence for interspecific hybridisation among the large *Arion* species, although not involving *A. flagellus*. More unexpectedly, the COI and morphological data suggest hybridisation involving species pairs in *Deroceras* (Agriolimacidae) and *Limacus* (Limacidae). In the latter groups, introgression appears to have occurred in one direction only, with recently-invading lineages becoming common at the expense of long-established or native ones. The results show how even a well-studied, macroscopic fauna can be vulnerable to cryptic and undetected invasions and changes.

T11.O2

THE *ARION* SLUG INVASION

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The slug *Arion lusitanicus* Mabille, 1868, (syn. *A. vulgaris* Moquin-Tandon, 1855) is one of the hundred most invasive alien species in Europe. It is assumed to have originated from the Iberian Peninsula and has been introduced to many European and American countries in recent decades. It causes significant economic losses in agriculture and horticulture, and it strongly affects native related species probably by competition or hybridization. *A. lusitanicus* belongs to a complex of morphologically very similar species, which also includes *A. rufus* and *A. ater*.

In this PhD project, phylogenetic, population genetics and experimental approaches are used to determine the origin and route of the *Arion* invasion and the mechanisms of the invasion success. The initial phase of the molecular analyses has shown surprisingly large genetic divergence among often syntopically occurring *Arion* slugs. However, *A. lusitanicus* appears to be much less diverse than the native *A. rufus* throughout most of the range. This is consistent with a current invasion of Europe and Switzerland by *A. lusitanicus* during which repeated bottlenecks and founder events are expected to lead to a reduction in genetic diversity.

The breeding experiment aims to assess the inter- and intraspecific interactions of *A. lusitanicus* and the Swiss native *A. rufus*. Growth, reproductive success and potential hybridization between the species under different conditions are evaluated. The first results suggest that *A. lusitanicus* is indeed a better competitor than *A. rufus*.

Further research and analyses will aim to identify additional ecological parameters contributing to the success of this invasive slug.

T11.O3

INTERACTION BETWEEN AN INVASIVE SLUG *ARION LUSITANICUS* AND AN AGGRESIVE WEED *TARAXACUM OFFICINALE*

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Grazing by *Arion lusitanicus* (Mabille) of inflorescences of dandelion (*Taraxacum officinale* agg.) was observed at a grassy site with an abundant slug population. The slugs climbed flowers and consumed the petals. Of the 40 % of the flowers grazed by this slug most died before seed dispersal. An experiment with artificial cutting of petals demonstrated that viability of seeds from inflorescences that survived slug grazing was little affected. Slugs also climbed to maturing capitula and seed was eaten from 10 % of the closed inflorescences. The slugs thus may destroy nearly a half of the maturing capitula before seed dispersal. In addition to seedling predation by *A. lusitanicus* which is an important source of dandelion mortality, grazing of flowers may also be an important source of mortality at sites where this slug is abundant.

The work was supported by grant 526/09/1436 of the Grant Agency of the Czech Republic.

T11.O4

INDIGENOUS AND INTRODUCED GASTROPODS, AND THEIR TREMATODES: IMPLICATIONS FOR BIODIVERSITY

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Parasites play a decisive role in sustaining the structure and biodiversity in freshwater ecosystems, both through their hosts and via other free living species that rely on these hosts. Introduced gastropods can aggravate the situation either by transmitting invasive parasites or through increased resistance to native parasites which allows them to outcompete native snails. For example, gastropod biodiversity in Israel has significantly changed since the introduction of two invading thiarids: *Thiara scabra* and *Tarebia granifera*. Nonetheless, biodiversity surveys often sample host and parasite richness at different points in time. Consequently, it is difficult to assess the relative role of biotic vs. abiotic factors in maintaining species richness, and to identify patterns and trends of biodiversity decline. A comprehensive survey of 41 natural freshwater sites was conducted during the years 2011-2012. The survey targeted both indigenous and introduced freshwater gastropods, including their trematodes. In total five indigenous and two introduced species of gastropods were identified morphologically. Nine species of trematodes were identified using molecular methods. One trematode species was found to infect all seven species of gastropods, and three additional trematode species were found to infect 5-6 species of gastropods. Introduced gastropods were rarely found to be infected. Taken together, these results suggest that introduced gastropods may outcompete their indigenous counterparts via increased resistance to native parasites. A better understanding of the players affecting freshwater gastropod fauna in Israel will assist in developing effective eradication and containment schemes to the benefit of agriculture and public health.

T11.O5

HABITAT QUALITY INFLUENCES THE TOLERANCE OF THE ASIAN GREEN MUSSEL *PERNA VIRIDIS* TOWARDS HYPOXIA

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As a consequence of growing human populations in coastal areas and the resulting transport of nutrients into the sea, hypoxia caused by microbial activity is an increasingly severe phenomenon in shallow-water systems. The Asian green mussel *Perna viridis* has

a large indigenous and non-indigenous circumtropical distributional range and is often found in polluted, eutrophic habitats where it shows a high resistance to environmental stress. Since the mussel's stress tolerance is discussed as one reason for its invasiveness, it is important to understand how habitat conditions enhance the ability to survive stressors. Since for persistent invasion the entire lifecycle must be accomplished successfully, it is relevant to assess stress sensitivity at different ontogenetic stages. In laboratory experiments, we investigated the mussel's tolerance to hypoxia, exposing a) individuals of populations from polluted versus unpolluted habitats on the Island of Java, Indonesia, and b) mussels of four different size classes (5-8.9 mm, 9-11 mm, 11.1-14 mm, 14.1-18 mm) to low oxygen concentrations for 2 and 3 weeks, respectively. We found that - in contrast to the mussels from the unpolluted site – hypoxia (1 mg/l dissolved oxygen (DO)) was not lethal for mussels from the polluted environment. The latter also survived longer under 0.5 mg/l DO. Hypoxia (1 mg/l DO) was not lethal for the intermediate sizes (9-14 mm shell length), whereas it was for mussels larger than 14 mm (mean time to death (LTmean) = 11 days). The smallest mussels showed low survival under both, hypoxia (LTmean = 15) and normoxia (LTmean = 16). We suggest three different ecological mechanisms, i.e. adaptation, acclimation and food availability, as potential causes for the higher resistance to hypoxia in mussels from the polluted habitat. Furthermore, we explain the size-dependent tolerance differences by the reallocation of energy from stress compensation towards reproduction during the post-metamorphic development.

T11.O6

THE INVASIVE *CORBICULA FLUMINEA* POPULATIONS IN PORTUGAL

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The Asian clam *Corbicula fluminea* is an invasive species (NIS) originally from Asia that has been spreading worldwide causing major ecological and economic impacts in freshwater ecosystems. The successful invasive behaviour of *C. fluminea* may be related to their natural traits. Records indicate that in Portugal, *C. fluminea* was firstly detected in the Tejo River in 1980 and a few years later in other Portuguese ecosystems. Previous studies in the Minho and Lima Rivers (North of Portugal) employing the mitochondrial DNA cytochrome c oxidase subunit I (mtDNA COI) gene, have shown the prevalence of one main haplotype which is similar to the European haplotype I, North American haplotype form A and the FW5 Asian haplotype and three other rare haplotypes were also detected only in the Minho River. However, *C. fluminea* populations from the South of Portugal namely, Tejo, Guadiana, Sado, Mira Rivers have not been assessed thus far. In this context, the main objectives of this study are to assess the genetic variability between the *C. fluminea* populations from the North and the South of Portugal employing mtDNA COI gene analyses. The obtained results will be compared with other available worldwide data of *Corbicula* species from the native and invaded regions applying population genetics and phylogeographical inference methodologies. This genetic characterization may provide insightful information regarding the invasive behaviour of these *Corbicula fluminea* populations in Portugal.

T11.O7

THE MOST AGRESSIVE FRESHWATER INVADERS: PARALLELS, CONTRASTS, SPREAD, AND ECOSYSTEM IMPACT OF ZEBRA AND QUAGGA MUSSELS

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Dreissena polymorpha, the zebra mussel, and *Dreissena rostriformis bugensis,* the quagga mussel, continue to spread, both in Europe and North America, at virtually all spatial scales, causing serious economic damage and altering the aquatic communities and ecosystems they invade. While the zebra mussel is among the best studied freshwater invertebrates, we do not always have comparable information for quagga mussels, which limits our ability to predict the spread and ecological impacts of this important freshwater invader. Although zebra and quagga mussels are closely related species, share a common native habitat, life history, and dispersal potential, the zebra mussel rate of spread has been higher than that of quagga mussel at most spatial scales throughout their invasion history. The estimated lag time between initial introduction and maximal population size is 5 times shorter for zebra mussels than that for quagga mussels, which may be an important factor affecting the speed with which this species can spread. The ecological impacts of both species are associated with their role as ecosystem engineers, and the magnitude of their effects is determined by the population density in a given waterbody. The ecological effects of quagga mussels may be similar to those of the zebra mussel, or they may be greater given that quagga mussels appear to utilize a wider range of habitats within lakes than do zebra mussels, and are therefore capable of attaining much larger overall population sizes, particularly in lakes with large profundal zones. Because the vast majority of observations of quagga mussel impacts on aquatic communities and environments have been conducted in waterbodies previously colonized by zebra mussels, it is very difficult to distinguish between the effects of zebra and quagga mussels.

T11.P1

INTERACTION BETWEEN AN INVASIVE SLUG *ARION LUSITANICUS* AND AN AGGRESIVE WEED *TARAXACUM OFFICINALE*

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Grazing by *Arion lusitanicus* (Mabille) of inflorescences of dandelion (*Taraxacum officinale* agg.) was observed at a grassy site with an abundant slug population. The slugs climbed flowers and consumed the petals. Of the 40 % of the flowers grazed by this slug most died before seed dispersal. An experiment with artificial cutting of petals demonstrated that viability of seeds from inflorescences that survived slug grazing was little affected. Slugs also climbed to maturing capitula and seed was eaten from 10 % of the closed inflorescences. The slugs thus may destroy nearly a half of the maturing capitula before seed dispersal. In addition to seedling predation by *A. lusitanicus* which is an important source of dandelion mortality, grazing of flowers may also be an important source of mortality at sites where this slug is abundant.

The work was supported by grant 526/09/1436 of the Grant Agency of the Czech Republic.

T11.P2

PREFERENCE OF *ARION LUSITANICUS* FOR SEEDLINGS OF HERB SPECIES

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Seedlings are highly vulnerable developmental stage of vascular plants and slugs are their important consumers. They trace palatable species of seedlings even when they are sparsely scattered in the undergrowth. In searching for seedlings slugs apparently compensate their poor mobility by an extraordinary sense enabling orientation at distance. This may be shown by their preferences for particular species of seedlings. We established and compared preferences for species of seedlings in *Arion lusitanicus* (Mabille). It was a dominant species (>98 % of slug population) in the field experiment where seedlings of 25 species of wild herbs were 4 days offered for predation, in 5 replicates. The proportion of consumed seedlings of particular species varied between 15.3±8.82% (*Cerastium holosteoides* Fries) and 99.2±0.72% (*Spergula arvensis* L.). Six species were significantly less and 3 species significanntly more consumed then the reference species *Taraxacum officinale* Weber ex Wiggers (74.2±13.19%). In a multi-choice laboratory experiment *A. lusitanicus* was offered with seeds of 11 herb species. Consumption in a 12 h experiment varied between 0.0% (*Euphorbia peplus* L.) amd 66.6±7.85% (*Cichorium intybus* L.). Field and laboratory consumption was positively but not significantly correlated (R=0.5347, P<0.1). Nine species of seedlings were less and one more preferred than *T. officinale*. The results show that *A. lusitanicus* is capable to distinguish and precisely locate presence of particular species of seedlings, widely scattered in a grassy undergrowth (natural experiment) or densely aggregated (laboratory experiment).

The work was supported by grant 526/09/1436 of the Grant Agency of the Czech Republic.

T11.P3

EXPANSION OF THE CHINESE POND MUSSEL (*ANODONTA WOODIANA*) POPULATION IN POLAND

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Wide-area terrain research done last years in Poland showed that population of Chinese pond mussel *Sinanodonta woodiana* (Lea, 1834) (Bivalvia, Unionidae) rose and is in a good state. The species was already identified in several water reservoirs across Poland. The population bulk and specimens size are different depending on habitat conditions. Sets of *Sinanodonta woodiana* specimens from reservoirs were collected and measured (size, the number of growth rings, shell thickness, weight). On this basis some additional quantities were calculated (age, shape index). These actions allowed to determine some environmental factors that are conductive to the population vitality. The results were confirmed with statistical analyses (e.g. factor analysis, canonical analysis, discriminant analysis) which helped to conclude about colonization progress of this invasive species and its habitat preferences. Using sclerochronological data the survival analysis was also done. Based on the multiple regression it occurred that the number of mussels is depended on longitude and proximity of other greater water reservoirs nearby. Moreover bigger reservoirs determine better conditions to settle. More mussels occurred in the east of the country. The further into south, the more biomass can be obtained. The number of mussels increased if a reservoir was less square in the shape. Older mussels occurred in deeper fish ponds. The less reservoir depth and less sediment thickness, the bigger mussel specimens live in fish ponds. If a reservoir is greater and the number of pond draining is lower, greater mussels can be encountered.

T11.P4

ANODONTA WOODIANA (LEA, 1834) – A REVIEW OF ITS EUROPEAN DISTRIBUTION

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The freshwater mussel *Anodonta woodiana* (Lea, 1834) (Chinese Huge Mussel) is one of the largest invasive Unionid species present in the European Fauna. The species is native to South Eastern Asia, Indochina, China, Korea, Japan, Taiwan and the Amur Basin in Eastern Russia. Zhadin classified the species in the *Anodonta* genus, while Falkner assigned the species to the *Sinanodonta* genus. *A. woodiana* was found for the first time in Europe in Romania in 1979 from fish farms at Cefa-Oradea. Its presence was linked with a 1960 import of Chinese Carp infested with the glochidia of the mussel, from the

Yangtze Stream Basin (China). Other infested fish stocks were brought to Romania at Nucet fish farm, from the Amur River, between 1963 and 1965.

This paper investigates the historic and current biogeographic range of this invasive species based on 50 citations collected from the scientific literature. The mussel was reported from the following European countries: Austria (2011), Belgium (2009), Bulgaria (2006), Croatia (2006), Czech Republic (1997), France (1989), Germany (2011), Greece (2008), Hungary (1984), Italy (1998), Moldova (2011), Poland (1993), Romania (1979), Serbia (2005), Slovakia (1999), Slovenia (2012), Spain (2009), Sweden (2008), The Netherlands (2008) and Ukraine (2005).

A. woodiana invaded European water rapidly with major consequences like competition for food and for host fish species with native mussels.

T11.P5

CORBICULA FLUMINEA INVASION IN LAKE MAGGIORE (ITALY): A THREE-YEAR FIELD MONITORING

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Corbicula fluminea (Müller, 1774) was recorded for the first time in Lake Maggiore in 2010. Recently, possible introduction in the Lake was suggested as coming from a population settled in River Ticino outlet. This study focused on spatial and temporal variations in abundance, biomass and population structure of *C. fluminea* in Lake Maggiore during the period 2010-2013. Clams were quantitatively sampled at four sites (Angera, Arona, Brebbia and Feriolo) located in the Southern part of the littoral area, characterized by diverse type of habitats and different degree of anthropogenic disturbance. Biomass was calculated based on dry weight of subsamples of clams collected at sampling sites. Age of individuals was estimated from shell length. Invasions dynamics was reconstructed from spatial differences in size/age distribution patterns and the contribution of the last recruited cohort to total population density.

The results revealed two main reproductive periods in this environment - spring and autumn. We found also that contribution of young-of-the year individuals was highest in the northernmost site Feriolo. A remarkably higher population density at Angera and Brebbia (with peaks of 1652 ind.m^{-2} in April 2011 and 2800 ind.m^{-2} in March 2012 respectively), together with the contribution of up to three-years-old individuals could stand the so-called “log-phase” (spread of an established population) of the invasion process. On the opposite, the size distribution and density observed at Arona (maximum of 136 ind.m^{-2}) in April 2013 suggested a decline of *Corbicula*. However, the northward spreading of the species was confirmed in summer 2011 when clams were found at a new location on Lombardy shore, thus giving the possibility to study “lag-phase” (initial dispersal and establishment of self-sustaining population) of *C. fluminea* invasion dynamics.

T11.P6

POPULATION GENETICS OF *ANADARA KAGOSHIMENSIS* (TOKUNAGA, 1906) FROM TWO EUROPEAN SEAS

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Anadara kagoshimensis (Tokunaga, 1906) [often locally misidentified as *A. inequivalvis* (Bruguière, 1789)] is an anadarid species originating in the Indo-Pacific region and first found around 1966 in the Adriatic Sea and in 1983 in the Black Sea.

In this study we used DNA microsatellites to analyze its genetic variability at two geographic scales, a small (between two populations at the Romanian Black Sea coast) and a large one (between the Romanian populations and an Italian population in the Adriatic Sea).

The observed genetic diversity was moderate (Jost Dest=0.3) and primarily accounted by the variability between the Black and Adriatic Sea samples. All three populations exhibited a moderate level of inbreeding, as measured by the inbreeding index F_{IS} (0.158-0.251), and a significant deficit of heterozygotes, as also observed in other marine bivalve species. No gene flow was observed between the two seas, and these results are consistent with the hypothesis that the colonization of the Black and Adriatic Seas arose as independent events. As *A. kagoshimensis* exhibits a life cycle with pelagic larvae, the presence of a bi-directional gene flow was tested between the two surveyed Black Sea populations, expecting that the dominant direction of the coastal currents would drive the genetic structuring of the populations. Although the main Black Sea current flows from North to South, direction reversal was reported in various regions of the Romanian coast. In our study, the recent immigration rates estimated using a Bayesian approach identified a significantly higher gene flow from South to North along the western Black Sea coast. Possible causes of the reversal of the main current have been identified as the change in wind speed/direction and the variation in the discharge of the Danube into the Black Sea (which generates a density gradient in the sea).

T11.P7

THE GIANT AFRICAN SNAIL *ACHATINA FULICA* AND ITS ROLE IN THE EPIDEMIOLOGY OF EOSINOPHILIC MENINGITIS IN SOUTH AND SOUHTHEAST BRAZIL

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The metastrongyloid nematode *Angiostrongylus cantonensis* is the most important etiological agent of eosinophilic meningitis in humans. The life cycle occurs among

rodents and many different molluscs acting as intermediate hosts whereas freshwater shrimp, fishes, frogs and flatworms are paratenic hosts, among others. This parasite, widespread in Southeast Asia and some Pacific islands, has now dispersed to other regions, including South America and Brazil. The spread of this emerging zoonosis is correlated with increased tourism, commerce, and the diversification of habits and customs in certain countries, factors that have facilitated the dispersal of the definitive and intermediate hosts of *A. cantonensis.* In addition, the introduction of non-native molluscs plays an important role, as has been observed with the giant African snail, *Achatina fulica*, in Brazil and the South American freshwater snail *Pomacea canaliculata* in China. Brazil is nowadays experiencing the explosive phase of *A. fulica* invasion and we report here the results of the search for specimens of this species infected by *A. cantonensis* from the South and the Southeast regions of Brazil from 2010 to May 2013. South region: infected specimens were found in the municipality of Florianopolis, State of Santa Catarina; as for southeast, there were found in the State of Rio de Janeiro (municipalities of Niterói, Nova Iguaçu, Queimados and Rio de Janeiro) and in the State of São Paulo (municipalities of Jundiaí, Rio Claro and São Paulo). Taking in account the number of infected specimens in addition to huge populations of *A. fulica* in all 26 States of the country, except Rio Grande do Sul, remarks on the role of this species in the transmission of eosinophilic meningitis in Brazil are also presented.

T11.P8

BACKGROUND LEVELS OF MARKERS OF ENERGY RESERVE AND RNA/DNA RATIO OF *CORBICULA FLUMINEA* (MÜLLER, 1774) IN THE RIVER MINHO ESTUARY

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The Asiatic clam *Corbicula fluminea* (Müller, 1774) is a bivalve native to the freshwaters and estuaries of South-East Asia. Outside its natural range *C. fluminea* is considered as an exotic invasive species worldwide. The first records of this species in the River Minho (NW Spain) date back to 1989.

In the last few years, some researchers have begun to use some markers of energetic reserves as a tool for analyzing the effects of different types of stress on organisms and how they affect their populations. In this work we have studied the background levels of proteins, glycogen, and the RNA/DNA ratio of individuals of different ages. These metabolic indices are also used as indicators of the physiological state of the organisms during different reproductive periods and growth, as well as indicators of nutritional status.

The studied specimens were collected in the River Minho estuary during the summer of 2010, at a sampling site located at 21 km from its mouth. In these samples we selected several representative individuals of each cohort. Foot and gills of these individuals were extracted to determine, in each cohort, the background levels of the three selected molecular biomarkers.

We identified nine cohorts, where protein levels ranged from 21.53 ± 5.47 mg/g in the cohort 1 to 45.17 ± 5.62 mg/g in the cohort 8, undergoing a steep increase between cohorts 1 and 2, which is followed by a significant decrease in the cohort 3. In the case of glycogen values ranged from 0.77 ± 0.33 mg/g in the cohort 5 to 9.57 ± 1.60 mg/g in the cohort 6, which is also the steepest increase between cohorts for this biomarker. Finally, values of RNA/DNA ratio ranged from 3.99 ± 0.86 mg/g in the cohort 8 to 10.91 ± 4.95 mg/g in the cohort 5.

Our results show that variations in the markers studied in this population of *C. fluminea* are mainly related to the growth and reproductive cycle of this species.

T12

COLOUR IN MOLLUSCS

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Colour is a fascinating feature in animals. Its functions include concealment, communication and regulation of physiological processes, and it is often linked with specific behaviour. The relative importance of those functions differs among taxa, sexes, and age stages, and the resulting coloration is a compromise among concurrent selective forces. Some really spectacular colour forms can be found in molluscs, from strikingly diverse shell colours in some snail species, through fairytale body colouration in opistobranchs, to cephalopod appearance that can change with a speed unparalleled in the animal kingdom. The purpose of the symposium is to bring together researchers working on mollusc colouration. The leading idea is that studies on colour, so strongly appealing to our aesthetic sense, can also bring answers to central questions in ecology, behavioural and evolutionary biology.

T12.O1

ONE POLYMORPHISM, TWO SPECIES, SEVERAL QUESTIONS: WHAT DOES THE SHELL COLOUR AND BANDING POLYMORPHISM OF *CEPAEA* TELL US?

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The two common *Cepaea* species of western and central Europe share a common shell colour and banding polymorphism and have a similar range of known morphs. They have widely overlapping geographical and habitat ranges. Morph-frequency variation as a response to climatic or predator selection is known in both. Nevertheless, the patterns of variation are very different in each. The historic data from the Evolution Megalab is used to explore these differences across their ranges and to look for interactions in mixed populations. Appearance alone cannot explain these differences, and a combination of population histories and differences in behavioural and physiological properties among the morphs of each species must be involved. In both species, the polymorphism also tells us about the scale and extent of genetic differentiation among populations; the scale can be very small, and this bears on speciation when selection or founder effects are involved.

T12.O2

EVOLUTIONARY IMPACTS OF NON-NATIVE SPECIES: ANTAGONISTIC CHANGES IN COLOUR POLYMORPHISMS OF LAND SNAILS BETWEEN LOCAL POPULATIONS AND METAPOPULATIONS

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Introduced non-native species have posed major threats to the native species in oceanic islands. A number of studies have shown that non-native species have caused serious extinctions of endemic island species. However, less attention has been paid to the evolutionary impacts of non-native species on native species. In the present study, I show that alteration of habitat conditions due to grazing by introduced goats and habitat-dependent impacts from invading malacophagous flatworms have changed the frequency of shell-colour morphs of the land snails *Mandarina chichijimana* within local populations and/or metapopulations in the southern region of Chichijima Island. The frequency of the bright morph significantly increased within local study populations over a 20 year time period. This increased frequency occurred because the island vegetation became degraded and drier due to grazing by introduced goats, and drier habitats are more advantageous for the bright morph than for the dark morph. In contrast, at the metapopulation level, the frequency of the bright morph decreased. This change at the metapopulation level was caused by the selective extinction of local populations. Grazing by the goats affected bush habitats more seriously than forest habitats, resulting in the selective extinction of the bush-inhabiting snail populations that were dominated by the bright morph. However, the frequency of the bright morph at the metapopulation level increased after an invasion of malacophagous flatworms into the study area three years ago. These predators prefer forest habitats, resulting in the selective extinction of the forest-inhabiting snail populations that were dominated by the dark morph. These results suggest that the introduction of non-native species can affect the genetic and phenotypic traits of native species. In addition, the spatial heterogeneity of the landscape and metapopulation dynamics can constrain adaptive evolution to changing environments.

T12.O3

PARALLEL POLYMORPHISM IN SOME SPECIES OF THE FAMILY *BRADYBAENIDAE* IN MOUNTAIN CONDITIONS

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Some species of the *Bradybaenidae* family such as: *Ponsadenia duplocincta*, *Bradybaena phaeozona*, and *Bradybaena plectotropis*, which are widespread in the Tian-Shan Mountains, are marked by bright parallel polymorphism in banding pattern, banding intensity, and shell color. The typical morph was highlighted for all studied species, which is 70-100% in the researched area. For *P.duplocincta* along with polymorphic populations in some parts of the studied area were found monomorphic populations. A correlation was found between the banding pattern, intensity of bands and shell color with habitats. The diversity and morph frequency of all studied species maintain certain stability for the researched years. The heterogeneity of the mountain area, the diversity of micro-climatic conditions create an exceptional diversity of habitats and spotty distribution of biotopes, because of that, there is a uniqueness of each population, but at the same time the similarity of pheneface of each studied canyon was marked. It should be noted the originality of each canyon’s populations, characterized by a certain morph frequency. This indicates, that the adaptive value of studied shell’ traits of the land snails, may be in relationship with the mountain habitat conditions.

T12.O4

COLOR IN CEPHALOPODS: THE PASSING CLOUD DISPLAY

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Cephalopods are noted for their ability to change their external colors. The ancient branch of nautiloids does not change either its body colors or its shell color, although the shell coloration is distinctively individualistic. Members of the other order of Cephalopods (Coleoidea) all can change their body color by use of chromatophores, skin cells that contain various colors that are exposed when the cell is expanded by muscle action. In addition, cephalopod skins contain leucophores, which show white when expanded and iridophores, which reflect blue blue/green coloration. Use of these color cells give the cephalopods a considerable palette to show multiple colors and patterns of colors on their skin which are used for camouflage and signals to other cephalopods and possible predators.

A particularly interesting skin display used by some cephalopods is the Passing Cloud which is a wave or multiple waves of dark flowing across the cephalopods' skin on a pale background. Although the wave appears to move across the skin, there is no movement by the animal other than the opening and closing of its color cells. Thus the wave is effected much like pixels on a computer screen. The Passing Cloud is interesting because we know so little about the context in which it is used and the neurology in which it is achieved. Hence it is interesting from behavioral, physiological, neurological and ecological points of view of which we know little.

T12

T12.O5

SNEAKY SEX IN SYDNEY HARBOUR

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In the world of cuttlefish, its not always brawn over brains that decides who gets the girl. Cuttlefish are known to use their colour change ability in sexually deceptive strategies such as female mimicry. Their unique colour change ability combined with a high level of intelligence allows for deception to be a successful alternate mating strategy. I will present a recently identified form of sexual deception employed by males of the species *Sepia plangon,* the mourning cuttlefish, an endemic Australian species found commonly within Sydney harbour. This behaviour involves the deceptive male splitting the colouration of his body in two halves to allow him to simultaneously court a female and deceive a rival male. The deceptive male divides his colouration along gender lines, showing typical male colouration on one side facing the female, whilst showing typical female colouration on the other side of his body facing a rival male. Within a specific social context this deception occurred 39% of the time. This type of sexual deception could provide insights into how intelligence is shaped by the demands of a complex social life.

T12.O6

MECHANISMS, ULTRASTRUCTURE AND PARTICLE MODELING OF FLASHING IN *CTENOIDES ALES*: “DISCO CLAMS”

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Molluscs showcase a myriad of underwater color patterns and light displays. These displays are most effective in shallow water, as light attenuates rapidly with depth, leaving limited wavelengths available for reflection. The bivalve clam *Ctenoides ale*s resides at depths up to 20m and often in small crevices, where ambient light is dim and wavelength-restricted. Despite this, the species has evolved a reflective mantle edge that emits a remarkably bright light display, leading to the common name, “disco clams”. The display has captured SCUBA divers’ imagination for decades, and is so vivid it was originally confused for bioluminescence. The display is produced through reflection, and a new particle modeling technique demonstrates how incredibly efficient the clams are at reflecting visible light. *C. ales* is the only known bivalve species with a behaviorally controlled photic display, yet virtually nothing was known about its mechanism or function. Research utilizing transmission electron microscopy (TEM) indicated the presence of electron-dense reflective vesicles averaging 0.34μm in diameter on the ventral half of the mantle lip of *C. ales*. The TEM of the congener *C. scaber*, which does not produce a light display, lacked any similar cells. Spectrometry and hyperspectral imaging indicated the reflected light is shifted toward blue wavelengths with a peak around 475-550nm. High-speed video revealed that the mantle edge rapidly furls to expose the reflective tissue, and then unfurls to hide the reflective tissue, producing the flashing phenomenon. Particle modeling based on radii and volume density at 480nm showed that the reflective vesicles are optimally sized and spaced to reflect visible light. The combination of mantle lip movement and precise intracellular structural arrangement of reflective spheres produce the photic display, and are both unique to the species.

T12.P1

HOST PREFERENCE AND COLORATION OF SYMBIOTIC GASTROPODS (EULIMIDAE)

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The family Eulimidae is a diverse group of highly specialised marine gastropods comprising about 1500 recent species which exclusively inhabit echinoderms. The taxonomy and life history of eulimids are poorly studied. There are no complete lists of species, and no data on their preference for different host species for many regions.

As result of previous investigations in Nha Trang Bay (South-China Sea) 17 species of eulimids were found, that doubles number of species recorded in the literature for Vietnamese waters. Formerly 7 eulimid species were recorded for the province of Khanh Hoa, where Nha Trang Bay is located.

The aim of the study was investigation of some aspects of host-symbionts relationships. Different echinoderms species were manually collected in Nha Trang Bay at depths from 0 to 15 m, using SCUBA equipment. Each host individual has been placed in zip-lock bag to avoid loss of symbionts. On the boat, specimens were examined visually to remove all associated symbionts and washed in a 6% magnesium solution. Hosts and symbiont specimens were fixed in ethyl alcohol for further identification, measurement and photography. Alive individuals were photographed under water or in aquaria.

As a result gastropods host preferences were found only for classes and genera levels of the echinoderms.

Most found eulimids had transparent shell and bright colored body. Almost all of them were well-visible on their hosts. They prefer the oral surface of the echinoderms and become less attractive for other marine organisms. In most cases the bright coloration allows to distinguish different species with almost same weak shell morphology. For example, two species from crinoids, *Annulobalcis maculatus* and *Annulobalcis vinarius* can be easily distinguished by the color pattern. However it is still unknown whether the representatives of this family have any evolutionary tendency through mimicry or not.

T12.P2

TRANSCRIPTOMIC PROCESSES LEADING TO ALBINISM AND SHELL COLOR VARIATION IN THE PEARL OYSTER *PINCTADA MARGARITIFERA*

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The pearl oyster *Pinctada margaritifera* is highly exploited in French Polynesia for its natural capacity to produce pearls. Pearls' value varies depending on their color. It is known that the biomineralization processes involved in nacreous shell synthesis are identical to the ones involved in pearl synthesis; therefore we explored the genetic determinism of nacreous shell color variation in the pearl oyster *Pinctada margaritifera*. We identified genes responsible for color synthesis and color variation by carrying out a comparative analysis of the transcriptome between normal (colored) and various types of albino individuals of *Pinctada margaritifera*.

Mantle tissue from normal colored specimen and 2 types of albinos were used to produce subtractive and suppressive hybridization libraries in order to recover over-expressed genes for each phenotype. The libraries generated *c*. 350 unique sequences from which 46 showed, through qPCR analyses, to be actively involved in the activation and inhibition of color synthesis in the nacreous shell. Important intra-phenotype gene expression variation was detected in the normally colored specimens, highlighting the complexity of coloration synthesis in the nacreous layer. Genes known to be involved in shell biomineralization of the aragonite and calcite layers and genes responsible for melanin biosynthesis showed significant gene expression variation among the different shell color phenotypes.

T12.P3

LAND SNAIL IN PAINTING ART

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Land snails are sometimes pictured on old paintings. We attempted at using this information to trace variation in European land snail fauna. Species affiliation and shell colour and banding morph frequency were recorded on panels of 26 painters in 10 public galleries. *Cepaea nemoralis* (L) was pictured on 30 panels of 16 painters showing 41 individuals. Yellow base colour (78% individuals) and 00300 shell banding morph (76%) followed by 12345 morph (17%) dominated the pictured population. There was no difference in proportion of colour (yellow vs. pink) and shell banding (00300 vs. all others) morphs portrayed at panels of three painters who pictured ≥6 individuals (Fisher exact test: P=0.070 – P=0.450). Most panels were painted between 1680-1720 following period of cold climate which might favour pink and 12345 confluent morphs. The role of painters aesthetic preference (for rare morphs) and composition of natural populations in shaping morph proportions of pictured populations could only be speculated. *Cepaea hortensis* (O.F. Müller) was portrayed in 2 panels, always as yellow unbanded morph. At least four other land-snail species (*Arianta arbustorum* (L.), *Fruticicola fruticum* (O.F. Müller), *Helix* sp., *Trichia*? sp.) were portrayed at 6 pictures finished between 1470-1720. Decorative art may provide some information on composition of earlier land snail faunas which is, however, difficult to interpret.

Supported by the Ministry of Agriculture of the Czech Republic, Project No. 0002700604.

T13

THE ROLE OF CEPHALOPODS IN THE WORLD'S OCEANS: A SYMPOSIUM IN HONOR OF MALCOLM CLARKE

(sponsored by Cephalopod International Advisory Council – CIAC)

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Cephalopods are crucial parts of all marine ecosystems, yet we know very little about them. Neritic and commercially important species are best understood, but approximately 45% of all cephalopod species are non-commercially important mesopelagic or bathypelagic species. The open-ocean pelagic environment is the largest and least understood marine biome.

Cephalopods are notoriously difficult to collect. Trawls inevitably damage delicate specimens, and catch rates are low due to net avoidance and patchy distributions. Although often compared to fishes, cephalopods have many features, including a unique morphology and high metabolic rates, which distinguish them from fishes. Many basic questions regarding population sizes, distributions, and reproduction are virtually unknown for the deep-sea cephalopods, but a major source of information comes from their natural predators. Cephalopods play an important role in the diet of whales, seals seabirds, and fishes, but the role of cephalopods as predators has been more difficult to assess.

New techniques such as stable isotope analysis, molecular barcoding, and non-invasive imaging, have the potential to add significant detail to our understanding of how cephalopods function in their environment. The increasing availability of manned and unmanned submersibles with video cameras provide unique insights into how cephalopods occupy their environment.

Malcolm Clarke's seminal work on cephalopod beaks and statoliths, and on the biology and ecology of whales, opened new avenues for research on trophic interactions in marine ecosystems, and highlighted cephalopods central role in all marine ecosystems. He published extensively on oceanic and deep-sea squids, their vertical distributions, their role as prey for marine mammals, and how to improve trawl capture rates. In addition to his research, Malcolm Clarke helped assure the continuation of cephalopod research by mentoring and creating a legacy of cephalopod researchers, and by co-founding the Cephalopod International Advisory Council (CIAC) the only international association of cephalopod researchers.

This cross-disciplinary, CIAC-endorsed symposium will provide a forum for oral and poster presentations focused on the many roles cephalopods play in the marine environment. The session will cover a wide range of topics, including biology, distribution, abundance, diversity, evolution, fisheries and food-web dynamics, honouring Malcolm Clarke´s career.

T13.O1

MALCOLM CLARKE'S LIFE IN SCIENCE

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Malcolm's scientific life started in the era of whaling and ended in the era of whale watching and his science charted this transformation. His career started aboard a pelagic whaling factory ship and it ended with him running his own private whale museum on the Azores. In the course of his research he unravelled many mysteries about the life of sperm whales and especially the squid they feed on. He was one of the most influential marine biologists of the 20th century and was elected to the fellowship of the Royal Society for his exceptional contribution to scientific knowledge. An inspirational figure and a most a generous spirit he was a friend, teacher and a great colleague to many marine scientists worldwide. We will remember him with great fondness.

T13.O2

MALCOLM CLARKE AND CEPHALOPOD BEAKS: THE PAST, PRESENT AND FUTURE IN ASSESSING CEPHALOPODS IN THE DIET OF TOP PREDATORS WORLDWIDE

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Dietary studies on predators are essential to understand the role of cephalopods in the marine ecosystems. Cephalopods in the diet of top predators are still mainly identified by using their chitinized upper and lower beaks, technique highly developed by Malcolm Clarke. In this presentation, we describe the cephalopod diet of key 20 major cephalopod predators worldwide (including wandering albatrosses, sperm whales, lantern sharks and Patagonian toothfish), compare the various methods to assess cephalopods in the diets of predators (i.e. identifying and measuring cephalopod beaks versus using stable isotopes, fatty acids and DNA techniques), evaluate critically whether the number of upper and lower beaks differs in diet samples collected and discuss the potential biases in the estimation of cephalopods in predator diets worldwide. Our results show that the predators that heavily feed on cephalopods (> 60% by mass), clearly feed mostly on species from the families Histioteuthidae, Cranchiidae, Ommastrephidae, Gonatidae and Onychoteuthidae, that the ratio of upper to lower beaks in diet samples from predators varied greatly in a single year, between years, and biases were greater for certain cephalopod species, resulting in an underestimation of their relative importance. Therefore we recommend cephalopod researchers that works on predators diets to: 1) Count both upper and lower beaks (and cite them in their papers), 2) Measure the lower rostral length (LRL) of lower beaks, 3) Assess if the number of upper beaks exceeds the number of lower beaks (always meant by prey species; i.e. identify both upper and lower beaks), and if so, the estimation of biomass should be made by measurements using published LRL/body mass relationships and then extrapolate this with the number of upper beaks and 4) Promote future research focusing on studies that provide

information on Upper Rostral Length (URL)/size and/or URL/body mass relationships of cephalopods. Also, we recommend that the description of new species should also include a good description of the beaks, which will in turn allow a better description of the cephalopod component of the diet of top predators. These recommendations are essential to enable improved information for the assessment and management of cephalopod fisheries from an ecosystem perspective (particularly those cephalopod species that numerous predators feed on) and improve future marine food web models.

T13.O3

THE ROLE OF CEPHALOPODS AROUND SOUTH SANDWICH ISLANDS FROM TOOTHFISH DIETS

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Cephalopods have an important role in the Antarctic food webs, however the knowledge about their ecology is very poor mostly because they are extremely difficult to catch using nets. The Patagonian toothfish, *Dissostichus eleginoides,* and the Antarctic toothfish, *Dissostichus mawsoni,* are two well-known cephalopods predators, which are commercially exploited. The aims of this study were to characterize and compare the cephalopod component of the two *Dissostichus* species around South Sandwich Islands, a poorly known area of the Southern Ocean. Furthermore we assessed if there were differences in the distribution of cephalopods between north/south of the Weddell Front as well as trophic level and the habitat of key cephalopod species by stable isotopes analyses.

Cephalopods occurred in 24% of *D. eleginoides* stomachs and in 77% of *D. mawsoni* stomachs. *Kondakovia longimana* was the most important cephalopod species by number of lower beaks on *D. mawsoni* (122 beaks, 65,2% of lower fresh beaks) and on *D. eleginoides* was once more the most important jointly with *Moroteuthis knipovitchi* (5 beaks each one, 45%). In terms of estimated mass, *K. longimana* was by far the most important squid (96.4% of the cephalopod component on *D. mawsoni* and 89.3% of the cephalopod component on *D. eleginoides).*Therefore, the two toothfish species preyed almost the same species. Despite the clear segregation of the fish species, with *D. eleginoides* being distributed further north, our results suggest that the effect of Weddell front do not affect the distribution of cephalopod species. Comparing the $\delta^{13}C$ signature with other studies confirm that the same cephalopod species can live on waters further south and in sub-Antarctic waters. On the other hand, the $\delta\,^{15}N$ signature shows that the same cephalopod species on different locations have different feeding behaviour, such as *K. longimana*. Our study provides valuable information for the feeding ecology of toothfish in the Antarctic around the South Sandwich Islands as well as the food web structure, and the role of cephalopods, in that area.

T13.O4

WHAT CEPHALOPODS TELL US ABOUT THEIR PREDATORS

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Much information may be gathered about teuthophagous predators by examining their cephalopod prey. In this study, I review food preferences of several Mediterranean predators and discuss what these data reveal about predatory behaviour.

The swordfish, *Xiphias gladius*, prefers muscular, i.e. high energy content, squids in a broad size spectrum. The occurrence of neatly sliced squids in its stomach shows that it uses its sword to kill or maim prey. The predominance of water column dwelling *Todarodes sagittatus* in summer and demersal *Illex coindetii* in winter as prey indicates a seasonal shift in its feeding habits.

The albacore, *Thunnus alalunga*, prey spectrum, viz. *Heteroteuthis dispar*, *T. sagittatus* juveniles, *Histioteuthis* spp. juveniles, suggests they feed in the water column upon small prey.

The blue shark, *Prionace glauca,* is a sluggish predator that prefers juveniles of large cephalopods and large slow swimming cephalopods.

The blackmouth catshark, *Galeus melastomus*, preys upon small cephalopods, biting pieces off the trailing part of their body, which shows its prey pursuing behaviour. Predation occurs both on the bottom and in the water column close to the bottom. Different cephalopods are found in different size catsharks, indicating an ontogenetic shift in diet.

The velvet belly, *Etmopterus spinax*, feeds on both oceanic and demersal small cephalopods seized close to the bottom. Often, pieces bitten off various parts of the prey body (trailing, leading and sides) are found in this sharklet stomach, thus revealing group predation. The digestion stage of prey varies throughout the day, which indicates circadian predatory activity.

Risso's dolphin, *Grampus griseus*, feeds mostly on bioluminescent squids suggesting that it detects its preys by their luminosity.

The loggerhead turtle, *Caretta caretta*, feeds on comparatively slow moving cephalopods, both in shallow coastal waters, on the bottom (*Sepia officinalis*), and in deep offshore waters, in the water column (*Histioteuthis reversa*).

T13.O5

TROPHIC ROLE OF *ILLEX ARGENTINUS* IN THE ECOSYSTEM

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Illex argentinus, as several other ommastrephid squids, has been considered a keystone species in the marine ecosystem of the Southwestern Atlantic Ocean. Several papers have been published describing the prey spectrum of *I. argentinus* through the entire geographical distribution; we reviewed and compared the prey spectrum of *I. argentinus* between different regions using material (stomach samples 2012) and data of identified content (all published papers), determining that *I. argentinus* diet was mainly composed by myctophid fish (34% of the diet). Eight myctophid species were observed as prey items and the presence in the feeding habits of *I. argentinus* changed according to the latitudinal distribution. *Gymnoscopelus* and *Protomyctophum* genus were present in the diet of the southern distribution while *Diaphus* genus in the northern. The presence of amphipods, copepods and euphausiids increased in the southern (39% of the diet). Cephalopods as prey items were preset in the whole area (27%) but they were more important in the northern. In a preliminary Ecopath model developed with these data we observed that *I. argentinus* plays an important role in the ecosystem as a transfer of energy from the lower to higher levels with a trophic level of 3.95 being one of the most important predators of demersal fish, crustaceans and other cephalopods (mainly species of the *Doriteuthis* genus).

T13.O6

LARGE-SCALE NON-INVASIVE SCANNING PERMITS A NOVEL APPROACH TO STUDYING CEPHALOPOD MORPHOLOGY

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The estimated 800 extant cephalopod species are comprised of two distantly related groups, the Nautiloidea and the Coleoidea. Major morphological differences between *Nautilus* and all other extant cephalopods make traditional phylogenetic analyses difficult due to the inability to polarize character states. Higher-level systematics are unstable, with multiple alternate hypotheses proposed. Furthermore, results from molecular and morphological analyses are often contradictory. External anatomy and internal hard parts such as the gladius, cuttlebone, and radula provide reliable characters and landmarks, but there are only a few parts to assess. Soft tissue characters may be affected by collecting damage and distortion due to fixation, while extensive dissection is invasive and may be impractical for rare or otherwise valuable specimens. In order to mitigate some of these problems, we here assess the potential of two non-invasive imaging techniques to reconstruct organ-level anatomy and the relative position of hard and soft tissues within cephalopods. Magnetic resonance imaging (MRI) and micro-computed tomography (μCT) can be employed for complementary whole specimen imaging of soft and hard tissues. These techniques provide rapid access to 3-dimentional (3-D) data on complex anatomical features, allowing for an accelerated comparative analysis across taxa. In addition, new systematic characters may be found,

such as the architecture of the circulatory system or the precise 3-D arrangement of cephalopod brains *in situ*, which are inaccessible with traditional, invasive methods.
The four representative genera *Nautilus*, *Doryteuthis*, *Sepia,* and *Bathypolypus* were scanned using the two imaging modalities. Brain, statocyst, statolith, and cuttlebone morphology are shown to be useful complex character sets, among others. Importantly, type material can be imaged without any negative impact. Our case study shows the potential value of a large-scale scanning effort for cephalopods, and provides the means to reinvigorate comparative cephalopod morphology using 21st century technologies.

T13.O7

IDENTIFICATION OF DEEP-SEA CIRRATE OCTOPOD HATCHLINGS USING HIGH-FIELD MAGNETIC RESONANCE IMAGING

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Dr. Malcolm Clarke's seminal book, "A Handbook for the Identification of Cephalopod Beaks" showed that a complex morphological character could be used to identify cephalopods in stomach contents, and spurred a new generation of ecological research into diets, predator-prey interactions and marine food webs.
In the current study, we use magnetic resonance imaging (MRI) to identify two rare, deep-sea, cirrate octopods hatchlings collected from Kelvin Seamount (New England Seamount Chain), and Goode Seamount (Corner Rise Seamount Chain) in the northwest Atlantic Ocean during the 2005 North Atlantic Stepping Stones cruises. Based on the lack of a secondary web, the U-shape of the internal shell, and the single nerve bundle that passes through the white body the specimens are identified as *Grimpoteuthis* sp. Taxonomic uncertainty within the genus and the absence of species-specific characters in octopod hatchlings prevents species-level identification, but new soft-tissue characters such as the shape of the shell cartilage are proposed for further investigation.
We conclude that wide-spread adoption of MRI technology can reinvigorate comparative morphology, spur new avenues of research in Cephalopod systematics, and provide new data from rare or otherwise precious specimens that may not be available for standard dissection.

T13.O8

IS THE SQUID EMBRYONIC STATOLITH HOLLOW?

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Squid statoliths are paired calcareous concretions essentially composed of calcium carbonate crystallised as aragonite and found inside cranial fluid-filled cavities, the statocysts - the main organ of detection of gravity and movement. Statolith use as an ageing tool was validated in the 1980s, when the daily periodicity of the growth increments was confirmed by chemically marking these structures in animals maintained in aquaria. Although statolith analysis has brought major advances in the knowledge of squid population-dynamics, little is known about the processes involved in statolith's calcification and increment deposition (e.g. during embryogenesis). We collected recently-spawned egg masses of the European squid, *Loligo vulgaris*, and after hatching (at 13-15ºC), statoliths were removed from the paralarvae and preserved at -20ºC. Prior to confocal analysis, statoliths were submitted to Alizarin red S (ARS) staining (5% of ARS in 0.1% KOH) to verify the presence of calcium content. In addition, images from optical microscopy and scanning electron microscopy (SEM) were acquired. The findings obtained by SEM, suggest that the embryonic statolith is hollow in some of the area between the nucleus and the natal ring. ARS stained samples analysed in confocal microscopy, and auto-fluorescence observation, confirmed the previous observation.
This surprising structural feature in the origin of $CaCO_3$ sensorial structures has never been described before and suggests a production, with minimum of material and energy expenditure.

T13.O9

COMPARATIVE MORPHOLOGY OF PARALARVAL BEAKS FROM REPRESENTATIVES OF THREE MAJOR SQUID FAMILIES (CEPHALOPODA: TEUTHOIDEA)

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The morphology and morphometry of beak and arm-crown development of *Chiroteuthis* cf. *veranyi*, *Liocranchia reinhardti*, and *Doryteuthis opalescens* paralarvae were examined. Measurements taken from upper (UJ) and lower (LJ) jaw structures were compared against ML by multiple linear regression to determine relative

influences on growth, and between species by ANOVA to identify differences. Considerable morphological changes were observed at early sizes of *L. reinhardti* and *D. opalescens*. Coloration was observed mostly in these two species. Lateral walls and hood (UJ) and wings and lateral walls (LJ), the most important structures in predicting paralarval size for all species, were more developed in *L. reinhardti*, for which the rostrum (LJ) was also important. Rostrum robustness and strength was higher in *L. reinhardti*, intermediate in *D. opalescens*, and lower in *C.* cf. *veranyi*, hinting at the respective prey type. Teeth (LJ) and slit, characteristics of ancestral cephalopods, were observed, disappearing completely and partially on the largest specimens of *L. reinhardti* and *D. opalescens*, respectively, and remaining in all sizes of *C.* cf. *veranyi*. Our results suggest that their presence in early paralarvae could be an adaptation to facilitate the ingestion of pre-digested flesh, and an indication that ontogeny might be recapitulating ontogeny.

T13.O10

NEW DATA ON SEXUAL DIMORPHISM IN ARMS AND VERTICAL DISTRIBUTION OF *LYCOTEUTHIS LORIGERA* AND *NEMATOLAMPAS REGALIS* (CEPHALOPODA: LYCOTEUTHIDAE)

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Lycoteuthis lorigera and *Nematolampas regalis* are known for their extraordinary extension of arms in mature males: arms II in *L. lorigera* and arms III in *N. regalis*. Photophores exist on the extension of both species. Studies of new material in the Museum of Victoria reveal that arm III of mature males of *L. lorigera* is also extended, although the extension is not as robust as that of arm II. Both arms II and III of mature females are not extended. Studies of the material in the Museum of New Zealand reveal that in mature male *N. regalis*, with the exception of arms III, no other arms are extended. No extension of arms exists in mature females of *N. regalis.* Opening-closing net samplings indicate that in the open water where the water depth is over 1000 m, during the day, the great majority of the population of *L. lorigera* live below 300 m, but none at the bottom, and at night it rises to above 300 m. In the shallower depth where the bottom depth is between 400 and 800 m, the catches of the open midwater trawls also indicate that the animals rise to the upper 300 m at night and the majority of the population live below 300 m during the day. Four bottom trawl catches were made during the daytime at 452-555 m. Bottom trawls did not catch *Lycoteuthis* at night. For *Nematolampas regalis*, in the open water where the bottom is over 1000 m, the majority of the population live in the upper 100 m at night, although some were captured at 400 m. The daytime distribution is unknown.

T13.O11

MALCOLM, MAN OF MEGA MAMMALS AND MONSTROUS MOLLUSKS

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Malcolm was a man in motion. It made no matter whether he was on a whaling ship surrounded with sperm whale guts in search of squids, roofing his house, building a swimming pool with linoleum, or painting a landscape of a near-by scene, Malcolm was active! This tribute talk is a personal remembrance of a long and productive friendship and collaboration.

T13.O12

A MOLECULAR SEARCH FOR THE GIANT SQUID *ARCHITEUTHIS*

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Despite its charismatic appeal to both scientists and the general public, remarkably little is known about the giant squid *Architeuthis*, one of the largest of the invertebrates. Although specimens of *Architeuthis* are becoming more readily available owing to the advancement of deep-sea fishing techniques, considerable controversy exists with regard to topics as varied as their taxonomy, biology and even behaviour. In this study, we have characterized the mitochondrial genome (mitogenome) diversity of 43 Architeuthis samples collected from across the range of the species, in order to use genetic

information to provide new and otherwise difficult to obtain insights into the life of this animal. The results show no detectable phylogenetic structure at the mitochondrial level and, furthermore, that the level of nucleotide diversity is exceptionally low. These observations are consistent with the hypotheses that there is only one global species of giant squid, *Architeuthis dux* (Steenstrup, 1857), and that it is highly vagile, possibly dispersing across oceans through a drifting paralarval stage. Demographic history analyses of the genetic data suggest that there has been a recent population expansion or selective sweep, which may explain the low level of genetic diversity.

T13.O13

LULA 1000 – THE NEW SCIENTIFIC EYE ON THE AZOREAN DEEP SEA

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Here we present current and past work of the Rebikoff-Niggeler Foundation (FRN) a non-profit institution which was established in 1994 on the island of Faial/Azores. The FRN is named after Dimitri and Ada Rebikoff-Niggeler, a Franco-Suisse couple who dedicated their lives to the development of underwater technology. The main objectives of the foundation are to support and assist marine research and marine conservation by providing deep-water diving facilities. Several projects have been carried out over the last years, ranging from bio-erosion studies, habitat mapping of deep water corals, genetic sampling of deep-sea species, to archaeological investigations. Besides the research projects, FRN publishes photos and videos on the marine environment.

The central platform for their work is their manned submarine. In former years with LULA 500 the foundation was able to dive in 500 m depth, but nowadays the new manned submarine LULA 1000 allows to investigate the Azores archipelago in up to 1000 m depth. The large dome in front of the research submersible gives three persons a spectacular view on the sea bed and surrounding waters, resulting in an excellent tool for in situ observations. LULA 1000 is equipped with HD TV cameras, still cameras, a manipulator that permits the collection and storage of objects up to 25 kg, HMI lights for daylight illumination, hydrophones and a CTD sensor for oceanographic data e.g.. This summer, FRN will focus their observation on deep sea cephalopods. We hope to record rare and new images of these animals to help to understand more about their biology. Therefore LULA 1000 will dive in the hunting grounds of sperm whales, which are important predators of deep sea squids, in the south of Pico and Faial.

T13.O14

ANTIOXIDANT DEFENSE AND HYPOXIA TOLERANCE OF JUMBO SQUID (*DOSIDICUS GIGAS*) THRIVING IN OXYGEN MINIMUM ZONES

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Jumbo squid (*Dosidicus gigas*) is a large oceanic squid endemic off the Eastern Tropical Pacific that undertakes diel vertical migrations into mesopelagic oxygen minimum zones (OMZ). One of the expected physiological effects of such migration is the generation of reactive oxygen species (ROS) at the surface, promoted by the transition between hypoxia and reoxygenation states. The aim of this study was to investigate the energy expenditure rates and the antioxidant stress strategies of juvenile *D. gigas* under normoxia and hypoxia, namely by quantifying the: i) oxygen consumption rates, ii) antioxidant enzyme activities , including superoxide dismutase (SOD), catalase (CAT) and glutathione-S-transferase (GST), iii) heat shock protein response (Hsp70/Hsc70), and iv) lipid peroxidation (malondialdehyde levels, MDA).

Metabolic rates of jumbo squids were significantly decreased under hypoxia (70%, $p<0.05$), but, despite reduced energy production, Hsp70/Hsc70 expression was elevated ($p<0.05$), which may be interpreted as a strategy to prevent post-hypoxic oxidative damage during the squid's night upwards migration to the surface ocean. Antioxidant enzyme activities in *D. gigas* were generally low and in the range of other squid species, but MDA concentrations (indicative of cellular damage) did not significantly change between normoxic and hypoxic conditions ($p>0.05$), demonstrating an efficient antioxidant defense system. SOD and CAT activities were enhanced ($p<0.05$) under normoxia that seem to constitute an integrated stress response at shallower depths by buffering increased ROS formation, and, in addition, might even be a strategy to cope with the reoxygenation/recovery process. GST activity was similar between normoxic and hypoxic treatments ($p>0.05$), indicating that antioxidant defense is species and tissue specific. The understanding of the physiological strategies that are linked to oxygen deprivation and reoxygenation (e.g. metabolic suppression and preparation for oxidative stress), may provide valuable information about how this species is quickly responding to the impacts of environmental stressors coupled with global climate change.

T13.O15

UNKNOWN LARGE PELAGIC INCIRRATE OCTOPUS FROM THE SOUTHERN OCEAN

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In December 2013 the UK ChEsSO (Chemosynthetically-driven ecosystems in the Southern Ocean) consortium explored the segment E2 of the East Scotia Ridge in the

Southern Ocean. The cruise JC80 on board of RRS James Cook was equipped with the ROV Isis to study the hydrothermal vents of the East Scotia Ridge. On 9th December the ROV Isis dived to "Dog's Head" vent field (56°05S 30°19W, 2650m). During the decent, Isis had an encounter with a large pelagic incirrate octopus at ~450 m depth. Four long, fringed arms and a bit of mantle appeared on the monitor of the forward looking camera and the arms passed by for several meters before disappearing downwards and the lights of the ROV were switched off. No pelagic octopus of this size is known from the Southern Ocean and the video footage will be shown in the hope that experts in the audience can help in identifying the species further.

T13.O16

IN MEMORY OF A FRIEND, TEACHER AND MENTOR

C.C. Lu

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Malcolm was a wonderful friend, teacher and mentor to multiple generations of marine scientists. In this talk, I remember our work together, the many ways he shaped marine science as well as his generous spirit and great energy.

T13.O17

THE SCIENTIFIC ROLE OF MALCOLM CLARKE IN THE AZORES

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Once one of the best cephalopod and deep diving cetacean experts in the world, Malcolm Roy Clarke (1930-2013), chose Pico Island in the Azores (Portugal) as his last home. But it was not retirement that kept him from working until his last days. We provide an overview of the regional scientific role of Malcolm Clarke by going through its published and unpublished work, teaching and public outreach during his 'Azorean' period, from late 80's onward. Malcolm early collaborations with the recently created Department of Oceanography and Fisheries, from the University of the Azores go back to 1981, working with sperm whales in S. Roque, Pico Island. In the early 90s he bought a house in Pico, settling for good with residency in 2000. In the Azores, Malcolm started a series of dietary studies on top predators such as sperm whales, blue sharks or swordfish. Together with Phil Pascoe, Dorothy Clarke, Helder Silva and Helen Martins, following one of his most famous lines of research, they collected over 50000 squid beaks (mandibles). His presence and work influenced researchers to publish on cephalopods and on the diet of other species such as seabirds, demersal and deep-sea fishes and also on cetaceans. Malcolm other works on cephalopods included taxonomic keys for the Azores, studies on growth, and reviews on the vertical distribution and association to seamounts. He supervised several students during this period and lectured an international course on cephalopod beak identification in Horta, Faial. In the Azores, one of his major achievements was the design and development of a Museum on "Squids and Sperm whales" with his wife at his own house, which opened to the public

in 2003. In 2012 it was acquired by the Regional Government guaranteeing the continuity of Malcolm's passion of revealing the incredible world of squid and deep diving whales. JNGP was supported by the doctoral grant (ref. M3.1.2/F/062/2011) from FRC, the Regional Directorate for Education, Science and Culture of the Regional Government of the Azores.

T13.O18

CLIMATE CHANGE IMPACTS ON COASTAL CEPHALOPODS DIVERSITY

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Climate change scenarios have predicted an average sea surface temperature (SST) rise of 1–6 °C by 2100 and species are expected to respond to this warming by shifting their latitudinal range and depth. Coastal marine systems are among the most threatened by climate change and ocean warming is expected to negatively impact their survival. Species distribution models (SDM) have been broadly used to access the impacts of climate change on biodiversity patterns. In this study, we explore the potential impact of climate change on the composition of coastal cephalopods, at a global scale. Using an ensemble forecast approach, we used SDM´s to project the potential distribution of 156 cephalopods species by 2050, under the Intergovernmental Panel for Climate Change (IPPC) A1B scenario implemented with the ocean circulation model ECHAM5/MPI-OM. We then aggregated geographically the species-level projections to analyze the projected changes in species richness and composition. Our results show that projected changes in assemblage composition are caused by different processes (species replacement vs. nestedness) in several areas of the world. We also investigated the change in body-size distributions at grid-cell scale for present-day and future time periods. Finally we discuss the ecosystem impacts potentially induced by climatic change during this century and the global patterns of such impacts.

T13.O19

DISTRIBUTION PATTERNS SHORTFIN SQUIDS (CEPHALOPODA: OMMASTREPHIDAE) IN THE PORTUGUESE NORTHWEST COAST

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The shortfin squids *Illex coindetii*, *Todaropsis eblanae* and *Todarodes sagittatus* are the most common ommastrephid species in Portuguese waters. They are demersal, neritic and oceanic squids, caught near the bottom during the day on the continental shelf and slope of the Atlantic Ocean. The ommastrephids occupy an important position in the marine foodweb feeding on a wide range of meso and epi-pelagic fish species and are a key prey for swordfish, sharks, tunas, cetaceans and marine birds. As fisheries resources, ommastrephids are by-catch reported together in the official Portuguese statistics and the specific composition of the total landings is unknown. This study aims firstly to assess the proportion of each species in the northwest coast landings, and then based in geo-referenced fishery-independent data, trawl discards data and biological data to identify geographical and seasonal abundance and distribution patterns of each species. In the period between January 2002 and December 2008, both landings and abundance of these ommastrephids decreased, particularly in period between January 2006 and December 2008. Trawling discards data show that the species most discarded is *I. coindetti,* probably due to its low commercial value. Landings showed a seasonal pattern, with peaks in early spring and autumn. Landings of *I. coindetii* and *T. sagittatus* were higher in early spring and autumn/winter, respectively and low during the rest of the year. The only permanently commercially landed short fin squid in the Portuguese coastal region is *T. Eblanae* whereas the other two species are seasonal components of the fishery. The *I. coindetti* and *T.eblanae* are sympatric species in relation to habitat, although with different biological cycles: while *T. eblanae* is equally frequent all year around, *I.coindetii* seasonally migrates from higher latitudes in winter to south during summer and autumn. *Todarodes sagittatus* does not complete the whole life cycle in coastal Portuguese waters, migrating initially onto the slope and subsequently inshore to the shelf trawling grounds, being more frequent in the autumn near the slope.

T13.O20

DISTRIBUTION OF CEPHALOPOD PARALARVAE IN TWO CONTRASTING SITES OF THE IBERIAN–CANARY CURRENT EASTERN BOUNDARY UPWELLING SYSTEM: CAPE SILLEIRO (42ºN) AND CAPE GHIR (30ºN)

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This work was made under the framework of the multidisciplinary project "**Ca**naries–**Ib**erian Marine Ecosystem **Ex**changes (CAIBEX)", to define and compare the cephalopod assemblage in relation with mesoscale dynamics between the coastal-shelf areas and the adjacent ocean. Lagrangian experiments were carried out to track upwelled water masses with a drifting buoy in the seasonal upwelling system off Cape Silleiro (41-43ºN, CAIBEX-I) and the quasi-permanent upwelling system off Cape Ghir (30-32ºN, CAIBEX-III). Day and night mesozooplankton samples were collected near to the drifting buoy at 5, 100 and 500 m depth with bongo nets.

Genetic barcoding allowed the identification of eight species belonging to four cephalopod families (98 octopodids, 16 loliginids, 15 ommastrephids and 4 sepiolids) in CAIBEX-I, mainly over the shelf of the coast of Spain and Portugal. Contrarily, up to twenty cephalopod species belonging to twelve families were found in CAIBEX-III off the coast of Morocco, including the neritic families found in CAIBEX-I (115 loliginids, 35 octopodids, 10 sepiolids and 4 ommastrephids), plus oceanic mid-water families

(21 onychoteuthids, 18 brachioteuthids, 14 pyroteuthids, 13 undefined oegopsids, 11 enoploteuthids, 3 cranchids and 1 mastigoteuthid).

Neritic species were found exclusively over the shelf, while oceanic species were present over the slope. The only exception was *Octopus vulgaris*, found at both domains, increasing in size towards the ocean. These results evidence that *O. vulgaris* accomplish its planktonic stage in the ocean, coupling their vertical distribution with off-shelf physical forcings.

Barcode identifications allowed increasing the distribution area of three sepiolid species to the south as well as identifying the smallest early stages of *Ancistroteuthis lichtensteinii* in the Atlantic. Furthermore, all the confusing loliginid paralarvae were identified to species level revealing the importance of *Alloteuthis media* (n=111) and *A. subulata* (n=18) in both surveys, while *Loligo vulgaris* (n=2) was found only off NW Iberian Peninsula.

T13.O21

CEPHALOPODS AS VECTORS OF HARMFUL ALGAL BLOOM TOXINS IN MARINE FOOD WEBS

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Here we summarize the current knowledge on the transfer and accumulation of harmful algal bloom (HAB)-related toxins in cephalopods (octopods, cuttlefishes and squids). These mollusks have been reported to accumulate several HAB-toxins, namely domoic acid (DA, and its isomers), saxitoxin (and its derivatives) and palytoxin and, therefore, act as HAB-toxin vectors in marine food webs through predator/prey interactions. The common octopus (*Octopus vulgaris*) and the common cuttlefish (*Sepia officinalis*) have been found to accumulate and store considerably high levels of DA (amnesic shellfish toxin) in several tissues. The highest values are usually observed in the digestive gland (DG) – the primary site of digestive absorption and intracellular digestion. The available information on the accumulation and tissue distribution of DA in squids (e.g. stranded *Dosidicus gigas*) is scarcer than in other groups. Regarding paralytic shellfish toxins (PSTs) in *O. vulgaris*, PSTs accumulate to the greatest extent in DG > kidneys > stomach > branchial hearts > gills. Analyses undertaken in *D. gigas* also revealed a wide range of PST levels in both stomach and DG. Unlike *O. vulgaris* and *D. gigas*, which accumulate PSTs in their viscera, and have a more diverse toxin profile, the Australian *Octopus* (*Abdopus*) *sp.5* accumulates and retains STX in the arms, with no levels ofother derivatives being found in the arms. Palytoxins are among the most toxic molecules identified and stranded octopods in Italy revealed high contamination levels of these compounds, with ovatoxin (a palytoxin analogue) reaching 971 μg kg^{-1} and palytoxin reaching 115 μg kg^{-1} (the regulatory limit for PlTXs is 30 μg kg^{-1} in shellfish). Although the impacts of HAB-toxins in cephalopod physiology are not as well understood as in fish species, similar effects are expected since they possess a complex nervous system and highly developed brain comparable to that of the vertebrates.

T13.O22

WHO KNOWS, ONLY THE HOST KNOWS; SEPIOLID SQUIDS AS EVOLUTIONARY DRIVERS OF BACTERIAL SPECIFICITY IN AN ENVIRONMENTALLY TRANSMITTED SYMBIOSIS

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The beneficial association between sepiolid squids (Cephalopoda: Sepiolidae) and their bioluminescent bacterial partners has been a unique model for understanding how animal hosts can select for a particular bacterial symbiont among the vast array of microbes in the ocean. Squids in the genus *Euprymna* are found primarily in the Indo-west Pacific and are allopatric, whereas their *Vibrio* bacteria are cosmopolitan and can be found throughout the world's oceans. Despite their distribution, marine Vibrios are highly specific for their *Euprymna* hosts, yet the evolution of this specificity has yet to be resolved. By using a natural recombinant homologous cloning method termed gap repair, we manipulated three main symbiotic operons (*lux*- bioluminescence, *msh*- mannose sensitive hemagglutinin (recognition), and *pil*- pili for attachment) from different *Vibrio fischeri* strains isolated from two geographically distinct squid host species (*E. tasmanica*- Australia and *E. scolopes*- Hawaii) to determine if these genes are responsible for the specificity observed among closely related host/symbiont pairs. Through colonization studies performed in naïve squid hatchlings from both host species, we found that all loci examined are important for specificity and host recognition in both *E. tasmanica* and *E. scolopes*. Interestingly, competitive ability of these symbiotic loci depended on the locus tested and the specific squid species in which colonization was measured, since both *Euprymna* species did not favor the mutated native *V. fischeri* equally. Our results demonstrate that not only multiple bacterial genetic elements determine *V. fischeri* strain specificity between two closely related squid hosts, but also host environment has an important role in shaping a successful association.

Deciphering how the evolutionary history of specificity between closely related sepiolid squids occurred may give insight to the function of competence and inter-strain genetic specificity in this dynamic beneficial symbiosis.

T13.O23

ARM AUTOTOMY IN OCTOPUS *ABDOPUS ACULEATUS* ON MACTAN ISLAND, PHILIPPINES

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Animals have evolved a diverse set of defense mechanisms including cryptic and startling displays, flight response, and inking to escape their predators. Arguably one of the most extreme tactics is autotomy, the voluntary shedding of a limb or body part. This behavior is immediately beneficial in the escape and survival of the organism from its predator. However, it simultaneously incurs long-term costs to activities where the

lost limb plays a vital role, such as locomotion. A taxonomically diverse set of organisms exhibits this ability, but is studied almost exclusively in jointed animals like reptiles, echinoderms, and crustaceans. Little is known about how this defense mechanism compares in soft bodied animals like molluscs.

A few species of octopus have anecdotally been reported to exhibit arm autotomy. We studied one species, *Abdopus aculeatus* that is abundant in the field and frequently losses and regenerates arms. Surveys were conducted in July 2011 and April 2013 on Mactan Island, Philippines to compare frequency of autotomy between sites and between seasons. General habitat descriptions and distribution of dens were recorded to determine what ecological pressures may be responsible for the observed frequency of arm loss. Behavioral experiments and observations were also conducted in a controlled laboratory environment to determine what predators are likely inducing arm autotomy and whether the autotomized limb distracts the predator from pursuing the octopus. Trigger fish were the primary predators nipping at octopus arms and consuming the autotomized limb. A high degree of autotomy was also sustained from fishermen during collections. This information will give us a better understanding about the factors involved in autotomy of soft bodied animals.

T13.O24

SQUID FLY IN A 15M DIAMETER TANK - AGAIN!

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In 1975 we brought *Illex illecebrosus* into Dalhousie University's 15m diameter Pool Tank for the first time, and the first night some of them flew out and killed themselves by landing on the surrounding deck. We discovered that leaving a single small "moon" light on stopped them from flying. This year we hope to bring them back again and film them flying under infrared as part of our new study of squid flight. Many squid do fly, and glide at least 50m at a stretch, as hard as some may find that to believe! This project will be part of the Ocean Tracking Network, which has lines of ultrasonic receivers around the world. We will put acoustic tags on squid to track them as they cross the 200km Halifax Line and many receiver lines along the US coast as they swim south to lay eggs in the Gulf Stream to complete their life cycle. It may even be possible to document how much time they spend flying in the wild by attaching GPS satellite tags that monitor when and how far they travel in the air. We are betting they fly at night, especially when there is no moon, but only tags can answer that question for sure! We may even be able to tag squid with radioisotopes as the Australians have done to follow multiple generations as juvenile squid return from the Gulf Stream to coastal waters. We hope that this study will provide accurate information on the location of the winter spawning ground, migration patterns between northern and southern stock components, the autumn spawning migration route, and what fraction of the stock inhabits waters beyond the continental shelf. This information is critical for fisheries management of *Illex* stocks.

T13.O25

CEPHALOPODS IN THE FOOD AND FEEDING NETWORK OF MARINE LIFE. LEGACY OF MALCOLM CLARKE

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Cephalopods were regarded as important in known marine environments by researchers of old (Aristoteles) and new (Clarke). To determine this importance is difficult, however. It is attempted here using species numbers and abundance (highest instantaneous biomass and yearly average production). Generalization level for the group stands now at 7% (in species numbers, 48 species for which good data exist, 700 total number of species), 30% (in highest instantaneous biomass) and 10% (in yearly average production). Predators of cephalopods belong to the following Classes (only marine species): Cephalopoda (700 species, 35 mln t biomass, 100 mln t production, opportunistic and specialized feeders), Chondrichthyes (250 species, opportunistic feeders), Osteichthyes (16000 species, opportunistic feeders), Reptilia (100 species, opportunistic feeders), Aves (500 species, opportunistic feeders) and Mammalia (100 species, opportunistic feeders). Therefore, 700 species of Cephalopoda are against 17000 species or so, and their moderate biomass of 35 mln t is against of some most successful species on Earth including man (such as marine birds and mammals). Predatory pressure upon cephalopods then is enormous. However, most of these links are of open opportunistic-opportunistic type which always gives chance of recovery because predation switches off on much higher level of abundance of prey than that of the specialists. Cephalopods are efficient as predators, catching mainly crustaceans (15000 species), fishes (16000 species) and cephalopods (700 species). This efficiency was quantified for the Benguela Ecosystem, with the modelling effort showing relative importance of fish and cephalopods. Biomass and even more production of marine crustaceans is enormous, and can easily sustain cephalopod survival. In addition, predation of cephalopods upon crustaceans is mostly one-way, whilst links to fishes consist of multiple loops. Physiological, life-cycle and behavioural advantages also have a role, especially when comparing energetic costs, learning abilities and survival proportions between larval & juvenile stages and adults.

T13.P1

ASSEMBLING THE GENOME OF THE GIANT SQUID, *ARCHITEUTHIS DUX*

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The giant squid *Architeuthis dux* belongs to the oceanic squids suborder Oegopsina. Among cephalopods, the Oegopsina dominate the pelagic, open ocean environment. Diversity at the family and generic levels is relatively high with 24 families and 69 genera described so far. They are characterized by rapid growth, short life spans, early maturity and rapid population turnover. Squid play an important role in oceanic ecosystems, both as predators and prey for other animals, such as fish, birds and cetaceans.

Little is known about *Architeuthis* species. There appears to be certain hotspots of *Architeuthis* findings, especially around Newfoundland, the Bay of Biscay in the NE Atlantic, South Africa, South Australia and New Zealand. A total length of 15m for females and 10m for males is accepted as a reasonable estimate, based on documented measurement of individuals by scientists.

We have extracted DNA from an *Architeuthis dux* specimen and the assembly is being done by combining sequencing data from Illumina (paired-end libraries and Moleculo reads) and 454 technologies. Complementarily, we are sequencing the transcriptome of ten other oegopsin species that will be used for genome annotation. The comparative analysis between oegopids will allow us to gain some insight into the evolution of this fascinating group.

T13.P2

TEMPORAL AND SPATIAL DISTRIBUTION OF CEPHALOPOD PARALARVAE MEASURED WITH DIFFERENT SAMPLING GEARS AND SAMPLING STRATEGIES

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The abundance of the main cephalopod paralarvae present in the Ría of Vigo (NW Spain) was compared using different sampling gears and experimental designs. Oceanographic cruises were undertaken at night during summer and early autumn in 2008, 2009, 2010 and 2012. Sampling strategy consisted on four parallel transects following a bathymetric gradient (40, 60, 80, 110 m). Within surveys carried out in 2008 and 2009 two samples per transect were collected with a bongo net: one at the surface (0-5 m), and a double oblique trawl for the water column. A multinet trawl gear was used in 2010 and 2012, following different experimental designs: samples were taken close to the bottom and at the surface of each transect in 2010, while a stratified sampling strategy was implemented from the bottom to the surface in 2012.

Our results showed that comparing both sampling gears, bongo sampling overestimated the abundance of the paralarvae found at the bottom layer (80% for *Octopus vulgaris*, 48% for sepiolids and 32% loliginids), because most of the animals were collected through the water column as the bongo went down or ascended from the bottom. Furthermore, bongo column samples collected less cephalopod paralarvae than multinet (almost 31-fold for *O. vulgaris*, 9-fold for loliginids and 14-fold for sepiolids), given that it spent less time filtering water at a given depth.

Comparison between multinet sampling strategies showed that if only surface and bottom waters are sampled great part of the abundance is underestimated (17-fold *O. vulgaris*, 8-fold Loliginids, 6-fold sepiolids and 3-fold ommastrephids), because most of the paralarvae were in the column

Apart from environmental conditions that may mask the abundance, the stratified sampling strategy with the multinet is the most accurate gear, giving the best vertical resolution, avoiding underestimations.

T13.P3

THE RARE BECOMES USUAL: NEW OCCURRENCES OF BIFLAGELLATE SPERMATOZOA IN CEPHALOPODA

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Ultrastructural studies of cephalopod sperm morphology have shown that spermatozoa can be considered important characters for phylogenetic studies. It was largely predicted that the cephalopod spermatozoon possesses the well-known disposition of acrosome, nucleus and flagellum. Whereas there are a wide range of acrosomal and nuclear morphologies, the flagellum is much simpler with the 9 + 2 uniflagellar axoneme. Recently were found three sepiolid squid species (*Sepiola atlantica*, *Euprymna scolopes*, and *Euprymna tasmanica*) that possess biflagellate spermatozoa. The aim of this work is to add new occurrence of biflagellate spermatozoa in Cephalopoda. We had collected the species *Rondeletiola minor* and *Sepietta neglecta* by bottom trawling over the fisheries bank "A Selva" (NW Atlantic). Electron microscopy techniques allowed spermatozoa ultrastructure analysis of *R. minor* and *S. neglecta*. Both of them show the same morphological structure, possessing biflagellate mature spermatozoa exhibiting the typical axonema 9+2, with no acrosomal gland. This observation is in agreement with the morphology found in *S. atlantica*, *E. scolopes* and, *E. tasmanica*, but contrasts with other known cephalopod species with uniflagellate spermatozoa, which possess the acrosomal gland, including other sepiolid squid species. The spermatozoa found here possess two triplet centrioles positioned within the nuclear invagination where each flagellum originates: each is harnessed to the plasma membrane by a membrane skirt. Microtubules are arranged parallel to the sperm longitudinal axis. The ultrastructure appears intermediate between the primitive Nautiloidea sperm type and modern

Coleoidea. This observation implies multiple independent evolutionary events of both biflagellate and uniflagellate sperm. Thus, sperm morphology seems more related to fertilization adaptation than phylogeny.

T13.P4

MOLECULAR SYSTEMATICS AND ECOLOGY OF *GRANELEDONE* (FAMILY MEGALELEDONIDAE) AND OTHER DEEP-WATER OCTOPUSES

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We present molecular data investigating the phylogenetic relationships of *Graneledone*, *Tetracheledone*, *Vosseledone* and *Praealtus*. Using five mitochondrial and three nuclear genes, we show that *Tetracheledone* and *Praealtus* are junior synonyms of *Graneledone*. A short region of the mitochondrial 12S gene was sequenced from *Vosseledone* and, based on the limited available sequence data, it seems that this genus is also a junior synonym of *Graneledone.* Additionally we present DNA barcode data from a 654 base pair region of mitochondrial cytochrome oxidase subunit 1 (COI) from nearly 100 individuals of *Graneledone*, *Thaumeledone*, *Megaleledone* and *Velodona*. These reveal undescribed species of *Thaumeledone*. Additionally a statistical parsimony analysis places *Graneledone verrucosa*, *G. pacifica*, *G. boreopacifica* and *Praealtus paralbida* as well as specimens of *Graneledone* from the Falkland Islands and South Georgia (previously identified as *Graneledone* sp.) in a single haplotype network, suggesting more detailed investigations of relationships among these putative species are required. Our data confirm the circumantarctic distribution of *Megaleledone setebos.*

T14

TAXONOMY AND ECOLOGY OF FRESHWATER MOLLUSKS IN THE MOLECULAR AGE

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The recent triumph of molecular methods in phylogenetics and ecological studies has influenced greatly virtually all spheres of zoological expertise. Using of diverse molecular tools has became standard for malacology, too. Over a long period, the freshwater mollusks taxonomy was based almost exclusively upon macromorphological traits including characters of shell, radula, genitals and so on. Now it is a time to discuss how deeply the classical approaches were changed since the ‘molecular revolution’ in taxonomy has started. Is there a possibilty to create ‘integrative’ systems of largest taxa of freshwater mollusks (Unionidae, Sphaeriidae, Viviparidae, Lymnaeidae, Planorbidae) to stop endless discussions on species concepts for freshwater snails and bivalves? What are the consequences of such molecularization for the classification of the taxa above species level? Are there ‘cryptic’ molecular species among freshwater mollusks? Another important sphere of investigation is so called ‘molecular ecology’. There are many ways of application of molecular tools to molluscan ecology and it is interesting to see how much progress has been made in our understanding of population structure of freshwater mollusks, their migration and invasions, biotic interactions and so on.

T14.O1

CUTTING THE GORDIAN KNOT OF NOMENCLATURE – HOW TO DEAL WITH OLD NAMES?

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Species delimitations are genuine scientific hypotheses, which nowadays can and should be improved by considering a maximum of data field in the sense of an “integrative taxonomy”. Accordingly, species delimitations are no sacred actions but represent regular scientific work. On the one hand they should be cited as such like all other scientific hypotheses. On the other hand, however, there is no scientific need of special protection of insufficient or even erroneous hypotheses.

Whereas the methodology of analyses has been substantially improved during the last years, the nomenclatorical (“naming”) aspects usually are entirely ignored in respective examples. Typically, after inferring cryptic species, authors are faced with a large number of old names in the literature, often severely insufficiently described and coupled with incomplete or even unknown or lacking type specimens. The freshwater gastropod family Valvatidae serves as an example for these conditions including about 60 valid species but over 200 named extant taxa. Possible solutions with accompanied problems are presented and discussed: (1) Classic, detailed historical analyses including literature and type studies of all old names will cause a delay in research for years and - more problematic - usually are not conclusive. (2) Applications of pure MOTU numbers are difficult to compare worldwide and will cause taxonomic chaos in the future. (3) Drastic reduction of available taxa due to insufficient description will need many decisions of the Nomenclature Commission, again is very time-consuming, and will blame the old authorities. (4) Ad hoc erection of new species names causes the danger of producing synonyms.

In conclusion specimens from type localities should be incorporated as far as possible to clear up the original name among species clades. Concerning old, possible synonyms new names are considered as the best available solution under the given circumstances.

T14.O2

FRESHWATER MOLLUSCS FROM THE SÃO FRANCISCO RIVER BASIN, NORTHEAST OF BRAZIL

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The construction of water infrastructure projects usually causes changes in the fauna composition and in the surrounding area. The governmental Project "Integração do Rio São Francisco" is one of the most important public policy on water resources nowadays, aiming to guarantee water supply for socio-economic development of the States more vulnerable to dry in the Northeast of Brazil. In order to investigate the occurrence of freshwater molluscs and search for *Biomphalaria* specimens infected by *Schistosoma mansoni* Sambon, 1907 in that region, a malacological survey was carried out between 2010 - 2012 in 25 municipalities from five States (Bahia, Ceará, Paraíba, Rio Grande do Norte and Pernambuco): Angicos, Aparecida, Açu, Bonito de Santa Fé, Cabrobó, Caicó, Cajazeiras, Ipueiras, Itajá, Jardim de Piranhas, Juazeiro, Jucurutu, Mauriti, Monte Horebe, Orocó, Paulista, Pena Forte, Pombal, Salgueiro, São Bento, São Fernando, São Rafael, Sobradinho, Sousa and Terra Nova. A total of 101 sites were sampled and the specimens of each sample were preserved in Railliet-Henry's fluid after relaxation in a 0,1% hypnol solution. The following species were identified: *Asolene meta* (Ihering, 1915), *Biomphalaria schrammi* (Crosse, 1864), *Biomphalaria straminea* (Dunker, 1848), *Corbicula fluminea* (Müller, 1774), *Corbicula largillierti* (Philippi, 1844), *Drepanotrema anatinum* (d'Orbigny, 1835), *Drepanotrema cimex* (Moricand, 1839), *Drepanotrema depressissimum* (Moricand, 1839), *Drepanotrema lucidum* (Pfeiffer, 1839), *Melanoides tuberculatus* (Müller, 1774), *Physa acuta* Draparnaud, 1805, *Physa marmorata* Guilding, 1828, *Plesiophysa guadeloupensis* (Fischer in Mazé, 1883) and *Pomacea figulina* (Spix in Wagner, 1827). *Anodontites* sp., *Diplodon* sp., *Eupera* sp., *Gundlachia* sp., *Hebetancylus* sp., *Heleobia* sp. and *Pomacea* sp. were also obtained. No *B. straminea* specimen was found infected by *S. mansoni*. The present study extended the geographical distribution of the natural vector of schistosomiasis in Brazil, *B. straminea*, as well as the exotic species *M. tuberculatus* and *P. acuta*.

T14.O3

NEW IDEAS ON CHARACTER EVOLUTION IN THE UNIONIDA

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Confusion resulting from different analyses of the higher level Unionida bivalve phylogenesis has impeded attempts to understand evolution within the group and to establish a stable, phylogenetic classification system. Previous and often conflicting estimates of Unionida phylogeny, especially those dealing with interfamilial relationships, stem principally from an insufficient amount of data. For example, the two largest published analyses of Unionida phylogeny both utilized a total of only 1,182 characters. An additional source of data is the comparison of the male and female mitochondrial DNA which are reciprocally monophyletic. Doubly Uniparental Inheritance (DUI) of male and female mitochondrial DNA analyses in Unionida support a long history, over 200 million years and document the long stability of the clade, lacking the masculinization characteristic of Mytilidae. Family level monophyly is supported for Hyriidae, Margaritiferidae and Unionidae but current family level separation within the Etherioidea is not supported. Etherioidea lack any evidence for DUI. Recently published subordinal nomenclature proposed by Hoeh and co-authors (Unionoina and Hyrioina) rejects the traditional, two superfamily nomenclature (Unionoidea & Etherioidea) as proposed by Parodiz and Bonetto. A new dataset consisting of data from seven genes [four mtDNA and three nDNA genes (5243 bp)] and 44 morphological and anatomical characters was analyzed. New phylogenetic analyses indicate that hyriids, rather than margaritiferids, are a product of the basal cladogenic event in the ancestral Unionida lineage. Three separate cemented unionoid lineages exist: *Pseudomulleria*, is confirmed as a member of the Unionidae, *Acostaea* is a Mycetopodidae and *Etheria* is separate. Current analyses strongly support (1) the glochidium as the ancestral Unionida larval type, (2) cementation having evolved independently at least three times within Unionida bivalves and (3) doubly uniparental inheritance of mtDNA (DUI) having been lost in the ancestral etherioid lineage.

T14.O4

INCONGRUENCE BETWEEN MTDNA AND NUCLEAR DATA IN THE FRESHWATER MUSSEL GENUS *CYPROGENIA* (BIVALVIA: UNIONIDAE)

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Identifying appropriate taxonomic or evolutionarily significant units is a challenging but crucial step for developing conservation strategies for freshwater mussels, the most endangered fauna in North America. Recent studies have shown that mussel

species designated by morphological characters alone are not always congruent with evolutionary lineages identified using molecular markers. For example, under recent taxonomy *Cyprogenia* specimens found west of the Mississippi River have been ascribed to *Cyprogenia aberti* (Conrad 1850), and specimens found east of the Mississippi River have been identified as *Cyprogenia stegaria* (Rafinesque 1820), although shells morphologically resembling both species have been found to co-occur in some states. Previous molecular studies using mitochondrial DNA sequences indicated that both *C. aberti* and *C. stegaria* are not reciprocally monophyletic group, suggesting that the genus *Cyprogenia* is in need of a major systematic revision. This study focuses on using mitochondrial and microsatellite data to review the delineation of the two *Cyprogenia* species. We collected 132 *C. aberti* and 47 *C. stegaria* from four states surrounding the Mississippi river. A region of the mitochondrial ND1 gene was sequenced to examine range-wide genetic variation for these cryptic species. We also used 9 microsatellite markers to estimate genetic structure and gene flow among populations. Bayesian analysis based on the ND1 sequences identifies two deeply divergent clades that differ by 15.9%. Individuals represented by these two mtDNA clades occur sympatrically in most of our sampling locations. In contrast, analysis of microsatellite genotypes supports recognition of three allopatric clusters that reflect the pattern of major hydrologic basins seen in other aquatic organisms. The observed incongruence between mtDNA and microsatellite data may be explained by several factors including incomplete lineage sorting or ancestral hybridization. These results highlight the potential problems of relying on a single locus marker such as mitochondrial genes for delineating species.

T13.O5

GENETIC VARIATION, POPULATION STRUCTURE, AND PATTERNS OF POST-GLACIAL COLONIZATION FOR UNIONIDAE IN THE NORTH AMERICAN GREAT LAKES

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Declines in North American unionid mussel populations have left 70% of species vulnerable to extinction. Continuous population declines as a result of pollution, habitat degradation, and invasive species in the last century have resulted in a dire need for conservation actions; however, a good understanding of patterns in genetic population structure often inhibits conservation strategies and management. The geologically young (ca. 15,000 y.o.) Laurentian Great Lakes are the largest freshwater system in the world and habitat for 47 of the ~300 species of North American unionids. Some important hypothesized routes of entry for aquatic organisms into Great Lakes at the end of the Wisconsin glaciation include: (1) the Wabash-Maumee spillway and the Chicago-Illinois River spillway connecting early lakes Erie and Michigan, respectively, to the Mississippi River watershed and (2) a connection between early Lake Ontario and the Mohawk River draining to Hudson River and the Atlantic Ocean. We have tested these hypotheses and compared the post-glacial origins of five freshwater mussel species in the Great Lakes basin (*Quadrula quadrula, Lampsilis cardium*, *Lasmigona costata*, *Venustaconcha ellipsiformis*, and *Ligumia nasuta*). Nuclear microsatellite DNA markers were genotyped or fragments of mitochondrial DNA were sequenced to analyze the genetic diversity and structure of these unionids in the Great Lakes and beyond. Patterns of genetic diversity and population structure were interpreted with respect to routes of post-glacial colonization. Our findings indicate that the pattern of post-glacial colonization varies among species with some entering via some species showing evidence of entry via single routes (*Q. quadrula*, *V. ellipsiformis*, and *L. nasuta*) and others showing patterns consistent with entry via multiple routes (*L. cardium* and *L. costata*). Understanding these patterns for unionids in the Great Lakes will help formulate evolutionarily sound management guidelines and provide insight for augmenting and re-establishing populations of species of conservation concern.

T14.O6

DO CONSERVATION EFFORTS REALLY TARGET THE MOST VULNERABLE TAXA? A VIEW FROM EUROPE

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Nonmarine molluscs are amongst the most imperiled animals. When it comes to invertebrates, conservation efforts revolve a handful of species, which are promoted as being keystone, flagship or umbrella species. How successful has this strategy been to conserve the freshwater mollusks of Europe?

Two species guilds stand out as the most vulnerable: unionoid bivalves, because of their complex life cycle and high sensitivity to water quality; and hydrobioid snails, because of their restricted ranges and stenoecious ecology.

France is home to eleven Unionoid species, three of them being listed in the European Habitat and Species Directive and protected by the French law. Two of them are widespread European species. Amongst the 191 French hydrobioids, 117 endemic species have been evaluated by the IUCN in 2011, revealing about half of them are threatened. Paradoxically, on the 21 hydrobioid protected species, only 4 are threatened and 11 have been categorized as "least concerned". None are listed in the European Directive.

An analysis of the economics of freshwater molluscan conservation shows that efforts are unbalanced and do not target the most imperiled species. The freshwater pearl mussel *Margaritifera margaritifera* has become a remarkable flagship species: it alone collects 80% of conservation budgets allocated to mollusks. However, it is arguably a poor umbrella species, as its habitat is naturally species-poor. By contrast, modern molecular systematics are revealing valid species of unionoids that remain outside the legal conservation agenda. The hydrobioids have an even worse destiny. Hard to see, difficult to identify, they are anything but charismatic. Their environment is poorly known and the keystone species concept does not apply either. As a consequence, and in spite of the existing regulatory framework, they are ignored by the managers and conservation agencies. Despite the current regulatory framework, we will continue loosing the European freshwater mollusks.

T14.O7

FRESHWATER GASTROPOD DIVERSITY OF EUROPEAN LAKE SYSTEMS OVER THE LAST 23 MILLION YEARS - STATE OF THE ART AND OUTLOOK

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More than one thousand gastropod species are currently known for European freshwater systems. Apart from faunal lists and a few general overviews, studies on the γ-diversities of European freshwater systems and the shifting biodiversity through space and time are entirely missing. For fossil assemblages, biodiversity estimates are likewise scarce and usually restricted to small regions. In many cases, even species lists do not exist and are hard to extract from the literature.

The present project is aimed at compiling freshwater gastropod faunal data from the huge amount of existing works. The γ-diversity of several hundred modern and fossil European lakes will be evaluated to provide a first detailed assessment of the faunal composition during the Neogene and Quaternary at species, genus and family levels. Important topics to be addressed are factors explaining the differences and changes in the γ-diversities through time as well as geographic gradients in species richness and/or faunal composition. Diversity data and inter-lake comparison will allow estimating endemism rates and quantitatively defining biodiversity hotspots in present and past lakes. The well resolved climate history of Europe during the last 23 million years will be a frame for linking species- and supraspecific compositions with climatic trends and events. Ideally, the project will shed light on the origin of modern lake faunas by the intense cooperation between zoologists and paleontologists. A major aim is to map a statistics-based Pan-European biogeography and palaeobiogeography of Neogene to Quaternary freshwater systems.

Data will be made permanently available for the public via the FreshGEN-database (Freshwater Gastropods of the European Neogene). Once established, this database will be open for geographic and/or stratigraphic expansion.

T14.O8

MARSUPIAL MOLLUSCS AS MODELS –EVOLUTIONARY SYSTEMATICS OF AUSTRALIAN FRESHWATER GASTROPODS

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While most marine molluscs are oviparous, viviparity is more often found among freshwater gastropods. Among the “marsupial” Thiaridae of Australian rivers two distinct reproductive modes were recently found to be realized. Ovo-viviparity, viz. releasing veliger from a brood pouch, can be found in only three species from the Jardinian province. In contrast, eu-viviparity, viz. giving birth to shelled juveniles, is found in all other eight species widely distributed over the continent. We focus here on *Sermyla* as a model system which occurs in Australia with two species, *riqueti* and *venustula*, and in which both viviparous reproductive modes are realized. To further investigate inter- and intraspecifc differences we use a set of morphological tools (e.g. biometry, geometric morphometrics) and molecular techniques (mtDNA and AFLP). The eu-viviparous *S. venustula*, with occurrences restricted to the northern provinces in Australia, revealed a high phenotypic plasticity in its conchology (i.e. significant differences in shell size and shape) and their reproductive biology. In contrast, *S. riqueti* with wider distribution and occurrences mainly in Southeast-Asia, has a much lower degree of intraspecific variation regarding shell size and shape. In addition, we found individuals from the Indonesian island of Sulawesi to have significantly bigger shells and a different reproductive strategy (ovo-viviparity). The molecular analyses using two mtDNA markers (COI and 16S) identified all *S. riqueti* that were found to be eu-viviparous as sister taxon to *S. venustula*, whereas *riqueti* from Sulawesi were not found to be closely related. The AFLP analyses of S. *venustula* revealed high intraspecific population differences as well as interspecific differences with *S. riqueti*. The study, therefore, not only indicates drainage based intraspecific differences in *venustula* but, based on molecular genetics and reproductive biology, suggests the existence of two distinct lineages within populations subsumed to date within the type species *Sermyla riqueti.*

T14.O9

THE STRUCTURE OF THE COPULATORY APPARATUS AS A TAXONOMIC TOOL FOR BITHYNIID SNAILS (GASTROPODA: PECTINIBRANCHIA: BITHYNIIDAE) OF WESTERN SIBERIA

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Five genera of the family Bithyniidae presented by 13 species are registered in the Western Siberian waterbodies. Traditionally, only conchological traits were used as diagnostic tool for identification of bithyniid snails in the region. We report some intergeneric and interspecific differences in the structure of the copulatory organ that are useful as an additional means for diagnostics.

Genus *Bithynia* Leach in Abele: penis sickle-shaped, somewhat massive, its finger-like outgrowth (FLO) is situated approximately in the middle of the penis. Penis is of uneven width: the base of penis is massive and wide, whereas its distal end narrow and slightly curved.

Genus *Opisthorchophorus* Beriozkina, Levina et Starobogatov: penis sickle-shaped, thin, oblong; its width remains the same in all parts of the organ. Its distal end pointed; it is very long and curved. The narrow FLO is in the lower third of the organ.

Genus *Digyrcidum* Locard: penis sickle-shaped and curved, with sharp distal end. FLO is placed near to the distal end of the organ

Genus *Boreoelona* Starobogatov et Streletzkaja: penis sickle-shaped, of the same width in all parts, visibly pointed near the distal end. FLO is relatively small as compared to the penis total length, lies near the penis base.

Genus *Paraelona* Beriozkina et Starobogatov: morphologically the penis is similar to that of *Bithynia* but species of the two genera may be easily distinguished by their conchological traits.

The current list of the bithyniid snails of the Western Siberia is as follows:

Bithynia curta Garnier in Picard; *B. producta* (Moquin-Tandon); *B. tentaculata* (L); *B. decipiens* Millet; *Opisthorchophorus baudonianus* (Gassiez); *O. troschelii* (Paasch); *O. abacumovae* Andreeva et Starobogatov; *Paraelona socialis* (Westerlund); *P. milachevitchi* Beriozkina et Starobogatov; *Boreoelona sibirica* (Westerlund); *B. contortrix* (Lindholm); *Digyrcidum bourguignati* (Paladilhe), *D. starobogatovi* Andreyeva et Lazutkina.

T14.O10

TAXONOMY AND ECOLOGY OF THE GENUS *SEMISULCOSPIRA* IN THE MOLECULAR AGE

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The application of molecular markers/phylogenetics to taxonomically difficult mollusk clades has in some cases been an unqualified success, *e.g.*, it has greatly improved our understanding of oyster systematics, taxonomy and ecology. This happy outcome has been less prevalent for some freshwater snail taxa due to extraordinary levels of within-population genetic diversity, especially for mitochondrial markers, that are incongruent with phenotype-based taxonomies. Rather than clarifying systematic/taxonomic relationships, molecular data in such cases may compound preexisting ambiguities and lead to very divergent proposals for taxonomic revision. The Northeast Asian genus *Semisulcospira* exemplifies some of these difficulties. Molecular phylogenetic analyses reveal that populations of multiple nominal species in Korea and Japan have engaged in cryptic gene flow across >700 km of the generic range spanning ancient lake/fluvial habitat disjunctions as well as a major marine barrier. Given such complexity, how can we construct a meaningful taxonomy – a critical requirement for rational ecological studies and conservation planning? Insights from angiosperm systematics and taxonomy provide some useful pointers.

T14.O11

TAXONOMY OF *ASOLENE META* (IHERING, 1915) AND *ASOLENE SPIXII* (D´ORBIGNY, 1838) (CAENOGASTROPODA: AMPULLARIIDAE) FROM BRAZIL

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Ampullariidae are freshwater snails inhabiting tropical and subtropical regions in Asia, Africa, and theAmericas. They are often major constituents of freshwater ecosystems

and play important roles in food webs. Unfortunately, the detailed morphology of most ampullariids is poorly known and their classification is based primarily on often variable shell characters, resulting in taxonomic confusion. Among the four genera in South America, *Asolene* is one of the least studied. To clarify the taxonomy of *Asolene meta* and *Asolene spixii* and provide additional data to understand systematic relationships within the family we assessed morphological and molecular data from specimens collected from two populations in Brazil, including the type locality of *A. meta*. *Asolene meta* is restricted to northeast Brazil while *A. spixii* has a wider distribution in northern Argentina, Uruguay, Paraguay and southern Brazil. The shells are similar but the aperture of *A. meta* is rounded and in *A. spixii* it is more elongated. There are a few anatomical differences, primarily in the characters of the kidney and the penial sheath. The elongated anterior kidney in *A. meta* is larger than that of *A. spixii*, which is triangular. The apical penis sheath gland is larger and more voluminous in *A. spixii*, although both species share two internal glands in that occupy similar positions on the sheath. In both species, the rounded, non-calcareous and unpigmented eggs are deposited below water in gelatinous masses. The taenioglossate radula and the stomach are similar in both species. Molecular data from cytochrome *c* oxidase subunit I (COI) confirm that *A. meta* and *A. spixii* form reciprocally monophyletic clades that do not share haplotypes. However the two taxa are sister species in phylogenetic reconstructions of the genus. Additional morphological and molecular data are being collected to expand the characters available for clarifying the taxonomy of the species.

T14.O12

DOES ECOPHENOTYPIC PLASTICITY OBSCURE EVOLUTIONARY HISTORY? RELATIONSHIPS OF NEARCTIC *STAGNICOLA* (GASTROPODA: LYMNAEIDAE) USING GEOMETRIC MORPHOMETRIC AND PHYLOGENETIC METHODS

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Ecophenotypic plasticity is pervasive within freshwater mollusks, yet its relationship to evolutionary history within pulmonate gastropod taxa is largely still unknown. Within Nearctic regions, prior impacts of Pleistocene glaciations caused extensive and frequent restructuring of aquatic ecosystems, providing extensive opportunities for diversification and local adaptation of lineages in refugia as well as gene flow during secondary contact upon glacial retreat. The diffuse Neacrtic distribution of a morphologically diverse molluscan subgenus, *Stagnicola* (Gastropoda: Lymnaeidae), provides a unique system to examine the effects of these phenomena on the molecular and morphological diversification of North American freshwater species.

Molecular phylogenetic and geometric morphometric analysis of 13 populations of three North American *Stagnicola* species indicate that while shell morphology is strongly correlated with locality and morphospecies tend to cluster in defined areas of morphospace, this relationship is not reflected within the phylogeny. Rather, several genetically distinct COI clades occur within *Stagnicola,*with each clade comprised of distinct morphospecies and, in some instances, high degrees of intra-population divergence. In contrast, nuclear ITS-1 regions show relatively little divergence between morphospecies. Paired breeding experiments yielded no hybridization between nominal morphospecies. These results imply that (i) shell morphology of *Stagnicola* species is largely ecophenotypic and as such shell-based characters are unreliable in distinguishing members of this subgenus, (ii) recurrent introgressive hybridization has occurred between recently diverged lineages, and/or (iii) incomplete lineage sorting of haplotypes shared in glacial refugia, all of which hinder the ability to distinguish and reconcile relationships among *Stagnicola* species using single-gene approaches. Other molecular studies of heterobranch gastropods reveal similar trends, suggesting that universal underlying mechanisms are responsible for morphological and geographical molecular incongruities as those observed here. These patterns imply that historical ecological factors have driven the current genetic population structure and diversification patterns observed in such groups.

T14.O13

CAN DEER SPREAD SNAILS?

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Galba truncatula is one of the most important freshwater snails which may act as intermediate hosts of more species of trematodes that have medical and veterinary importance. In Hungary, Central Europe they play a role as vectors of several flukes in game animals. Deer living in flood areas along Danube River are highly infected with rumen and liver flukes the larvae of which develop in *G. truncatula*. Infection is confined solely to areas where lymnaeid snails have dense populations.

Some decades ago a liver fluke *Fascioloides magna* that have an American origin was spreading in deer in Gemenc area which is the largest game reserve in Hungary. When foci of infections were investigated it was revealed that intermediate snail hosts could be detected not evenly throughout the swampy area but only in dubs on dirty roads. The field roads in trenches have several long lasting puddles during wet summer because the wheels of vehicles compress the mud that prevents leakage of water out of them. Deer highly prefer to wallow in road puddles because this way they can observe their surroundings easily in order to run away in case of danger.

G. truncatula could be found almost exclusively in road wallows that were frequented by deer although there were no direct connections among them. The puddles where no deer wallowed were free from snails. As the most wallows sometimes dry up completely or winterkilled during frost, they obviously need to repopulate repeatedly. After lying on the mud animals can carry the tiny *G. truncatula* snails from one puddle to another by their sloppy fur. As the deer also defecate in wallows miracidia can easily develop and hatch from fluke-eggs in their droppings inside watery splash. In this way deer help the expansion of intermediate hosts of their flukes.

T14.O14

TAXONOMY, MORPHOLOGY AND DISTRIBUTION OF ANCYLINAE (GASTROPODA: PULMONATA: PLANORBIDAE) IN ARGENTINA

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Taxonomic studies on Ancylinae, freshwater limpets that inhabit continental limnic environments, are scattered and show a degree of systematic confusion of species identification in Argentina. The aim of the present study is to broaden the information on morphology in order to improve taxonomic knowledge and to update distribution of the species, based on literature records, revision of museum collections and field research. We identified new records and elevated to six the number of genera known at the moment, totalizing seven species. Shell morphology, muscles scars and radula distinguishes three groups of limpets. Ancylinae with shell apex on the anterior region: *Anancylus rosanae* Gutierrez Gregoric, 2012; Ancylinae with an elevated shell: *Gundlachia ticaga* (Marcus & Marcus, 1962), *G. radiata* (Guilding, 1828); *Uncancylus concentricus* (d´Orbigny, 1835) and *Anisancylus obliquus* (Broderip & Sowerby, 1832); and Ancylinae with flattened shells:*Hebetancylus moricandi* (d´Orbigny, 1837) and *Ferrissia irrorata* (Guilding, 1828) *Ferrissia irrorata*, originally described from Antilles, is for the first time registered to Tucumán province (Northwestern Argentina). *Gundlachia radiata* is restricted to Northeastern Argentina (Corrientes province) and, together with *F. irrorata* could represent a recent introduction. The southernmost point of occurrence of these snails is the southwestern of Rio Negro province. Ancylinae are lacking from southernmost ecorregions as well as the desertic Puna ecorregion in north.

Financial support: CNPq (476682/2004-5), CNPq Protax (562291/2010-5), Conicet/ Argentina.

T14.O15

LYMNAEID TAXONOMY IN THE MOLECULAR AGE: ADVANCES AND PROSPECTS

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Traditionally, the system of the family Lymnaeidae (Pulmonata: Basommatophora) had been based on morphology. Since 1997, different molecular techniques are effectively used in lymnaeid molecular phylogeny and taxonomy bringing a new dimension into the old debates. Main advances of lymnaeid molecular studies are briefly reviewed, including:

1. Generic system of the family. Molecular data reveal two large phylogenetic branches of recent lymnaeids that justifies separation of two subfamilies: Lymnaeinae s.str and Radicinae Vinarski, 2013. The phylogenetic position of some peculiar taxa (i.e. genus *Lanx*) is still not clarified.
2. Coordination between genetic (evolutionary) distances and Linnaean ranks of the taxa. A decent correlation between ranks and distances provides an additional tool for systematization. Approximate genetic distances to characterize each level of taxonomic divergence (subspecies to genus) are provided.
3. Species delineation within lymnaeid snails. Incongruence between macromorphological and molecular data is frequently observed. This hampers species identification based on morphological traits.
4. Numerous examples of interspecific hybridization are observed by incongruence of morphology and nuclear markers on the one hand and mitochondrial genes on the other.
5. Phylogeography. Three Palaearctic species of the family have been densely sampled to date (*Lymnaea stagnalis*, *Radix balthica*, *R. labiata*). Though the ranges *L. stagnalis* and *R. balthica* are almost identical in the Palaearctic, their phylogeographic patterns are completely different. The phylogeographic structure in *R. balthica* is virtually absent, whereas in *L. stagnalis* we found three independent lineages having more or less distinct ranges.

Most recent papers on lymnaeid molecular taxonomy employ sets of standard genes (COI, cyt-b, ITS-2 etc) but is it possible that speciation events are caused by changes in the so called "speciation genes". In this case, molecular data alone are not enough for correct species delineation and identification. Possibly, we need a genome-wide comparative analysis to solve these problems.

T14.P1

FOLLOWING THE FOOTSTEPS OF LINNAEUS INTO THE 21TH CENTURY– THE FREDIE PROJECT ON BARCODING EUROPEAN FRESHWATER MOLLUSCS

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FREDIE – the acronym for '*Freshwater Diversity Identification for Europe*' – is a nationally funded project jointly conducted by three German Leibniz institutes, i.e. the Zoologisches Forschungsmuseum Alexander Koenig Bonn, the Institut für Gewässerökologie Berlin and the Museum für Naturkunde Berlin. During the last two years we built up an ethanol-stored collection with samples from our own fieldwork and material from project partners. Currently this collection comprises over 2.500 samples from over 550 sampling points, covering roughly 70 percent of the described European malacofauna (excluding Hydrobiidae and Sphaeriidae). Our aim is to combine a DNA-barcoding approach (essentially focussing on COI) with solid taxonomic expertise for European freshwater organisms (fishes, mayflies and molluscs), in order to develop an online identification system for species diversity of these taxa in Europe (www.fredie.eu). One goal of the project is to generate, with the help of several partners, a more reliable species evaluation based on reconciling molecular and morphological diversity vs. disparity patterns in these limnic groups of organisms in Europe. Interestingly, a brief overview of the available literature and databases revealed that the diversity of European freshwater molluscs in terms of species numbers varies between sources, as varying geographic areas are covered, and often different names are considered valid. Here we present the current status of the mollusc work-package, summarizing data for selected taxa with available information on synonyms, type localities and distribution with first DNA-barcoding results. In this context we will outline problems related to type-material (i.e. unknown or imprecise type localities, those that do no longer exist and, thus, no topotype material being available), resulting in the inability to generate exact "barcodes" for nominal taxa, which is essential for any taxonomic approach, including those utilizing molecular data.

T14.P2

COMPARING APPLES TO APPLES: CLARIFYING THE IDENTITIES OF TWO HIGHLY INVASIVE NEOTROPICAL AMPULLARIIDAE (CAENOGASTROPODA)

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Ampullariidae are a monophyletic family of freshwater gastropods. Recent molecular work began to clarify generic relationships, but current systematics remains unsatisfactory. With more than 300 available species group names for New World taxa alone, taxonomic confusion is rampant, as illustrated by two species that have been introduced widely and are difficult to differentiate conchologically, *Pomacea maculata* Perry, 1810 and *Pomacea canaliculata* (Lamarck, 1822). Misidentification hampers efforts to manage their spread and impacts as invasives, and prevents meaningful comparative analyses of their biology. We have clarified the taxonomy, described the morphological and genetic distinctiveness of the two species, and re-evaluated their biogeographic ranges. They differ most clearly genetically, with no shared haplotypes and a mean genetic distance of 0.135 at cytochrome *c* oxidase subunit I (*COI*). Differences in shell morphology are most obvious in recently hatched juveniles; the number of eggs per clutch is higher in *P. maculata*, and the individual eggs are smaller, so *P. canaliculata* hatchlings are nearly twice as large as those of *P. maculata*. Adult shells differ primarily in the angulation of the whorl shoulder and pigmentation of the inner pallial lip, with the latter a distinctive feature of *P. maculata*. They also differ in reproductive anatomy, most notably in *P. canaliculata* having two distinctive glandular tissues in the apical penial sheath gland, and *P. maculata* lacking a medial sheath gland but possessing a basal sheath gland. *Pomacea canaliculata* is restricted to a narrower southern range, whereas *P. maculata* ranges extensively throughout much of South America. *Ampullaria*

gigas Spix, 1827 and *Ampullaria insularum* d'Orbigny, 1835 have been synonymized with *P. maculata*. Neotypes have been designated for *P. maculata* and *A. gigas*, and a lectotype has been designated for *A. insularum*. A neotype has been designated for *P. canaliculata*.

T14.P3

GUNDLACHIA TICAGA (MARCUS & MARCUS, 1962) AND *GUNDLACHIA BAKERI* PILSBRY, 1913: IDENTITY CONFIRMED BY MORPHOLOGICAL AND MOLECULAR DATA

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Gundlachia 1849 Pfeiffer is a freshwater patelliform snail with the widest geographical distribution among the eight genera of Ancylini reported for the Neotropical region. *Gundlachia bakeri* was described to septate specimens found in an artificial lake at the city of Belém, Pará, Brazil whereas *Gundlachia ticaga* was described from aquarium specimens from the city of São Paulo. The two species are very similar, considering shell morphology (shell oval-shaped with a rounded apex inclined to right and protoconch almost totally covered with shallow punctuations), mantle pigmentation and muscle scars. Absence of radial lines on the teleoconch of *G. ticaga* has been considered a distinctive character. The fragility of characters resulted in the synonymization of the two species by some authors. The aim of this study was to recognize the identity of *G. bakeri* and *G. ticaga* based on morphological and molecular data. The comparative morphology of the shells and soft parts was carried out with the aid of optical microscope images and scanning. Molecular studies were performed after extracting DNA from the muscular foot, using 16S mtDNA as molecular marker. Taxa from *Ancylus* and *Biomphalaria* were used as outgroups. Phylogenetic subsequently performed with the sequences obtained revealed the existence of a well supported clade to the species of *Gundlachia*. The amplification sequences of the species *G. bakeri* and *G. ticaga* generate fragments of 430 base pairs that were grouped into two distinct clades, with high boostrap support (0.91). The species differ in morphology of the shell apical microsculpture, number of cusps in the rachidian tooth, shape of the adductor muscles and details of the reproductive system. We confirm the validity of these two taxa based on morphological and molecular data. Studies with other molecular markers using samples from watersheds are being analyzed to increase knowledge about the group.

Financial support: CNPq (476682/2004-5), Protax (562291/2010-5), Faperj APQ1 E-26/110.362/2012

T15

T15. O1

MATING BEHAVIOR IN *OCTOPUS OLIVERI*, A HAWAIIAN INTERTIDAL OCTOPUS

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Extremely little is known about *Octopus oliveri*, its life history, distribution, or behavior. *Octopus oliveri* was described by Berry in 1914 from the Kermadec Islands as a relatively small intertidal octopus. Since *Octopus oliveri* is found in Hawaii, the opportunity to study its life history and mating behavior has become possible.

As is true with most octopuses, female *O. oliveri* have two oviducts for sperm storage and may be able to store viable sperm for at least 100 days and up to 10 months. In addition, they mate with several males before laying their eggs at the end of their lives. This suggests that sperm selection or competition may be occurring, however it has rarely been studied in octopods and never in *O. oliveri*.

Four trials of behavioral experiments were recorded wherein six females were mated with three males in varying order, for a total of 24 females and 12 males. Video analysis of mating behavior shows the rates of aggression and duration of mating for 66 successful mating pairs. By observing the difference between the first, second, and third mating males, one may discern whether one male is more successful behaviorally than another in inseminating a female. The weights of both the males and females were recorded, as well as whether eggs were subsequently laid after mating and when.

This work is a first step in understanding this poorly described species and its role in the Hawaiian intertidal ecosystem.

T15.02

REPRODUCTIVE CYCLE AND FEMALE GONAD STRUCTURE OF THE SOUTHERN CARIBBEAN ENDEMIC GASTROPOD *VOLUTA MUSICA* (CAENOGASTROPODA: VOLUTIDAE).

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Voluta musica is an endemic volutid restricted to the Southern Caribbean and is a threatened species. The Venezuelan Red Book of Fauna included it under the category “Least Concern”; however, such statement lacks on biological available information that indicate an actual higher risk status. *V. musica* spawns egg capsules with 1-4 eggs immersed in an intracapsular fluid that allows them to develop and hatch as crawling juveniles. The present work describes the gonad structure, female gametogenesis and the reproductive cycle of *V. musica*. The ovary of *V. musica* has a digitiform shape, weakly ramified; the acini develop onto the inner side of the digestive gland, at the apical whorls of the spire. The acini are surrounded by a well developed connective tissue with scattered muscle fibers; the acinus wall is formed by somewhat elongated cells. Through the oogenesis four developmental stages were recognized: (1) oogonia, (2) previtellogenic oocytes, (3) vitellogenic oocytes, and (4) degenerative oocytes. Oocyte degeneration is an outstanding processes that take place nearly all year round. Oocytes in a degenerative state were recognized by a disintegrated cytoplasm, which becomes vacuolated, with irregular shape. The plasma membrane usually breaks and the vitellinic droplets fill the acinus. At this stage, the acinus wall cells shows brown bodies in their cytoplasm, suggesting their participation in the oosorption process. A number of hemocytes participate in the phagocytosis of broken oocytes, showing in their cytoplasm engulfed vitelline droplets. Other cell type, possibly derived from the acinus wall invade the center of the acinus after the oocyte lysis; these cells have a peculiar nucleus shape, that frequently appears as deeply cleft, remembering apoptotic cells. Very few ripe oocytes were only observed in February and March samples. The main reproductive period (higher number of egg capsules are found in the field) spans from April to November.

T15.03

SPERM PRECEDENCE IN THE HERMAPHRODITIC FRESHWATER SNAIL, *HELISOMA TRIVOLVIS*

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Our primary research goal was to determine the nature of sperm precedence in the freshwater snail, *Helisoma trivolvis*. Sperm precedence has been suggested as a way for female partners to choose among mates after mating has occurred, sometimes referred to as cryptic female choice, one aspect of sexual selection. Most studies of sexual selection have focused on gonochoristic species (with two separate sexes) as opposed to hermaphroditic species like the sperm storing simultaneous hermaphrodite *H. trivolvis.* Sperm precedence refers to the non random differences in fertilization success after copulation with multiple sperm donors has occurred. Because *H. trivolvis* store sperm, we predicted that sperm from the first mate would fill the spermatheca and thus second sperm success would be low. We investigated whether the first sperm contributor or second sperm contributor fertilized more offspring of *H. trivolvis*, using albinism as genetic marker to determine paternity. To ensure a varied genetic background, albino snails used in the study were descendants from F_2 albinos resulting from crosses between pigmented wild *Helisoma trivolvis* and lab-reared albinos. Albino snails were isolated until they reached maturity and were mated first with a pigmented snail and then an albino snail (or the reverse). Egg masses were collected at 1, 3, 5, and 11weeks after mating and embryos were examined under an inverted microscope at 40x. The presence or lack of eye pigmentation was used to identify paternity in these snail embryos. As expected, we found strong first mate precedence in *H. trivolvis* overall; about 85% of eggs were fertilized by the first partner, although there were individual differences in precedence. In addition, there was significantly lower first sperm precedence when an albino snail was the first mate, suggesting a slight preference for pigmented partners.

T15.O4

IMPACT OF GLOBAL WARMING ON THE SPAWNING SUCCESS AND EMBRYOGENESIS OF A SPECIALIZED SOFT CORAL-FEEDING NUDIBRANCH, *ARMINA MACULATA*

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Understanding how marine organisms will respond to future thermal scenarios is of great relevance, particularly during their early life stages, since these are expected to be the most vulnerable ones.

The present study aimed to investigate, for the first time, the spawning success and embryonic development of a specialized soft coral-feeding nudibranch, *Armina maculata*, under different thermal scenarios, which reflect: i) the present-day average spring (18 °C), early-summer (22 °C) and summer (24 °C) temperatures, and ii) the projected near-future warming (27 °C, +3 °C), a temperature that the species already experiences during heat wave events in Sado estuary. The optimal temperature for spawning was 22 °C and higher thermal scenarios caused a significant decrease in the spawning frequency (i.e. the number of egg masses laid per week). At the future warming scenario, spawning stopped after 3 weeks of incubation and the respective hermaphroditic spawners deceased after 7 weeks. Our findings also showed that embryonic development time was inversely correlated with temperature and that the projected near-future warming is expected to greatly reduce egg mass viability and cause deleterious effects on embryo's development (higher number of abnormalities), survival and growth.

T15.P1

ANATOMICAL CHARACTERIZATION OF THE *THAUMASTUS (QUECHUA) SALTERI* (SOWERBY, 1889) PENIAL COMPLEX AND SPERMATOPHORUS (PULMONATA, BULIMULINAE)

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Thaumastus (Quechua) salteri is a specie-type of the subgenera that has geographical distribution in the Peruvian Andean region of the Lambayeque and Cajamarca. Male genitalia were described in 2006 by PENA showing the subcylindrical, long penial complex with regular diameter and internally with short and straight muscular pilasters in the end region also showing wide, thick foiled glandular walls at the proximal region. Based on specimens from the Chota locality type, Cajamarca, that ejected the phallus with one spermatophorus during the relaxing process, it was possible to get transversal sliced images that permitted its morphological characterization. The collected specimens were relaxing under iced water for twenty four hours then preserved in alcohol 70^{o}GL where they stayed for almost ten years. The material was photographed with an Olympus E30 and after, the ejected phallus was transversally cut, rehydrated in alcoholic series until 30^{o}GL, buffered in phosphate solution, fixed in glutaraldehyde and osmium tetroxide 3%, dried at critical point, put in stubs and covered by gold. Later, all this was scanned by a DSM 950 Zeiss. The macroscopic images of the spermatophorus showed that in its apical and ejected portion there is one external and hard slide with many edges being one of them with prominent projections in the proximal portion; the terminal portion is nearly cylindrical and a little bit softer. The terminal phallus portion presents in a transversal view a muscular wall with longitudinal fiber layers surrounding a circular fiber tunica; the lumen with muscle-connective tissue casting the external wall of spermatophorus. In the median phallus region the muscular projections (pilasters) viewed in high resolution, present a ciliated epithelial coat with a granular aspect material at the penial and vas deferens lumen tubes. The results were confronted with the ones obtained by BREURE (1978) with optical microscopy for the *Thaumastus (Quechua) taulisensis* Zilch, 1953.

Autorization's collect process- Instituto Nacional de Recursos Naturales, Peru. INRENA DGFFES-DCB-006/2003

T15.P2

ON TRACKING THE FATE OF PARASPERM IN GASTROPODA

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Parasperm are a significant component of the ejaculate of many gastropod species. These sterile germ cells are much larger than the fertile 'eusperm' and usually contain copious secretion granules. Electron microscopic examination of the female bursa copulatrix has shown that some parasperm are phagocytosed, whereas others are digested extracellularly but the fates and function of parasperm secretions are unknown.

We obtained sperm samples from seminal vesicles of ripe male *Littorina littorea*, *Fusitriton oregonensis* and *Plicopurpura patula* and used Percoll® gradients to isolate parasperm from eusperm. Purified samples of each sperm type were treated with RIPA lysing buffer (Sigma) and run on SDS PAGE to separate proteins. Individual protein bands were cut out from gels under sterile conditions and analyzed by means of liquid chromatography-tandem mass spectrometry (QSTAR Elite LC MS/MS) to determine amino acid sequences. The proteins, or their homologues, were subsequently identified from these amino acid sequences by a MASCOT-DB search. Several proteins unique to parasperm were found, but one band that was prominent in all three snails is a 'heat shock' protein of approximately 110KD, homologous with a number of other HSPs on record in this size range. The main purpose of this study was to identify a protein unique to parasperm and now that we have done that, to generate a parasperm-specific antibody that will enable us to track the fate of parasperm in female snails and learn more about their function.

T15.P3

VERTICAL TRANSMISSION OF BACTERIAL SYMBIONTS IN THE FAMILY ASTARTIDAE (BIVALVIA)

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The periostracum of the species from the family Astartidae is characterized by having a pitted surface. The presence of bacteria inside the pits has been previously reported for *Digitaria digitaria* (L., 1758) and this seems to be the general rule for the other genera of the family. In order to check the relationship between the bacteria and the bivalves, we studied the pathway of transmission using semi-thin sections and transmission electron microscopy. The presence of bacteria inside bacteriocytes inside the gonads of *Digitaria digitaria* and *Astarte cf. undata* Gould, 1841 has been observed. In *Goodallia triangularis* (Montagu, 1803), a brooding species, the bacteria appear inside the oocyte. These results point out an endosymbiosis, a mutually obligate association in which the symbiotic bacteria are maternally transferred. This is assumed to involve co-evolutionary interactions.

T15.P4

EVALUATING THE MATING GROUPS' HYPOTHESIS IN POPULATIONS OF *ECHINOLITTORINA LINEOLATA*

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Marine organisms with planctotrophic larvae are expected to present genotypic frequencies in Hardy-Weinberg equilibrium. Despite this, there are many cases in which fine scale population structure and homozygote excess are observed. One hypothesis for this is the existence of mating groups, which we tested using *Echinolittorina lineolata*, a gastropod whose larvae recruit on the rocky shores of the Brazilian coast. Previous studies have reported excess of homozygotes in this species. Our sample site was a beach in São Paulo State where we chose five rocks. All the littorinids were removed from the rocks in June of 2012. All the juveniles were collected after 40 days and again 40 days later. Molecular analyses were performed for 11-15 juveniles from each sample, using two mitochondrial markers: cytochrome oxidase I and cytochrome b. The diversity indices were statistically similar for both collections. Analysis of molecular variance (AMOVA) did not point population structure, and the variability between individuals from the same rock was higher than the variability between rocks or between the two collection times. So far our results do not support the hypothesis of mating groups.

T15.P5

ABUNDANCE AND SPAWNING PATTERNS OF THE LIMPET *SIPHONARIA PECTINATA* IN CONTRASTING ENVIRONMENTS IN SW PORTUGAL

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The limpet *Siphonaria pectinata* is a marine pulmonate mollusc, which inhabits the intertidal zone of warm temperate and tropical rocky shores. In the European Eastern Atlantic coastline, this species is only common in continental Portugal, namely in the south. To our knowledge, there is not any published study focused on the ecology of this species in Portugal.

Surveys of intertidal communities and studies on limpet populations carried in SW Portugal have consistently found that this species can occur across all tidal levels, but its distribution and abundance show high variability at small spatial scales.

In our previous studies on limpet recruitment, recruits of *Siphonaria pectinata* (maximum shell length – MSL ≤ 2 mm) were commonly found in tidepools monitored every three months. Despite a high inter-annual variability in maximum densities of recruits, recruitment mostly occurred during summer-autumn seasons.

Preliminary observations indicate that spawning (egg-laying) by this species generally occurs during spring-summer seasons, but the time-span of spawning and the abundance of egg masses on the shore may vary greatly among contrasting environmental conditions: microhabitats (emersed-rock versus tidepools) and thermally different locations (a breakwater adjacent to an effluent of hot water from a local thermoelectric station versus nearby locations).

In order to study temporal and spatial patterns of population structure and spawning, we have counted potentially reproductive individuals (MSL ≥ 5 mm) and egg-ribbons present within fixed sampling areas, every month. Comparisons were made between the two microhabitats sampled in two locations and among locations at varying distances from the thermal effluent. Abundance of other limpets (*Patella* spp. MSL > 5 mm) was also registered within the same sampling areas. Temperature was semi-continuously recorded in all locations/habitats.

Physiological attributes of *Siphonaria* in coping with extreme thermal conditions and the potential role of competition with *Patella depressa* will be considered in the discussion.

T16
T16.O1

INVESTIGATING THE BIVALVE TREE OF LIFE -- AN EXEMPLAR-BASED APPROACH COMBINING MOLECULAR AND NOVEL MORPHOLOGICAL CHARACTERS

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To re-evaluate the relationships of the major bivalve lineages, we amassed detailed morpho-anatomical, ultrastructural, and molecular sequence data for a targeted selection of exemplar bivalves spanning the phylogenetic diversity of the class. We included molecular data for 103 bivalve species (up to five markers) and also analyzed a subset of taxa with four additional nuclear protein-encoding genes. Novel as well as historically-employed morphological characters were explored and we deconstructed widely used descriptors such as gill and stomach "types." Phylogenetic analyses, conducted using parsimony direct optimization and probabilistic methods on static alignments (maximum likelihood and Bayesian inference) of the molecular data both alone and in combination with morphological characters offer a robust test of bivalve relationships. A calibrated phylogeny also provided insights into the tempo of bivalve evolution. Finally, an analysis of the informativeness of morphological characters showed that sperm ultrastructure characters are among the best morphological features to diagnose bivalve clades, followed by characters of the shell, including its microstructure. Our study found support for monophyly of most broadly recognized bivalve higher taxa, although support was not uniform for Protobranchia. However, monophyly of the bivalves with protobranchiate gills was still the best-supported

hypothesis. Autobranchia, Pteriomorphia, Heteroconchia, Palaeoheterodonta, Archiheterodonta, Euheterodonta, Anomalodesmata, and a newly recognized clade (comprised of Euheterodonta excluding Anomalodesmata) were recovered across analyses, irrespective of data treatment or analytical framework. Palaeoheterodonta and Archiheterodonta formed a clade under many analytical conditions. [The Bivalve Assembling the Tree-of-Life project (http://www.bivatol.org) is supported by the U.S. National Science Foundation (NSF) Assembling the Tree of Life (AToL) program (DEB-0732854 / 0732903 / 0732860)]

T16.O2

ADDING STRUCTURE TO THE BIVALVE TREE OF LIFE

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Shell microstructures have often been used as characters in attempts to unravel the phylogeny of the bivalves. As part of the BivAToL project, we reviewed the use of particular characters and collected new data on exemplar taxa. Previously microstructural characters have been used as present/absent with no consideration of positional information or attempt to homologise shell layers. Our new survey used 21 characters, over half of them unused previously, developing a new scheme for homologising shell layers using the pallial myostracum as a datum. In the subsequent analysis, shell microstructure characters were shown to carry more phylogenetic signal than many other morphological systems.

Variation in shell microstructure is most variable in the outermost shell layer (M+2). Most striking is the apparent occurrence of derived microstructures in disparate parts of the tree, implying repeated evolution of specific microstructures such as foliated calcite which appears diphyletic within the pteriomorphs, and the occurrence of crossed-lamellar aragonite in both the archi- and euheterodonts as well as in the arcids within the pteriomorphs. Nacre is often thought of as primitive within the Bivalvia and yet it has a rather interesting distribution within the tree, with occurrences in the protobranchs restricted to the extant Nuculoidea and apparently as a derived condition in the anomalodesmatans. We will also chart the occurrences of other interesting shell characters such as periostracal calcification, tubules and so-called 'homogenous' structure.

This work is part of the The Bivalve Assembling the Tree-of-Life project (http://www.bivatol.org) supported by the U.S. National Science Foundation (NSF) (DEB-0732854 /0732903 / 0732860).

T16.O3

BIVALVIAN TRIPTYCH: BIVALVE SEASHELLS OF WESTERN SOUTH AMERICA

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The marine bivalve mollusks from Arctic Alaska, U.S.A., to northern Perú have been the subject of our two previously published books. We have begun research on a third eastern Pacific Ocean bivalve monograph, to be entitled *Bivalve Seashells of Western South America*. The study region originates at Punta Aguja, Piura, Perú (5.8°S), and continues south to the southern tip of Isla Chiloé, Los Lagos, Chile (43.4°S). As with the previous monographs, we will cover species that occur from the intertidal zone to the deep sea. As we have reviewed the literature for the Perú-Chile Province, we have noted a marked decrease in bivalve diversity compared with similar northern latitudes. In the Alaskan, Oregonian and Californian Provinces, we have documented over 470 bivalve species, in the Panamic Province 892 species, whereas we currently only have records for 217 species from the Perú-Chile Province. The decrease in the number of species present in the southern region may be a function of under-sampling, or may represent a much lower diversity, or a combination of both factors.

T16.O4

GLIDING CONVERGENCE FROM CONVERGENT, PARALLEL, AND DIVERGENT SHELL SHAPES: EVOLUTION OF COMPLEX PHENOTYPIC TRAITS IN SCALLOPS (BIVALVIA: PECTINIDAE)

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Convergence is where equivalent environments produce strong selection forces to generate similar phenotypic responses in organisms. This biological phenomenon provides strong evidence for adaptation because it links a specific morphology to a single function (one-to-one mapping). Alternatively, a more complex relationship may occur when convergent function is linked to divergent morphologies. This relationship is the many-to-one mapping, which predicts multiple, diverse forms can be attributed to a single convergent function. Scallops are great model organisms to study the many-to-one mapping because they exhibit a wide variety of shell shapes (morphology), yet they only have six recognized life habits (ecological function). One fascinating life habit is gliding, which is a unique swimming behavior that has been observed to have specific biomechanical requirements. Furthermore, gliding independently arose four times within scallops. Here we test the hypothesis that gliding scallops have converged to a single shell shape due to a direct link to the life habit (one-to-one). Alternatively, the shell shapes of gliders could be divergent, reflecting the shape of their respective ancestors, but have converged on the gliding life habit (many-to-one). In this comparative study, we quantified the shell shapes of nearly 600 individuals from 50 species that represent

four of the six life habits using landmark-based geometric morphometrics. We matched the scallop phylogeny with the morphometric data and reconstructed ancestral shell shapes to test for evolutionary patterns of convergence, parallelism, and divergence. Our results show that there are two distinct shapes linked to the gliding life habit and that the shell shapes of gliders arose through convergent, parallel, and divergent evolutionary patterns. This study supports the many-to-one mapping between form and function, and exemplifies the complexity of evolution that brings about such amazing diversity.

T16.O5

EVOLUTIONARY PATTERN OF SYMBIOTIC LIFESTYLE AND HOST ASSOCIATION IN THE BIVALVE SUPERFAMILY GALEOMMATOIDEA

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Galeommatoidea is a superfamily of tiny marine bivalves that have diversified in shallow waters. Interestingly, many members of this bivalve group live symbiotically on the body surface or inside the burrows of other marine benthic invertebrates, including crustaceans, holothurians, echinoids, cnidarians, sipunculans and echiurans. These symbiotic species exhibit high host specificity, commensal interactions with hosts and extreme morphological, behavioural and ecological adaptation to a symbiotic lifestyle. In addition, this superfamily includes many free-living species that are often attached to the undersurface of rocks in the intertidal zone. An intriguing question is how these diverse lifestyles and host associations evolved in this superfamily. Here, we present the first comprehensive molecular phylogeny of Galeommatoidea using three nuclear genes (18S, 28S and H3) and one mitochondrial gene (COI) from 40 galeommatoidean species belonging to 28 genera. As a result, six well-supported major clades were found within Galeommatoidea, which do not correspond to the traditional classification. All the major clades include symbiotic species, whereas two of them include free-living species. The analyses suggest that the colonisation of crustaceans, holothurians, sipunculans and echiurans occurred multiple times. Furthermore, the associated hosts were often divergent at the phylum level within the same major clades, suggesting that host switching between different phyla occurred repeatedly. Our results suggest that the colonisation of various host taxa and host switching have played an important role in the evolution and diversification of galeommatoidean bivalves.

T16.P1

DWARFISM IN AÇOREAN BIVALVES: A CONSEQUENCE OF EITHER LATITUDE OR PRODUCTIVITY (OR BOTH)?

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Bergmann's rule states that within a broadly-distributed taxonomic clade, species and populations of larger size occur in colder environments, whereas those of smaller size are found in warmer regions. The marine bivalves of Pacific islands, especially those occupying coral reefs, are relatively species poor in comparison with continental habitats. This may result from isolation, higher temperatures and low nutrient supplies. Conversely, the higher bivalve diversity of near-shore continental waters may reflect greater habitat diversity, for example, river and lagoonal estuarine systems, but also higher coastal productivity levels.

Açorean waters are relatively depauperate in terms of bivalve diversity, there being only some 50 species recorded to date. Most too are sub-tidal. Analysis of large numbers of bivalves, mainly shells, collected from dredging operations conducted first in 2006 and subsequently, has revealed that, overridingly, each species is but ~50% the shell length size of Mediterranean conspecifics. Bivalve size declines intra-specifically with decreasing latitude and this may apply to the Açorean species. Since, however, the islands are located at approximately the same latitude as the Mediterranean (and are influenced by these waters), the main reason for bivalve dwarfism in the archipelago appears to result from low, oceanic, productivity not latitude. This, in turn, is associated with low population sizes, save for *Ervilia castanea*, which here overwhelmingly occupies high-energy inshore habitats and associated higher productivities. Nevertheless, this species too is dwarfed by mainland conspecifics. Similarly, the introduced *Venerupiss decussata*, found solely within the lagoonal environment of Fajã de Santo Cristo on São Jorge, is somewhat smaller than its mainland conspecifics, although it is abundant enough to warrant artisanal exploitation. This study therefore argues for the role of nutrients, or rather their deficiency, in regulating Açorean bivalve species diversity and individual maximum size. In waters of locally higher productivities, however, population densities increase.

T16.P2

MORFO-ANATOMICAL COMPARISON OF GENUS *CRASSOSTREA* AND *SACCOSTREA* (BIVALVIA: OSTREIDAE: CRASSOSTREINAE)

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The taxonomy of almost all groups of Bivalvia is very confusing, there is a amount of species to be described, the other (known) still require a better definition. Knowledge of anatomy is extremely shallow and restricted to a few representatives. This happens even in groups of great commercial interest, such as oysters.

The identification of oysters is difficult due to the high degree of phenotypic plasticity. The pure use of external morphology has caused errors in identification and

classification. Diverse species occur sympatrically and are transported to aquaculture. Accurate identification of species of oysters is essential for research and aquaculture.

In Crassostreinae, the genus *Saccostrea* and *Striostrea* have a denticles in marginal valves, named "chromata", and in genus *Crassostrea* is absent, characteristic of genus. Anatomically, promial chamber is present in Crassostreinae and Pycnodontinae, absent in others Ostreidae.

Crassostrea oysters, in Brazil, are popularly known as mangrove banks. These banks are formed in the intertidal and subtidal environment, both in bedrock and in the roots of *Rhizophora* trees. According to the dissertation presented in IBUSP (Amaral, 2010), there are two species occurring in Brazil: *C. rhizophorae* only in mangroves (intertidal zone) and *C. brasiliana* found on the rocky shores and mangroves (subtidal).

Species of the genus *Saccostrea* are common in rocky shores of the Indo-Pacific. The taxonomy of this genus is unclear, as the morphological plasticity among the constituent species raises confusion in the identification.

Significant anatomic differences were found in almost all structures, allowing species differentiation and identification. The differentiation between the species *Crassostrea* based only on the shell is complicated, since the structure has phenotypic plasticity and maybe changes caused by adaptation to the environment.

This work presents morpho-anatomical comparisons between four species of each genus: *Crassostrea rhizophorae, C. brasiliana, C. virginica, C. gigas, Saccostrea cucullata, S. echinata, S. palmula* and *S. scyphophilla*.

T16.P3

A SURVEY OF BIVALVES FROM NORTHERN SEABOARD OF THE SÃO PAULO STATE, BRAZIL

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In Brazil, it is estimated that there are around 1000 species of bivalves, and just approximately 400 have been registered. Only in the São Paulo State it is supposed that there should be around 300 species, of which over than 190 have been described. Despite the wide bivalve's biodiversity in the region, the knowledge is still scarce, especially about deep waters, which only recently began to be exploited. Considering the lack of updated records about molluscan variety and localization of these organisms at the northern seaboard of São Paulo State, the present work aims to produce a survey of bivalve species that inhabit the São Sebastião Channel, between Ilhabela and São Sebastião municipalities, from harvestings made between 2010 and 2012 in the intertidal and subtidal zones. A total of 388 living specimens were collected, from 52 species of 34 genera, belonging to 18 families of five orders of Bivalvia. The families, quantitatively ordered, were: Tellinidae, Veneridae, Semelidae, Ungulinidae, Mactridae, Solecurtidae, Corbulidae, Cardiidae, Lucinidae, Petricolidae, Nuculidae, Psammobiidae, Donacidae,

Solenidae, Periplomatidae, Thraciidae and Arcidae. Among the identified species, *Caryocorbula caribaea*, *Codakia pectinella* and *Diplodonta punctata* were the most abundant in intertidal, while *Macoma uruguayensis* and *Pitar fulminata* in subtidal zone. Rare species were also found, such as, *Thracia similis*, *Solecurtus sanctamarthae* and *Phlyctiderma semiaspera*. All specimens were meticulously dissected and conserved in order to investigate gametes, anatomy, shells and molecules. Our results created an inventory of species occurrences capable of contributing to management plans and preservation of the northern seaboard of the São Paulo State, a fragile environmental heritage.

Financial Support: PNPD/CAPES 1106/2010 and FAPESP 2010/15486-8.

T17

T17.O1

HOX AND *PARAHOX* GENE EXPRESSION DURING DEVELOPMENT OF THE TROCHID GASTROPOD *GIBBULA VARIA*: HOW IDIOSYNCRATIC ARE MOLLUSCS?

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Hox transcription factors are expressed in distinct, often overlapping, domains along the developing anterior-posterior body axis of animal embryos. During the intracapsular development of *Gibbula varia* all eleven detected *Hox* genes are expressed in ectoderm-derived cells, only *Hox5* is additionally detected in the entoderm. *Lox5*, *-4*, and *-2* are expressed in the apical organ during trochophore stages, and in the cerebral ganglia during veliger stages. Further posteriorly, *Hox2*, *-3*, *-4*, *-5*, and *-7* contribute in patterning the other major ganglia. *Hox1*, *Post1*, and *Post2* genes are involved in shell morphogenesis and seem to have lost their role in neurogenesis. Additional expression domains of *Hox7* and *Lox4* are the larval prototroch and velar areas, which contrasts with the expression of these genes in annelids where most of *Hox* genes are expressed in posttrochal area and are involved in segmental determination. This may indicate a fundamentally different role of these genes in Gastropoda, or even in molluscs in general. Whereas *ParaHox* gene expression patterns are similar to that of annelids, *Gibbula Hox* genes do not show spatial colinearity or expression in any mesodermal cells. Both features may be correlated with synchronizing ecto- and mesodermal differentiation in segmented animals. This study was supported by the MOLMORPH network (Marie Curie Fellowships for Early Stage Research Training, MEST-CT-2005 - 020542).

T17.O2

POU GENE EXPRESSION IN THE CEPHALOPOD *IDIOSEPIUS NOTOIDES*

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Cephalopods are considered the most intelligent invertebrates and possess a suite of sophisticated sensory organs and a complex central nervous system (CNS). However, remarkably little is known about the molecular mechanisms underlying their brain development. *POU* genes encode transcription factors which contribute to the correct spatio-temporal expression of target genes during CNS development. Previous studies on these homeobox genes have mainly focussed on vertebrate and ecdysozoan model species.

The present study is concerned with the expression of three *POU* genes during development of the CNS of the pygmy squid *Idiosepius notoides*. The expression of *InoPOU2*, *InoPOU3*, and *InoPou6* has been investigated in early developmental stages up to posthatching individuals. All three genes are solely expressed in a limited time frame in distinct developmental stages of *I. notoides*. *InoPOU3* is weakly expressed in the anlagen of the cerebral and palliovisceral ganglia of stage 19 embryos. Subsequent developmental stages exhibit *InoPOU3* expression in parts of the supra- and subesophageal masses. In contrast, no *InoPOU2* and *InoPOU6* expression was observed until stage 24. All three genes are strongly expressed in the supra-and subesophageal masses in stages 24-26 when the individual brain lobes differentiate. None of the three genes is expressed in late prehatching stages or hatchlings.

The present data argue for a role of *InoPOU2*, *InoPOU3*, and *InoPou6* in the differentiation of cephalopod brain lobes. The expression of *InoPOU3* during stage 19 suggests its involvement in the formation of the early ganglia which give rise to all adult brain lobes. All three *POU* genes therefore are expressed in the neurogenesis of *I. notoides* as their orthologs in other molluscs (gastropods) and bilaterians (e.g. fruit fly and mouse).

T17.O3

LOOK OUT! REVEALING PHOTOSENSITIVE STRUCTURES AND THE CORRESPONDING MOLECULAR BASIS IN THE SCALLOP, *ARGOPECTEN IRRADIANS*

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The adult scallop possesses up to 200 mirror-type eyes along the edge of mantle tissue that lines the left and right valves of the animal. Like nearly all photosensitive structures in metazoans, scallop eyes require a G-protein coupled receptor (GPCR) opsin bound to a lightsensitive chromophore to respond to light. We have identified two different Gq-coupled opsin genes expressed in the eye of the scallop, *Argopecten irradians*. The two genes contain amino acid motifs necessary for chromophore binding and protein folding, suggesting that both are functional. Surprisingly, these scallop opsin genes differ by 45% at the amino acid level, which is twice as many differences as seen between red and green opsins used for colour vision in primates. These data suggest that the two Gq-opsin proteins may respond to different wavelengths of light, providing preliminary evidence that scallops use dichromatic vision in a similar manner as trichromatic vision in primates. Dichromatic vision would require that opsins are 1) expressed in the same retina and 2) differ in wavelength sensitivity (function). Here, we address if scallops have the ability to detect contrast (dichromatic vision) by examining spatial expression patterns of opsin, and estimating function by modelling the tertiary structure of the two gene products. Results from our *in situ* hybridization experiments of eyes and other potential light-sensitive tissues determined that at least one Gq-opsin gene is expressed in the tentacle nerves. Additionally, comparison of protein folding indicates structural quantitative differences between the two Gq-opsin genes, suggesting divergent wavelength sensitivities. Future work will complement our results by directly measuring the wavelength sensitivity of each Gq-opsin.

T17.O4

IDENTIFYING THE MOLECULAR LINK BETWEEN PHOTOSENSITIVE TISSUES AND THE EYES OF THE BAY SCALLOP, *ARGOPECTEN IRRADIANS*

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Molluscs utilize a vast array of photoreceptive structures, such as complex eyes capable of spatial vision or simple photoreceptive neurons found in the mantle tissue (extra-ocular photoreception, EOP). EOP is ubiquitous in molluscs, while spatial vision has evolved independently multiple times. This pattern suggests that, through the recruitment of photosensitive machinery from one system to another, EOP may be an evolutionary source of eyes. Scallops (Pectinidae) are well known for mirror-type eyes found along their mantle edge on modified tentacles, and represent an excellent opportunity to study the relationship of EOP and vision. Here we test whether the scallop eye shares phototransduction systems with EOP in the mantle by analyzing gene expression in visual (eyes), putatively photoreceptive (tentacle), and non-photoreceptive (adductor muscle) tissues from the bay scallop, *Argopecten irradians*. RNA was extracted from tissues collected after 9 hours in dark or 9 hours in light then sequenced on the Illumina HiSeq2000. This study tests three hypotheses: 1) If scallop tentacles function in EOP and not solely chemoreception, they will contain the molecular components of the phototransduction pathway, which are required for photoreception; 2) Photosensitive organs will show increased expression levels of phototransduction genes under light conditions when compared to the dark treatment; 3) If the molecular components for phototransduction in the scallop retina evolved from EOP, phototransduction genes will be co-expressed between eye and tentacle. Alternatively, if the scallop eye did not evolve directly from EOP, but instead by the co-option of genes from other sensory systems, then different genes should be utilized for phototransduction in the eye and tentacle. Results from this work represent the first molecular characterization of mantle-based EOP in bivalves and identifies possible links between two independent photoreceptive systems, thus implicating mechanisms that generated the diversity of molluscan eyes.

T17.05

DEVELOPMENT OF THE MANTLE EDGE IN *NODIPECTEN NODOSUS* (BIVALVIA: PECTINIDAE) AND ITS IMPLICATIONS FOR UNDERSTANDING THE FUNCTIONAL ONTOGENY OF SCALLOP PALLIAL FOLDS

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The mantle margin has particular roles in the life of bivalves, interacting with the environment and playing several different functions. Generally, this region is comprised of three distinct folds with large morphological diversity in Bivalvia. In Pectinidae, the mantle edge is especially complex, with tentacles and pallial eyes scattered all over both margins, and a large curtain-like fold called velum. Although pectinids are a well-studied group, there are no specific studies performed on their mantle edge

considering its anatomy and development. Moreover, little information on pallial structures' morphogenesis is available for the family. How does the formation of these complex traits occur? What tissue and morphological changes are involved during ontogeny? These are important questions in need to be answered. In this context, the present study contributes with detailed anatomical information on the mantle edge at larvae, post-larvae, juvenile and adult stages of *Nodipecten nodosus* (Linnaeus, 1758), by means of histological and Scanning Electronic Microscopy techniques. During *N. nodosus* development, the larval mantle margin has a single rim related to shell and periostracum secretion. The greatest changes in the mantle edge design occur after metamorphosis, with the differentiation of the pallial folds prior to the establishment of subsequent pallial structures. Muscular and epithelial tissues are constantly modified along this process, and remarkable modifications in type and position of cilia were observed as well. Pallial organs have distinct developmental timing; the velum is formed first, and other specialized organs, such as tentacles and eyes, are originated later. We hypothesize that functional aspects are deeply associated to the anatomical changes of the mantle margin during the transition from larvae to juvenile stages. Finally, these original results on pallial margin differentiation in Pectinidae will provide a basis for broad comparisons of mantle development across major bivalve taxa.

T17.O6

AVOIDING MISIDENTIFICATIONS BY ONTOGENY: AN EXAMPLE BETWEEN *AGATHISTOMA VIRIDULA* AND *A. HOTESSIERIANA*(GASTROPODA, TROCHIDAE, TEGULINAE)

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Tegulinae is a subfamily of the marine gastropod family Trochidae that comprises about 40 species in six genera. The species level identification is normally simple, with the exception of the *Agathistoma* species. This study will portray misidentifications that occur between *Agathistoma viridula* and *A. hotessieriana*, mainly in juvenile specimens. *Agathistoma viridula* ranges from Costa Rica to the state of Santa Catarina, southern Brazil, while *A. hotessieriana* ranges from Florida (USA) to the state of Bahia, northeastern Brazil. Both live inintertidal rocks with overlapping distributions in northeast Brazil. In this study, wecompare the morphology of both species, being the main differences in the shell, soft-body color and digestive system traits. The shells of *A. viridula* reach about 25mm in height,while *A. hotessieriana* only about 13mm; juveniles of *A. viridula* differ from *A. hotessieriana* in having amore discoid shell; the first three whorls are slightly concave and the basic color consists in an intense whitish yellow with red to purple axial blotches, while in *A. hotessieriana* the three first whorls are convex and the color isa mildwhitish yellow with light brown axial blotches. Regarding the soft parts attributes, *A. viridula* differs from *A. hotessieriana* by having a different color pattern on foot and cephalic tentacles; *A. viridula* has a lateral projection on ommatophore; the dorsal folds of the middle esophagus of *A. viridula* differs from that of *A. hotessieriana* by being smaller and the left dorsal fold running straight to the posterior esophagus; while in *A. hotessieriana* the left dorsal fold runs to the left side under the diverticulum. Although there is some intraspecific variation on radular structures, both species differ on the apical cusps of rachidian and marginal teeth, and on the base of lateral teeth.

T17.O7

SHELL ORNAMENTATION: VARIX FORMATION AND GROWTH IN *NUCELLA LAMELLOSA* AND *CERATOSTOMA FOLIATUM* (MURICIDAE: GASTROPODA)

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Gastropods produce some of the most beautiful skeletons of any animal, often with complex ornamentation. This ornamentation is thought to reduce predation vulnerability, as well as being implicated in other functions. How snails control the growth and spacing of shell ornamentation is a significant unsolved puzzle of gastropod biology. Here we studied the growth of varices, periodic blade-like thickenings of the aperture, in, *Ceratostoma foliatum* and *Nucella lamellosa* (Caenogastropoda: Muricidae: Ocenebrinae). *Ceratostoma foliatum* has regular, synchronized varices with 120° spacing, while *N. lamellosa* has irregularly spaced varices with 10-50° between them, which sometimes split or double. As a shell grows, varices encountered on the body whorl are believed to stimulate the formation of new varices at the aperture, synchronizing varix location and creating constant spacing. Body whorl varices and/or the apertural varix were removed to determine how their absence affected future varix growth in both species.

In *Ceratostoma foliatum,* the presence of previous varices appears to stimulate the growth of new varices, but is not the only cue. When a varix is removed, the corresponding varix on the new whorl sometimes does not form, leaving a gap of greater than 120°. The addition of a varix in a foreign location also stimulates new varix production.

Nucella lamellosa varices appear to be weakly affected by previous varix locations; snail where the varices were removed form more simple varices, with less split or doubled varices. The effect of varix removal varies with size; larger snails with varices removed grow faster and have less space between varices than control snails, while the same is not true for smaller snails. This may relate to the time or effort required to remove varices during growth, as varices become relatively larger in larger snails.

T17.O8

TESTING A MORPHOMETRIC DISCRIMINATION BETWEEN TWO SPECIES CLUSTERS BELONGING TO THE PROTOBRANCH GENERA *LEDELLA* VERRILL & BUSH, 1897 AND *YOLDIELLA* VERRILL & BUSH, 1897, BASED ON HINGE PLATE CHARACTERS

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Preliminary results have shown that the hinge plate characters may have a strong role in discriminating among species complexes of *Yoldiella* and *Ledella*. However, no attempts have been made to discriminate between these genera based on hinge plate characters. The present work does that based on a restricted number of species and, consequently, must be understood as a preliminary attempt towards a true discrimination among these genera, based on the hinge plate. The following species were used in this test: *Yoldiella* *lapernoi* Benaim & Absalão, 2011; *Yoldiella paranapuaensis* Benaim & Absalão, 2011; *Yoldiella jeffreysi* (Hidalgo, 1877); and four unnamed species of *Ledella*. The measurements taken for the hinge plate were made on lateral view (six measurements) and dorsal view (nine measurements). The statistical analyses were initiated by a preliminary Correlation Test to exclude the redundant variables. The remainder morphometric variables were used to test the discrimination between the two sets of species (one set of *Yoldiella* species and another set of *Ledella* species). We have used 56 valves of *Yoldiella* and 56 valves equally distributed over the four species of *Ledella*. Since we had a large number of *Ledella* valves, we performed the analysis a second time, changing the *Ledella* specimens to increase the strength of the results. The statistical analyses correctly discriminated 99,1% of the valves of the first analysis and 100% of the valves of the second one. These results show that the hinge plate is apt to distinguish between the genera *Yoldiella* and *Ledella*, restrictedly defined by these seven species, and suggest that it might be a good instrument to distinguish the two genera as whole.

T17.O9

COMPARATIVE ANATOMY OF THE FASCIOLARIIDAE *PUSTULATIRUS OGUM* AND *HEMIPOLYGONA BECKYAE* FROM BRAZIL (GASTROPODA: NEOGASTROPODA: PERISTERNIINAE)

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The Fasciolariidae comprises marine gastropods of the order Neogastropoda, with more than 200 species distributed worldwide in three subfamilies. Peristerniinae is represented in Brazil by the genera *Polygona*, *Hemipolygona*, *Pustulatirus* and *Leucozonia*. As the anatomical knowledge of fasciolariids is scarce, and as part of a greater study of its morphology, the Brazilian species *Pustulatirus ogum* and *Hemipolygona beckyae* (originally depicted in the genus *Latirus*) were examined. The descriptions of shell, head-foot, pallial complex, digestive, nervous, excretory and reproductive systems were undertaken. Anatomically, both have similar characteristics, in agreement with other Fasciolariidae; the main differences occurs in the radula, nerve-ring and penis. Their radulae are as characterized for the *Latirus sensu latu* complex, in which the innermost cusp of the lateral tooth is well developed but always smaller than the other cusps; this features differs from *Leucozonia*: this cusp is reduced or absent. The radula of *P. ogum* possesses the rachidian tooth with four cusps, differing from other examined fasciolariids. Nerve-ring varies mainly according to statocyst position and buccal ganglia commissure. The penis possesses a terminal tapering, as described for other fasciolariids; the length of which may be long (longer than half of total penis length) as in *H. beckyae* or very short (shorter than half of total penis length) as in *P. ogum*. The meaning of the differences among soft-parts described here and that of other *Latirus sensu latu* species are still under analysis, depending on further study on more related taxa.

T17.O10

GASTROENDOSCOPY: AN INSIDE VIEW OF LIVE GASTROPODS

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The gastropod gill, or ctenidium, is the major structure in the mantle cavity. Its extensive area serves as the site for respiratory gas exchange and the cilia on its surface move water through the mantle cavity. Details of the anatomy of the ctenidium have been used to develop hypotheses regarding molluscan systematics and evolution. Despite its significance to the animal and to malacologists, images of the gill have been limited to studies of dissected and preserved material. To view live, functioning ctenidia, I inserted an endoscope through the apical opening of individuals of the keyhole limpet *Diodora aspera* and through the tremata of individuals of the red abalone *Haliotis rufescens*. The leaflets of living ctenidia are inflated, turgid structures that appear to completely fill the volume of the mantle cavity. They can contract using muscles in the walls of the leaflets and re-expand by inflating with blood. Flow through the gills of animals of both species in still water is extremely laminar, with parallel streamlines extending well outside the openings of the shell. Thus the ctenidia of live gastropods are dynamic, plastic structures that play an active role in responding to flow and particles moving through the mantle cavity.

T17.P1

EVOLUTION OF PARASITIC STRATEGY AND MORPHOLOGICAL DIVERSIFICATION IN THE GASTROPOD FAMILY EULIMIDAE

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Parasitism has evolved more than 60 times in the animal kingdom, with each lineage having pronounced species richness through host-parasite interactions. Parasitic animals have therefore had a significant role in the evolution of the entire life, but their history of diversification has been seldom discussed in a detailed phylogenetic context. Eulimidae is a representative lineage of parasitic gastropods in terms of its extraordinary species richness and wide variety of parasitic strategies (e.g. hemi-, ecto-, and endoparasitism). However, phylogenetic relationships, evolutionary history of host echinoderm utilization and acquisition of the different strategies have been essentially unknown for eulimids due in part to their rarity and inaccessibility.
Here we present the first comprehensive molecular phylogeny of the family based on five-gene sequences (ca. 3.6 kb) from 66 eulimids representing over 30 genera as well as from outgroup taxa including its sister family Vanikoridae. Bayesian and maximum-likelihood reconstruction of tree topology and ancestral character states revealed that (1) each of the five echinoderm classes except for Crinoidea is infected by multiple lineages of the parasites, (2) teleoconch and radula have been lost more than once in the evolution of eulimids since the late Cretaceous, and (3) globose to capuliform shells as well as endoparasitism have evolved independently in several of the lineages. The parallel acquisition of the broad shell and large attachment area may have been

adaptive consequences for avoiding predation pressure and/or dislodging by wave action in permanent ectoparasites and for reducing the cost of shell construction in endoparasites. Previous studies on parasitic animals have focused on the host-parasite interaction and host switching as the driving force for their diversification; however, the present results show that external factors, unrelated to host characteristics, can also greatly promote differentiated morphology and ecology and thereby the speciation of parasites.

T17.P2

NEW INSIGHTS INTO PALLIAL EYE DEVELOPMENT IN PECTINIDS REVEALED BY DETAILED MICROSCOPY STUDY OF *NODIPECTEN NODOSUS* (BIVALVIA)

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Pectinids, or scallops, are fan-shaped shell bivalves with a notable swimming behavior and epifaunal habit of life. Their eyes are situated along the middle pallial fold on both sides of the animal. The complexity of such organs has been attracting the interest of many zoologists since the XIX century, and, therefore, they have been intensively investigated, including physiological, anatomical and behavioral aspects. Nevertheless, eye development and morphogenesis remain scarcely studied, but these data are an essential component in the study of the evolution of complex traits in Bivalvia. Here, we provide detailed anatomical information on the development of the pallial eyes of the scallop *Nodipecten nodosus* by means of histological and Scanning Electronic Microscopy techniques. Pallial eyes are formed at the juvenile stage, few weeks after the metamorphosis. Initially, they occur as projections of the mantle bearing a pigmented epithelium and a spherical internal space. A cluster of cells fills this space and gives rise to important tissues: firstly the distal retina, then the proximal retina, and lastly the lens. At this stage, the reflector layer is already present, although its pigmented layer is not conspicuous. Remarkable changes in components' position, form and cell number were observed during eye development. The camera-type form is achieved earlier, followed by the expansion of the pigmented epithelium and eye stalk. It is generally assumed that, in adult scallops, pallial eyes have spatial vision with a complex mechanism of light and movement perception. The results obtained herein, however, suggest that developing eyes (present in early juvenile stages) are most probably not capable of more than a simple degree of photoreception.

T17.P3

WHAT THE GAMETIC MORPHOLOGY OF *FELANIELLA CANDEANA* TELL US ABOUT THE REMOVAL OF UNGULINIDAE FROM LUCINOIDEA?

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Species of Lucinoidea, particularly of the family Ungulinidae, are well known and abundant in diverse habitats where they are considered key elements in the trophic chain. Sexual cells features have been proved helpful in systematic reviews, phylogenetic analyses and reproductive biology studies. Using light and transmission electron microscopies, the spermatozoan and oocyte morphologies of *Felaniella candeana* were described. Some traits of the sperm cells such as the elongated nucleus, which tapers and exhibits a slight curvature, are modifications of the *primitive* type. The acrosomal vesicle is short, conical and contains a small amount of lytic substances. Mitochondria are laterally projected beyond the basis of the nucleus. The female gonad is composed by acinus surrounded by a thin wall that contains connective tissue and discontinuous layers of myoepithelial cells that develop large oocytes. The place of anchorage between the female gamete and the acinal wall is called stalk. Oogenesis in this bivalve seems to be classified into solitary type and the spawning patterns is denominated bradytictic. These suggest that *F. candeana* shows long periods of sexual cells production, trying to enhance reproductive success. A comparison of sperm ultrastructure among bivalves indicates that there is a certain correlation between the evolution of long sperm nucleus and large, yolk-rich eggs, proposing that the sperm nuclear shape is related to the size of the oocyte and the type of fertilization. One possible reason for the presence of an elongated sperm head is that this shape is more efficient than the *primitive* one for penetration into the jelly coat and cytoplasm of large oocytes. Recently, investigations suggest that Ungulinidae corresponds to a monophyletic group together with the clades: Arcticidae, Veneridae and Mactridae. The ultrastructural analysis of spermatozoa spawned by Ungulinidae reveals that these gametes resemble sperm cells produced by Veneridae, especially because of the presence of a nuclear curvature.

Financial Support: PNPD/CAPES 1106/2010, FAPESP 2010/15486-8 and PIBIC/CNPq.

T17.P4

MORPHOLOGICAL AND MOLECULAR IDENTIFICATION OF HYDROBIIDAE FROM BRACKISH LAGOONS IN SCOTLAND

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Four hydrobiid species are found in Scottish brackish lagoons; *Hydrobia acuta neglecta, Peringia ulvae, Ecrobia ventrosa* and *Potamopyrgus antipodarum.* Shell form is often used to differentiate between species but this is not reliable as it may be affected by

environmental and parasitic factors, consequently the accuracy of the published distribution is doubtful.

In April 2011, three lochs on North Uist (Outer Hebrides), were sampled for hydrobiids. Living specimens were identified using tentacle pigmentation patterns and a subsample of each phenotype from each loch underwent genetic analysis of the Cytochrome Oxidase I mitochondrial gene region. The species clades on the maximum likelihood tree show a general link with tentacle pigmentation patterns. The qualitative results suggest that tentacle pigmentation is a useful indicator of species identity, but that other features should also be taken into account.

T17.P5

MORPHOLOGICAL DIFFERENTIATION BETWEEN LARVAE OF TWO SPECIES OF *CRASSOSTREA* SACCO, 1897 (BIVALVIA, OSTREIDAE) FROM PARANÁ COAST, BRAZIL

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Crassostrea rhizophorae and *C. brasiliana* are native oysters of Paraná coast. The identification of larval shells of native species of *Crassostrea* Sacco, 1897 from plankton samples is a difficult task due to the similarity in size and morphology. Larva of both species has some characteristic features in common like an umbonate, inequivalve shell and provinculum bearing distinct teeth in some stages. Detailed studies of the morphology of larval shells along developmental stages and techniques of Scanning Electron Microscopy (SEM) supply information about modifications of the prodissoconch, important to differentiate con-generic species. In this work, the morphological characteristics of the prodissoconch were analyzed along the growth of laboratory reared larvae. Samples of larvae were collected during the cultivation and preserved in ethanol 70% and the dimensions of larvae, duration of larval period, growth of prodissoconch and number of teeth in the three larval stages: D-shaped larva, umbo larva and pediveliger were observed. For SEM analysis samples were treated with a solution of sodium hydroxide (5-10%) for the separation of valves and oven-dried before metallization. The result of the comparative study of growth of the prodissoconch of the two species indicated that *C. rhizophorae* has longer larval development period than *C. brasiliana*. Height in the umbo fase is more elongated in *C. brasiliana* larvae (211 µm) than in *C. rhizophorae* (145 µm). Height of pediveliger larvae of *C. brasiliana* reached 390 µm and of *C. rhizophorae* 337 µm. SEM analyses showed differences in the number of teeth of the prodissoconch of D-larvae of the two species with the presence of 2 teeth in the right and left valve of *C. brasiliana* and an edentulous provinculum in both valves of *C. rhizophorae*. Right valve of pediveliger larvae of *C. brasiliana* has 1 tooth in the anterior area and *C. rhizophorae* 2 teeth.

T17.P6

VARIATIONS IN THE EPITHELIAL GLAND CELLS IN *HELIX POMATIA, CEPAEA HORTENSIS* AND *ARION VULGARIS* – A COMPARISON

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Gastropods produce high amounts of mucus for different functions as defense, locomotion or protection against desiccation. As a consequence several gland types with different chemical compositions are present in the pedal epithelia. Although much is known about the gland cells in this animal group a direct comparison of the different glands is rare.

Within this study we analyzed on histochemical and ultrastructural level all epithelial glands of two different families (Helicidae *versus* Arionidae). Additionally micro computed tomography scans give an indication of the overall distribution of the gland cells. To visualize the carbohydrates more detailed, further immunohistochemical investigations are made.

The results indicate a great variety in the arrangement of the diverse cell types in the different species: *Arion vulgaris*, for example, has a large gland cell type in the body epithelium containing exclusively acidic proteins (Alcian blue staining at pH 1.0 and 2.5), while in *Helix pomatia* and *Cepaea hortensis* also carbohydrates (PAS staining) are present in this area. In the sole however, PAS-positive gland cells are present in all three species.

The question arises whether this variation in the gland chemistry and mucus composition is the result of different functions and/or related to the different living conditions of the animals. Further it will be interesting to find out whether the distribution of the pedal glandular system is related to the presence of a shell.

T17.P7

STRUCTURAL CHARACTERIZATION OF NEURONS AND GLIAL CELLS OF THE BIVALVE *SCROBICULARIA PLANA*

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The neurocytology of bivalves is poorly known and that of peppery furrow shell *Scrobicularia plana* was never studied. Better descriptions in this economically important bivalve are worthwhile because of a zoological interest and due to evidences that pollutants may disrupt its nervous system. *S. plana* does not have a single brain but rather three series of ganglia, which make the cerebral, pedal, and visceral ganglia

(interconnected by nerves), located in different parts of the body. To characterize the neuronal and glial cell types in this species we used light (LM) and transmission electron microscopy (TEM). Isolated ganglia were fixed for 3h in 2.5% glutaraldehyde, in 0.2M cacodylate buffer (pH=7.6) and post-fixed for 2h in 1% OsO_4 (same buffer). They were dehydrated and embedded in epoxy resin. Semithin sections were stained for LM with methylene blue-azure II, and ultrathin sections were counterstained for TEM with uranyl acetate and lead citrate. Silver staining techniques for neuronal projections were used at LM. Each ganglion has perineurium (outermost layer of collagen-like fibrous material with blood spaces), outer cortex, and inner medulla (or neuropil). Neurons exist throughout the cortex and glial cells stand in both cortex and medulla. Considering size and shape, two main types of neurons exist: big and intermediate/small. Two types of gliocytes also exist: dark and light. Neurons have roundish nuclei, having uncondensed or clumped chromatin. Some neurons contain cytoplasmic pigmented granules. The neurons are typically unipolar, but some (rarely) are bipolar; axons extend to the medulla. Synaptic contacts and vesicles occur both in cortex and medulla. Gliocytes are elongated or triangular, attaching to neurons or their projections. Generally, gliocytes are smaller than neurons, having higher nucleus to cytoplasm ratio. Yet, distinction between small neurons and gliocytes is not often clear and seems unreliable at LM. Underdoing studies will offer characterization refinements.

T18

T18.O1

MAKING SMALL DATA BIG: A SOLUTION FOR THE PUBLISHING BOTTLENECK IN BIODIVERSITY

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"Publishing bottleneck" is comparable to the "taxonomic impediment", but is caused by: (1) increasing amount of data due to the intensification of scientific exploration increases; (2) publishing in non-machine-readable formats, e.g. paper/PDF; (3) low uptake and inconsistent policies for data publishing; (4) pressure of administrators to publish in "high-impact" journals; (5) increasing difficulties with peer-review.

The *Biodiversity Data Journal* (BDJ) (www.pensoft.net/journals/bdj) and associated *Pensoft Writing Tool* (PWT) (www.pwt.pensoft.net) build on the experience of the highly successful ZooKeys and are launched within the EU-funded project ViBRANT. BDJ is the first work flow ever to support the full life cycle of a manuscript, from writing through community peer-review, publication and dissemination within a single, online collaborative platform.

BDJ publishes papers in all biodiversity science (taxonomic, morphological, genomic, ecological), with no lower or upper limit to manuscript size. The main types of manuscripts are: (1) single taxon treatments (e.g., new taxa, new names/synonyms, re-descriptions); (2) data papers describing biodiversity-related databases; (3) sampling reports; (4) local/regional and habitat-based checklists/inventories; (5) ecological and biological observations of species/communities; (7) identification keys; (8) descriptions of biodiversity-related software tools.

Text and data submitted to *Biodiversity Data Journal* are formally peer-reviewed and evaluated for technical soundness and the correct presentation of appropriate and sufficient metadata through a novel *community-based pre-publication* peer-review and possibilities to comment after publication (*post-publication peer-review*). Authors may also opt for an entirely public peer-review process. Reviewers may opt to be anonymous or to disclose their names.

The Pensoft Writing Tool (PWT) provides a set of pre-defined, but flexible, article templates, and import function from external databases (Darwin Core data, bibliographies), including track change and comments tools, revision history, online collaboration between authors and external contributors (e.g., mentors, potential reviewers, linguistic editors). Submission to the journal is simply at the click of a button.

T18.O2

ACTIVITIES OF THE PHILIPPINE MOLLUSK SYMBIONT INTERNATIONAL COOPERATIVE BIODIVERSITY GROUP

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The Philippine Mollusk Symbiont International Cooperative Biodiversity Group (PMS-ICBG; www.pms-icbg.org) is an NIH-funded collaboration that combines research on molluscan diversity with discovery of natural products from bacteria that live symbiotically in mollusks. Targets of the natural product research are compounds of pharmaceutical interest and enzymes that might be used for biofuel production. Pharmaceutical targets are sought mainly in neogastropods, with focus on Muricoidea and Conoidea, but with sampling broadly across the Gastropoda. Cellulase activity is sought primary in the Teredinidae, but also assayed in herbivorous gastropods. On the biodiversity side, the project has assessed the lumun-lumun method of sampling which was developed in the Philippines, helped move the World Register of Marine Species towards completeness for valid species of mollusks, resulted in the description of several species of conoideans, and cultured new strains of bacteria from *Kuphus* and other shipworms. Combining discovery of natural products with biodiversity discovery is a promising avenue for accelerating work in systematic biology, particularly in light of recent advances in comparative genomics.

T18.O3

MOUNTAIN KILIMANJARO ECOSYSTEMS UNDER GLOBAL CHANGE: STORY FROM SNAILS

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Biodiversity maintained by tropical mountain ecosystems is threatened by the combined impacts of global warming and the conversion of natural to human modified landscapes. This paper presents preliminary findings of the on-going study on abundance, diversity and composition of land snails in human-disturbed ecosystems of Mountain Kilimanjaro. Using a combination of direct search (for hour) and litter-sieving techniques, snails were sampled in a plot of 2500 m^2 in 5 units of each habitat: disturbed forests, home gardens, grasslands, shaded coffee plantations, full sun-coffee plantations and maize fields. Total number of snails per plot ranged between 0 and 102, while the number of individuals per species ranged from 1 to 57. A total of 32 species were collected accounting for 42.1% of published species and diversity per plot ranged between 1 and 20. As natural areas are increasingly reduced into isolated remnants, the importance of secondary habitats for species conservation has as well increased.

T18.O4

MOLLUSCS ASSOCIATED WITH CORAL REEF ISLA LARGA, SAN ESTEBAN NATIONAL PARK, CARABOBO STATE, VENEZUELA

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Coral reefs are defined as the most diverse tropical coastal marine environments. The wide variety of organisms inhabiting different microhabitats, therefore these systems are determined as a complex community, include invertebrates, among them the molluscs, which have a high density and wide distribution throughout the food chain and in the reef system. Studies of the community provide information on biodiversity and ecology of this ecosystem. In Venezuela, in studies of the eastern part of the country, special attention is given to groups of mollusks that inhabit soft bottoms and cropping lines, but only a few works were made in reef systems. Therefore, the aim of this work is to generate taxonomic information on the mollusk biodiversity associated with reef in Isla Larga, in the San Esteban National Park, as a scientific contribution for conservation. As a result of the sampling areas in Isla Larga reef during the years 2006 to 2009, specimens of mollusks were collect on the depth gradient from 0 to 18 meters deep by Scuba diving. For the first time were identified in Isla Larga, PN San Esteban, 25 families within the Phylum Mollusca and 38 species contained in the classes Bivalvia and Gasteropoda. The species collected have been reported from others Caribbean coral reefs, as well as in other tropical marine systems, like sea grass, mangrove and reef lagoons. Isla Larga shows important taxonomic information from a small area surveyed. Therefore, these findings strongly suggest that there should be an increased effort on more survey areas in the Parque Nacional San Esteban.

T18.O5

UNRAVELLING TAXONOMIC COMPLEXITIES IN THE ENDEMIC SOUTHERN AFRICAN GENUS *CHONDROCYCLUS* (CYCLOPHORIDAE)

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Chondrocyclus are small operculate land snails inhabiting leaf litter of forests. They are characterised by an ornate periostracum with axial pleats, hairs or flange-like extensions and a horny operculum with a spirally coiled fringe of fused bristles. The species have a fragmented distribution throughout eastern and southern South Africa, tied to the presence of forest and thicket. They belong to the tropical family Cyclophoridae, a group well represented in Asia and Madagasar, but with only 18 described species in mainland Africa, nine referred to *Chondrocyclus*. The genus was last reviewed in 1939, but species were overlooked since worn shells look alike, and few anatomical details were known. An up-to-date revision is provided and species-level taxonomy extensively updated in the light of new morphological data. Comparative morphological observations are provided for the protoconch, periostracum, operculum, radula and penis, all characters which exhibit phylogenetically consistent variation. Three main lineages are identified, each comprising two or more sub-lineages, based on the periostracum and a combination of the characters investigated. Two species from north of South Africa, occurring in Malawi and Zimbabwe respectively, are removed from *Chondrocyclus* based on the operculum and periostracum. *Chondrocyclus* is thus known only from South Africa although further collecting is likely to produce records from Swaziland and Mozambique. All species, barring the widely-distributed *C. isipingoensis*, are narrow-range endemics, emphasising the importance of conserving South Africa's remaining forests. The geographical distributions of the respective lineages are interpreted in the light of regional vegetation patterns and historical environmental phenomena which affected forest cover during the Plio-Pleistocene. Current understanding of the distribution of lineages based on morphology lays the foundation for further research and questions are highlighted around which hypotheses can be formulated.

T18.O6

MANGROVE-ASSOCIATED MOLLUSCS OF SOUTHEAST ASIA: DIVERSITY AND DIVERSIFICATION

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Mangrove forests are an iconic but threatened environment in SE Asia. While floristics and ecology have been widely studied, the evolution and diversity of the invertebrate fauna are poorly understood. The mangrove-associated molluscs of the Indo-Pacific are not very diverse, with around 100 species dominated by only three gastropod familes: Potamididae, Littorinidae and Ellobiidae. For the first two of these families, near-complete species-level molecular phylogenies and distribution data are now available, enabling reconstruction of historical processes of diversification and documentation of modern patterns of diversity. Mangrove littorinids (genus *Littoraria*) have a relatively long pelagic larval life of up to 10 weeks and most show wide, overlapping distributions in the central Indo-Pacific, with speciation only in peripheral areas (the 'stack of pancakes' model). In contrast, the potamidids have short-lived larvae (less than 2 weeks) and show very different patterns. For example, *Cerithidea* species show small, narrowly allopatric ranges, implying speciation within SE Asia (the 'mosaic' model). Several cases of coincidence among the boundaries between sister species suggest that vicariance speciation has occurred across recognized biogeographic barriers, including the 'Wallace Line' that is famous in the terrestrial realm. Now that distributions of mangrove molluscs are known in some detail, it is possible to plot species diversity across the region. Whereas mangrove plants conform to the familiar pattern of maximum diversity in the Coral Triangle of eastern Indonesia, mangrove molluscs are most diverse in the southern South China Sea and Java Sea, with implications for conservation efforts.

T18.O7

TAXONOMY, BIOGEOGRAPHY AND ECOLOGY OF TERRESTRIAL MOLLUSCS OF THE ATLANTIC FOREST IN PARANÁ STATE, SOUTHERN BRAZIL

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The tropical forests, subtropical and arid regions around the planet harbor a remarkable diversity of terrestrial molluscs that have intrinsic importance as vital elements in the natural environment where they evolved and are functionally important for the maintenance of ecosystems in which they live. Although research has advanced globally in recent decades, knowledge about this malacofauna remains in its infancy in Brazil, where it is estimated that less than 1/3 of its diversity is known. Considering the rapid rate of degradation of natural environments because of human development and vulnerability of terrestrial molluscs in relation to habitat loss, there are certainly species that are at risk of extinction before being properly known. In this context the focus is on the land of the State of Paraná, located in southern Brazil (25°15'04''S 52°01'17''W), bordered on the north by the São Paulo State, between the Atlantic Ocean (East) and Argentina (West). The surface of the region is distinguished by presenting five zones with limited geographic landscapes by mountain ranges, which are distributed 16 watersheds. The east-west extension of the state was originally covered by Atlantic Forest biome (83%), interspersed with non-forested formations (17%), which due to the longitudinal variation there are five distinct vegetation units that correspond to geographical areas. Given this panorama, the first step to fill part of this gap in scientific knowledge is an urgent need to conduct species surveys and the data publication that make this malacofauna known as well as the threat it faces. Based on the premise that terrestrial gastropods are sedentary animals that have intimate dependence of biotic and abiotic conditions related to the ecosystem in which they live, the fundamental hypothesis of this study is that these molluscs constitute a good model for analysis of biogeographic and ecological data. The work was divided into tree stages: 1° gathering of information about the species of molluscs of the Paraná State in the literature and in the museums collections (MHNCI, MZSP, MNRJ, ANSP, MCZ) and information on the geological evolution of the region; 2° Activity in field: species surveys in natural areas using standardized collection method; 3° Analysis Laboratory: 3.1: Systematic analysis; 3.2: To determine the richness, abundance and distribution of terrestrial mollusks in Paraná in macroecological approach; 3.3: To seek congruent distribution patterns among different species natural landscapes of Paraná based on phytogeographic units and delimit areas of endemism; 3.4: To assess the influence of vegetation types on the composition and stratification of terrestrial molluscs in Paraná and evaluate the influence the composition of litter on the community microgastrópodes (analyzed by GIS ArcGis and interconnected by statistical generalizations, e.g. Perarson's correlation, PCA and ANOSIM). We obtained 149 species (104 macrogastropodes and 45 microgastropodes), included in 53 genera and 25 families. Of this total, 38 species are believed to be new to science. We recorded 15 species non-Stylommatophora (9 Helicinidae, 3 Gymnomorpha, 2 Diplommatinidae, 1 Potieriidae). From this total were 23 exotic species, including two invasive species. The evaluation revealed a biogeographical and ecological series

unpublished results for understanding the patterns and processes on the diversity of terrestrial molluscs in the largest remaining of preserved Atlantic forest in Brazil, considered high-priority area to biodiversity conservation.

T18.O8

PHYLOGENY OF THE CAENOGASTROPODA – A MORPHOLOGICAL PERSPECTIVE

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The largest phylogeny only based on non-molecular characters, i.e., morphology, was recently published (Simone, 2011 – 305 taxa, ~1000 characters, ~3.500 states), raising a myriad of implications, including: 1. Comparison with molecular approaches of molluscan and gastropod phylogeny; 2. Insertion of any further taxon anatomically studied in the enormous data-matrix, in order to analyze its possible relationship under a morphological point of view; 3. Discussion on the possible utilization of any given structure to base taxonomy; 4. To base morphologically taxa so far only defined in molecular base; 5. To demonstrate that the morpho-anatomy has been prematurely neglected in Malacology, and that the issue is still source of important data and interpretations. All these features will be exposed under a comparative scenario and illustrations, in order to reintroduce of extra-molecular approaches in Malacology, to explore its importance and fundaments, and to show how important is to transfer to morphology conclusions only or mainly based on molecular scenarios. These aspects gain importance in a specialty that mostly deals only with shells. Examples of completely new taxa that have been found in Brazilian deep-waters, as well as polemic taxa, mainly from deep hot-vents, in such the taxonomy has been controversial, can be perfectly analyzed under the new matrix, with more secure taxonomical implications.

T18.O9

THE PRESENT KNOWLEDGE OF THE TAXONOMY OF TRIPHORIDAE (GASTROPODA) FROM BRAZIL

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The family Triphoridae comprises several species described worldwide, being usually recognized by their left-handed shell (although species of Metaxiinae are dextral), presence of three holes (aperture, anterior canal and posterior canal) and rhinioglossate dentition. It is considered as one of the "Big Five" families of marine mollusks in terms of richness. Although well studied in the Pacific, Europe and Caribbean, Triphoridae had never been subject of a large revision in Brazil, where many species need to be reported or described. Previously to this study, there were only 13 species (some of them are actually misidentifications) listed from the Brazilian coast, through general catalogues of mollusks or isolated registers of species. As part of a project aiming to know the real diversity of Triphoridae from Brazil, several works were published or are being prepared. A revision of Metaxiinae replaced the single species previously reported by five species, one of them new. The review of Triphorinae from a particular

region, the Vitória-Trindade Seamount Chain (southeastern Brazil), revealed 13 species, of which seven were new records of Caribbean species and two were new species. The current works on Triphorinae includes its review on another locality, the Campos Basin (southeastern Brazil), which adds 13 taxa to Brazil, nine of which will be described as new species; the study of about ten undescribed species from the Potiguar Basin (northeastern Brazil); the generic allocation of a deep water new species from Abrolhos bank (northeastern Brazil); and a large revision on the genus *Inella*. These studies indicate that at least 60 species need to be named or reported to Brazil. This project alerts for the importance of the alpha-taxonomy, enabling posterior studies on zoogeography, phylogeny and ecology, which can include the feeding association of triphorids on sponges and the importance of color on triphorids.

T18.O10

DECONSTRUCTING *DENDROPOMA:* A SYSTEMATIC REVISION OF A WORLD-WIDE WORM-SNAIL GROUP WITH DESCRIPTION OF NEW GENERA (CAENOGASTROPODA: VERMETIDAE)

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Identifying natural groups within the caenogastropod family Vermetidae has proven challenging. The sessile lifestyle of vermetids, with associated xenomorphically-distorted, overgrown, and corroded shells, has resulted in a long and confused taxonomic history based primarily on adult shell characters. In this study, we use morphological, anatomical, and molecular data to clarify systematics and phylogenetic relationships within the genus *Dendropoma* s.l. We assess generic names previously used in the *Dendropoma* group for availability. We describe 21 species, eight of which are new, place them into four robustly supported genera, two of which are new (*Dendropoma s.s.*, *Novastoa*, “new-genus-1”, “new-genus-2”), and describe the current state of knowledge of the distribution of these taxa. The genus *Dendropoma s.s.* is well supported in our phylogenetic analysis, and is additionally supported by reproductive traits and a novel mitochondrial gene order. Two subclades within *Dendropoma s.s.*, not formally recognized in this study, are characterized by convex or concave exterior surfaces of the operculum. The opercula of examined species within the genus *Novastoa* feature a well-developed mammilla on the internal surface and upright tightly packed spiral lamina on the external surface. The genera *Novastoa* and “new-genus-1” form a well-supported monophyletic group with the genus *Dendropoma s.s.*, although sister group relationships among these genera are not resolved. The fourth genus, “new-genus-2”, is more closely related to the vermetid genera *Eualetes*, *Thylaeodus*, and *Petaloconchus*, demonstrating that *Dendropoma s.l.*, is not monophyletic. The calcified operculum of “new-genus-2” is unique in the Vermetidae and examined species in this genus are also characterized by a translocation of the valine mitochondrial tRNA. Further study will encompass the full

range of morphological diversity in the Vermetidae to clarify the major lineages within this remarkable family of snails.

T18.P1

THE MOLLUSCA: A NEW REFERENCE

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After more than four years in preparation, a new molluscan text is nearing completion. This text will provide the first updating of the general molluscan literature in 15 years; a period of phenomenal advancement in knowledge, approaches, and methodologies in malacology. Extensively illustrated with hundreds of new colour figures prepared mainly by Julie Ponder, this text covers general biological topics as well as molluscan fossil history, and individual taxon treatments of major groups. General chapters bring together a diverse and extensive literature to cover topics such as morphology, physiology, immunology, circulatory and excretion systems, development, and reproductive biology. Taxon chapters provide overviews of phylogeny and classification as well as more specific and detailed coverage of biology, fossil record, and natural history. Individual chapters are also devoted to natural history (including ecology), human interactions, and current research topics. Phylogenetic trees are incorporated into many of the illustrations where they are informative and provide evolutionary scenarios for traits and taxa. Functional groups and guilds are also treated where they provide a better entree into the subject. While no single volume can truly cover the extensive depth and breadth of the molluscan literature, the text is heavily crossed referenced to several thousand publications. We expect publication in late 2014 or early 2015.

T18.P2

OPENING BIODIVERSITY DATA: DATA PAPERS AS INCENTIVE FOR RESEARCHERS AND INSTITUTIONS

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A Data Paper is a scholarly publication whose primary purpose is to describe a data, rather than to report a research investigation. As such, it contains facts about data, not hypotheses or results based upon data. Data Papers are designed to (1) provide a citable journal publication that brings scholarly credit to data publishers; (2) describe the data in a structured human-readable form; (3) bring the existence of the data to the attention of the scholarly community.

The description should include several important elements (usually called *metadata*), that document how the dataset was collected, which taxa it covers, the spatial and temporal

ranges of the data, information on data collectors and owners, software used to create or view the data, etc. The metadata can be used to form a data paper manuscript.

An important feature of Data Papers is that they should always be linked to the data they describe through an URL, ideally resolving a DOI. Conversely, the metadata describing the dataset held within data archives should include the bibliographic details of the Data Paper once that is published.

At the time of submission of the Data Paper manuscript, the data described should be freely available online in a public repository under a suitable data license, so that they can be retrieved for reuse, resampling and redistribution by anyone for any purpose, subject to one condition at most - that of proper attribution using scholarly norms.

GBIF and Pensoft pioneered a workflow between the GBIF's Integrated Publishing Toolkit (IPT) and the journals ZooKeys, PhytoKeys and MycoKeys to automatically export metadata into the form of a data paper manuscript. Recently, Pensoft launched a new Biodiversity Data Journal along with an article authoring platform called Pensoft Writing Tool (PWT). The workflow was piloted within the EU-funded projects ViBRANT and EU BON.

T18.P3

MOLLUSCA IN THE CATALOGUE OF LIFE: TOWARDS A GLOBAL CHECKLIST

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Mollusca represents one of the major gap areas in the Catalogue of Life (CoL). The overall completeness (species in the CoL/estimated species number) of the entire CoL is around 70%. The number of estimated living species in Mollusca ranges from around 85,000 to 150,000 hence the completeness in the CoL might range from 49% to only 28%. Especially large taxa with marine, freshwater and terrestrial species, like the class Gastropoda, have no Global Species Databases (GSDs) yet and consequently are extremely underrepresented in the CoL.

The strict marine classes Caudofoveata, Cephalopoda, Monoplacophora, Polyplacophora, Scaphopoda and Solenogastres (together 2,571 species) are provided by World Register of Marine Species (WoRMS) to the CoL. For the other two groups, Bivaliva and Gastropoda, the new procedure ProtoGSD was applied in i4Life project (EC-FP7-i4Life-project-261555). This brings data from different thematic databases (WoRMS of marine species, FADA of freshwater bivalves and MolluscaFW of freshwater gastropods) and regional databases (pulmonates from Australia – AFD Pulmonata and New Zealand – NZIB) together. The merging was not done automatically due to taxonomic conflicts. The WoRMS taxonomy was taken as a master classification and data from the other providers were added. The number of molluscan species in the CoL could be therefore fundamentally raised from 14,277 species in AC 2012 to 41,655 in the AC 2013 and its completeness was almost tripled (now approx. 42% by 100,000 species estimated). As CoL only includes the basic ranks (Phylum, Class, Order, Superfamily, Family, Genus and Species) in a simplified management classification some adjustments were needed to integrate the multiple intermediate ranks (e. g. Subclass, Infraclass, Suborder) widely used in molluscan classification.

ProtoGSD is an effective procedure to provide data with global coverage until GSDs are available. However, Gastropoda are extremely underrepresented in the CoL and especially land gastropods need further improvements.

T18.P4

DATABASING EFFORTS WITHIN THE DEPARTMENT OF MALACOLOGY AT THE MUSEUM OF COMPARATIVE ZOOLOGY (HARVARD UNIVERSITY)

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In 1859, Louis Agassiz founded the Museum of Comparative Zoology (MCZ) at Harvard University. The enthusiastic oversight of past curators namely John G. Anthony, William J. Clench, Ruth D. Turner and Kenneth J. Boss enabled the Department of Malacology at the MCZ to develop one the largest and most diverse collections in the world. The collection is rich in types, and currently includes over 377,000 cataloged lots and at least another 150,000 uncataloged lots. Overall strengths of the collections include western Atlantic species, North American Unionidae and Pleuroceridae, deep-sea mollusks, Teredinidae, Achatinellidae and other pulmonate groups.

Associated specimen data for all cataloged lots has been captured in our Museum wide database (MCZbase). Our data is fully searchable (http://mczbase.mcz.harvard.edu/SpecimenSearch.cfm) and is compatible with ongoing efforts of other external shared databases (i.e. EOL, GBIF, BISON). Additionally, MCZbase provides a means to illustrate species distribution maps, specimen images, literature and direct links to historical data written in our specimen ledgers. The uses of MCZbase are highlighted in this poster.

T18.P5

THE VOYAGE OF LA BONITE, 1836-1837
1. THE DRY MATERIAL AT THE NATURAL HISTORY MUSEUM, LONDON

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In 1854, 428 specimens collected during the circumnavigation of the corvette *La Bonite*, 1836-1837, were donated to the Natural History Museum in London.

In January 2012 I began the curation of 85 dry lots of this historically important collection which needed remedial conservation, comprehensive labeling and annotation as the material was cited in many relevant journals and books. As a result a large number of type specimens have been identified and were incorporated into the type collection.

T18.P6

MOLLUSCA SECTION IN NATIONAL MUSEUM OF WALES

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The Mollusca Section in the National Museum of Wales covers a wide range of taxonomic research in land, freshwater and marine molluscs. To assist this research we have established the capability to work at the molecular level to answer species level questions and to analyse higher-level phylogenetic relationships. To keep up with technological advances we also produce open online resources such as the taxonomic tool 'Marine Bivalve Shells of the British Isles' and the collections based 'Mollusc Types Catalogue'.

This poster demonstrates the wide capabilities of National Museum Wales in providing Worldwide Institutions with taxonomic knowledge from its staff and vital historical data from its extensive collections.

T18.P7

A PRELIMINARY ASSESSMENT OF THE FRESHWATER MUSSEL RESOURCES IN NATURAL HISTORY MUSEUMS

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Natural history museums around the world often contain collections of freshwater bivalves of the order Unionoida, encompassing 6 families. These resources vary with the focus, age of the museum and its geographical location. Many are composed primarily of dry shells; some have a small amount of alcohol preserved specimens, comprised mostly of local species. These same collections may hold primary type specimens, often unmarked as types. Most collections are composed of specimens collected by amateurs as well as prominent malacologists. Some museums have digitized their collections so the contents of the collections and type holdings are available on the World Wide Web. University museums, local museums as well as some large museums have collections that are undigitized and unreported. Today with the rapid decline in many aquatic species, historical specimens and locality data are valuable for conservation and understanding the former ranges of these rare, endangered or extinct taxa. Having access to georeferenced specimen occurrence data allows researchers to address important scientific and societal questions in areas such as endangered species conservation, environmental restoration, species habitat relationships and documenting global climate change. This poster is a preliminary compilation of unionoid museum data. These data will assist in locating specimens and types or collections that will be useful in: taxonomic and phylogenetic research, conservation, history of science and convincing funding agencies that modern specimen resources for the study of these animals are not currently available in museums today.

T18.P8

HAWAIIAN LAND SNAIL BIODIVERSITY: SYSTEMATICS, PHYLOGENETICS AND CONSERVATION STATUS OF A VANISHING FAUNA

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Although islands comprise only 5% of the earth's landmass, the study of their biota has been and remains critical to the development of major theories in ecology and evolution. The Hawaiian archipelago serves as a prime example. Of the islands' numerous spectacular radiations, one in particular has enormous potential to inform our understanding of speciation, island biogeography and evolutionary ecology: Hawaiian land snails. As few as 21 colonists from 10 families have resulted in an estimated 752-1461 Hawaiian land snail species. They exhibit an exceptional degree of endemicity (>99%), with many single island or even single ridge endemics. Unfortunately, like land snails globally, they are vanishing faster than we can study them due to habitat loss, invasive species, and climate change. An estimated 50-90% may already be extinct, but their real conservation status is unknown because most have not been studied in any detail for over 60 years. In order to address this lack of knowledge our Hawaiian Land Snail Biodiversity project aims to comprehensively update the taxonomic and conservation status for all Hawaiian land snail families using an integrative systematic approach, combining field surveys, phylogenetics, anatomical descriptions and biogeographic analysis. Our primary goals include: 1) completing a comprehensive and systematic survey of the remaining Hawaiian land snail fauna, 2) developing comprehensive phylogenetic hypotheses for all Hawaiian land snail species using material from the surveys in goal 1 and extensive museum material, and 3) completely updating the taxonomic framework of Hawaiian land snails and describe/redescribe taxa as necessary. This work is underway and we have already completed 431 surveys across the main Hawaiian Islands, recording 25644 specimens from >99 native species, many that were thought extinct. Considerable progress has been made in the phylogenetic reconstructions for several families (notably, Achatinellidae, Amastridae, Helicinidae, and Helicarionidae), revealing high levels of cryptic diversity.

T18.P9

DISTRIBUTION PATTERNS OF MANGROVE GASTROPODS FROM THE INDO-WEST PACIFIC

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Biogeographic studies on coral reefs in the Indo-West Pacific have revealed interesting patterns, especially the existence of a "Coral Triangle," hosting the highest diversity in the region. Mangroves in the Indo-West Pacific also possess high marine biodiversity, but the animal diversity within those coastal forests has been poorly explored and most invertebrate mangrove taxa await taxonomic revision. However, taxonomic knowledge is essential to properly address questions in many other areas, such as conservation, evolutionary biology, and biogeography. Our lab has undertaken extensive fieldwork in the mangroves of the Indo-West Pacific, particularly South-East Asia. All gastropod taxa are collected and species are being delineated using morphology and DNA sequences. Many groups of gastropods are found in mangroves, but the most diverse are by far the onchidiid slugs and ellobiid snails. Some interesting geographic patterns that we have begun to see will be presented, based on preliminary data from India, Singapore, Malaysia, Sumatra, Borneo, Northern Territory and New South Wales (Australia). Additional fieldwork is planned in other parts of the Indo-West Pacific, which will allow us to more accurately determine species diversity and patterns of geographic distribution. On a longer term, we are interested in comparing patterns of diversity and distribution across gastropod taxa or between neighboring mangroves and coral reefs.

T18.P10

HOW MANY LITTORAL MARINE MOLLUSCS ARE THERE IN THE AZORES?

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The majority of our knowledge of marine biodiversity is derived from data collections in museums and universities and also from scientific publication or research reports. The ATLANTIS database is one of the many databases that compile important information about species occurrences allowing a descriptive analysis of species distributions in the archipelago of the Azores. It encompasses a large subset of taxonomic groups, including terrestrial lichens, bryophytes, vascular plants, molluscs, arthropods, vertebrates and coastal invertebrates. From a total of 145825 marine point occurrences, a total of 864 species of coastal marine invertebrates and 198 species of algae are reported to be present in the Azorean archipelago. This database comprises 864 coastal marine invertebrates with distributional data on a 500 meters grid. Taxonomy, geo-referenced distribution data, species description, conservation status are some of the available information

within the database that was retrieved from published scientific literature dating back to 1858. One hundred and seventy six publications were carefully screened for records on marine invertebrate species and data on collection sites was included in the database. Coastal and marine species number is still underestimated in the Azores. However, a major effort was made to reveal a baseline taxonomic dataset and marine organisms perform about 23% of the Azorean registered biodiversity, where the Molluscs are the most representative Phylum (44.0% of marine invertebrates). Available information allows calculating the species richness, rarity or complementarity, and marine littoral molluscs' diversity (specific richness) is analyzed throughout the archipelago, in relation to the amount of publications and to the evolution of marine biodiversity research in the Azores. In fact, the knowledge on marine malacological biodiversity matches the evolution of research as number of publications on the issue increased over time, with an average of 1.8 publications per year until 1989 and an average of 9.3 between 1990 and 2010. The increasing number of publications in the last two decades resulted mainly from the establishment of a local scientific community in the University of the Azores, performing research in Malacology and organizing the scientific expeditions and Workshops of Malacology, organized by the University of Azores. In terms of spatial molluscan biodiversity pattern in the archipelago, São Miguel is the island with the highest molluscan species richness recorded with a total of 281 species, followed by Faial with 167 (less than 41% of the reported species number for São Miguel). However, sampling effort regarding this taxonomic group is not the same at all Azorean islands, as São Miguel and Faial are also de islands where most marine research has been focused, reflected by a higher number of scientific papers in the database. Therefore, higher research effort should focus in other areas of the archipelago before an inventory closer to completion could be attained.

T18.P11

CURRENT RESEARCH ON SHELLFISH WITH THE IBIS PROJECT

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Marine invertebrates provide important economic and food resources for humans. On the island of Ireland, the blue mussel *Mytilus edulis* aquaculture industry, the European flat oyster *Ostrea edulis* fisheries and aquaculture, and culture of the Pacific oyster *Crassostrea gigas* are current key commercial molluscs. With the new international IBIS project (funded from the European Union INTERREG IVA Programme 2012-2015), we are working to develop evidence-based management approaches for the environmental and commercial sustainability of native shellfisheries and aquaculture for a broad range of molluscan fisheries species. Field and laboratory research on *O. edulis*, *C. gigas* and *M. edulis* is being carried out to further understand their biology and ecology as a basis for informing policy, including improvements to yield but also direct empirical test of stress during handling and live transportation. To help predict impacts of near future climate change on shellfish stock management, our research includes laboratory manipulations

of other species that are caught wild with limited regulation (such as *Buccinum undatum*), which may be particularly vulnerable to future climate change, or may indeed provide the fisheries of the future.

T18.P12

REVISION OF THE AFROTROPICAL LAND SNAIL GENUS *AVAKUBIA* PILSBRY, 1919 (STREPTAXIDAE)

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Huge areas of central Africa are effectively *terra incognita* with respect to terrestrial Mollusca, not only due to undercollecting. Taxonomically "better known" species and higher taxa regularly turn out to be heterogeneous upon closer examination. This provides an impediment for biogeographic studies, for which land snails are otherwise eminently suited.

The present study of the streptaxid *Avakubia* is a good example. The taxon was introduced for a single shell of the type species *Gulella* (*Avakubia*) *avakubiensis* Pilsbry, 1919, from the eastern Democratic Republic of Congo (DRC). Between 1934 and 2010 the species was reported from scattered localities between Liberia and Uganda, covering a linear range of nearly 5000 km. This species was considered an example of a land snail distributed across the entire African forest belt. A second species, *Gulella* (*Avakubia*) *acuminata* Thiele, 1933, also introduced on the basis of a singleton, was reported again in 1998.

We studied all available material reported in the literature and additional museum specimens identified as *Avakubia* (including recently collected material), *ca* 150 specimens in all, of which 115 adult shells. On each adult shell 11 measurements were made and analyzed. Where possible, conchometric data were supplemented by soft part characters, and by data on protoconch and internal shell structures using SEM and micro-CT scan observations.

Material previously reported as *Gulella* (*Avakubia*) *avakubiensis* appeared to embrace six distinct morphospecies, each with a much more restricted range. On the basis of both conchological and anatomical characters we classify *Avakubia* as an independent genus with at least nine species. In addition, a superficially remarkably similar, but conchologically and anatomically distinct radiation is recognized with four species.

T18.P13

REDESCRIPTION OF *CORNISEPTA CROSSEI* (DAUTZENBERG & FISCHER, 1896) (MOLLUSCA, GASTROPODA, FISSURELLIDAE)

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The family Fissurellidae is composed by prosobranch gastropods of rocky habitats, from the foreshore area to the deep sea. They are characterized by a conical and patelliform shell with a wide aperture and an apical, subapical or marginal foramen.

The family classification is only based on morphological characters (radula, shell and mantle characteristics) and it's highly discrepant according to different authors, from two to five subfamilies. Although Fissurellidae species are often included in molecular phylogenies, there are few specific studies of this group and, therefore, a broader study of Fissurellidae species is necessary to improve the correct understanding of this family.

In this communication the species *Cornisepta crossei* (Dautzenberg & Fischer, 1896), which is only described in the original description, it's redescribed from a total of 263 specimens. The material was collected through the French campaigns Seamount I (1987) and Seamount II (1993) and several Spanish campaigns like Cangrexo 1991, DIVA-Artabria I 2002, DIVA-Artabria I 2003 and Sarridal 2007. The specimens were found in different Banks from NE Atlantic (Galicia, Atlantis, Hyeres and Irving Banks) and in the drop-off of the Galician coast, between 650 and 1191 m at depth.

This material was studied and a detailed study of the shell to the SEM is presented, describing the identifying characters. Besides, a biometric study with the corresponding form index is provided and unknown characters not considered in the scientific literature until now are described.

T19

T19.O1

THE LAND SNAILS OF PENNSYLVANIA, USA: LIKELY EFFECTS OF GLOBAL WARMING UPON SPECIES' DISTRIBUTIONS

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Land snails are relatively immobile animals whose latitudinal and altitudinal ranges may not readily shift in response to climate change. Even if capable of range shifts, high-altitude endemic snails may have little room in which to expand (in Pennsylvania, elevations 700-978 m represent only 2% of land area). We examined whether some land snail species in Pennsylvania are limited to upper elevations to assess whether climate warming poses a threat to them. We surveyed land snails at 108 sites across twelve regional transects at regular 100 m intervals of elevation from 100 to 900 m, and habitat characters at each site were measured. Nine species occurred primarily at higher elevations and are likely to experience population declines with climate warming. In addition, multivariate analyses of region, elevation, latitude, soil chemistry, and other habitat factors were used to describe habitats currently occupied by land snail species.

T19.O2

IMPACT OF ENVIRONMENTAL VARIABLES ON THE DIVERSITY OF FRESHWATER MOLLUSCS

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The Narmada river is one among the important river of India, which is subjected to the pollution day by day, due to various anthropogenic activities. Change in physico-chemical parameters of river due to pollution, imparts negative effect on the diversity of Molluscans. The present study was carried out for the period of 24 months from August 2009 to July 2011 at four selected stations viz S_1, S_2, S_3 and S_4 respectively. During the present study about 17 species of class Gastropoda and 8 species of class Pelecypoda were recorded. The molluscan diversity was maximum in April- May months and minimum in July- August months. The value of Shannon and Weaver Index (H) varied from 2.7 to 3.1, indicating the water quality and diversity of species. Both gastropods and pelecypods showed strong negative correlation with turbidity, nitrate, alkalinity and phosphate at all four stations, while strong positive correlation was observed between molluscan species and pH. Multiple k- dominance plot of all stations facilitated the discrimination of molluscs according to species' relative contribution to standard stock. The results of present study showed that the freshwater biodiversity is altered by the change in the physico-chemical parameters of river. Thus regular monitoring of water parameters is necessary in maintaining the diversity of Molluscs.

T19.O3

EFFECT OF TEMPERATURE ON EMBRYONIC DEVELOPMENT OF THE MARINE GASTROPOD *CHARONIA SEGUENZAE* (ARADAS & BENOIT, 1870)

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The encapsulated development of the marine gastropod *Charonia seguenzae* (Aradas & Benoit, 1870) was studied under 3 temperatures (17, 20 and 23 °C). One hundred eighty (180) egg capsules that were deposited the same day, by the same individual (23,1 °C) and were at the same developmental stage (1 cell stage) were used. At the stage of blastula (7th Day After Deposition – DAD) they were separated in three groups of 60 capsules. One group remained at 23 °C and the other two were acclimated at 20 and 1 °C. Two randomly sampled capsules were collected from each temperature (every day during the first 5 days, D1-D5, every two days from D7 to D17 and every three days from D20 to eclosion), weighed, opened and the eggs, embryos or larvae were photographed under stereoscope. Stages of development, shape and dimensions were studied and measured on microphotographs. All developmental stages were described in relation to temperature and time. At 23 °C eclosion occurred 49 days after capsule deposition, at a free swimming veliger. Embryonic development at 23 °C was 17 and 24 days faster than 20 °C and 17 °C respectively. Temperature is a factor that affects not only the developmental rate but also the size of the embryos, with lower temperature leading to the eclosion of larger individuals.

T19.O4

TEMPORAL VARIATION IN REPRODUCTIVE PHENOLOGY OF *PATELLA* SPP.: PAST AND PRESENT

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Global changes occurring in the biogeochemistry of the oceans may influence the ecology of the biota. There is evidence that species are reacting to changes in climate through variations in the abundance and phenology with many species showing a poleward shift in their distributional range. The rocky intertidal is a relatively simple ecosystem but highly susceptible to anthropogenic activities and is thus an excellent model system for the understanding of the consequences of change in climate. This study presents a preliminary analysis of the changes in gonad phenology of *Patella aspera* over time. *Patella aspera* is being collected in various locations of the São Miguel Island (Azores) and their gonad development assessed visually using a trained observer. These data are then compared to unpublished data on gonad development collected in the period of

1985-1987through a chi-square test of independence.Overall, in contrast to the period of 1985-87, there was a much lower number of individuals reaching maturity (gonad development stages IV and V) in 2012-2013 and there was no clear peak in spawning. In addition, the resting period appears to be starting in June, one month delayed compared to data from 1985-87. These variations are important and may affect the population dynamics of the species.

T19.O5

δ^{18}O AND δ^{13}C RECORD OF *VIVIPARUS DILUVIANUS* (KUNTH) SHELLS FROM HOLSTEINIAN DEPOSITS AT ORTEL KRÓLEWSKI AND SZYMANOWO, EASTERN POLAND

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The research is conducted at 2 sites of lake deposits of the Holsteinian Interglacial (MIS 11) in Eastern Poland – Ortel Królewski and Szymanowo. Stable oxygen and carbon isotope composition of *Viviparus diluvianus* shells is investigated in 13 samples. Samples are arranged according to the shell shape changes, noted in different parts of the interglacial identified by pollen analysis. They are chosen in relation to the mean values of the slimness index, which correspond to the certain parts of the interglacial, characterized by definite climatic conditions. One sample comprises 3-5 complete, mature individuals of similar age (the same number of growth segments) living at different time (various pattern of growth lines).

Values of δ^{18}O and δ^{13}C at Ortel Królewski varies from -7.73 to -7.23‰ and from -10.06 to -9‰ respectively. Maximum of δ^{18}O corresponds with the *Taxus* zone of the Holsteinian and the highest slimness of *V. diluvianus* shells (1.41), whereas similar shells from the climatic optimum has the lowest values of δ^{18}O. This may result from deepening of the lake. Constant rise of δ^{13}C in the lowermost part of the profile points to amelioration of the climate. Maximum values in the intra-interglacial drying and cooling of the climate may be connected with the lake shallowing. At Szymanowo oxygen and carbon isotope curves represent intervals of -8,61 – -7,77‰ and -9,7 – -8,85‰. Samples are correlated with the final part of the climatic optimum and the post-optimal period. Depletion in δ^{18}O and δ^{13}C values confirms deterioration of the climatic conditions. Fluctuations in δ^{13}C curve towards higher values coincides with the cooling of the climate and periods of drop of the water level, noted in pollen and biometric studies of *V. diluvianus* shells.

Project financed by the National Science Centre, Poland, given on the base of decision DEC2011/03/B/ST10/06329.

T19.P1

T19

CHARACTERIZING DIVERSIFICATION PATTERNS AND DIET EVOLUTION IN CONE SNAILS

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Why are some clades more diverse than others? Evolvability, or a lineage's intrinsic capacity to adapt and diversify, is thought to account for differences in diversity between clades. One component of evolvability is modularity, or the degree in which characters (e.g., phenotype, genes, developmental networks) are able to evolve independently. Over long evolutionary time-scales, lineages with greater evolvability should (1) exhibit higher levels of diversification rates and species richness and (2) exhibit greater levels of phenotypic variance.

I propose to test these predictions in cone snails. Cone snails within the diverse genus, *Conus* (>500 spp.) are a group of predatory snails that typically feed on worms, molluscs, or fish, and capture their prey using a cocktail of venomous neurotoxins (conotoxins). This group is appropriate for two reasons. First, conotoxin genes are well-studied – gene duplication and strong diversifying selection across conotoxin gene superfamilies is thought to allow this group to specialize and partition resources. Gene duplication can increase evolvability because the copied gene is allowed to evolve independently, potentially facilitating the rise of new phenotypes. This provides a natural way to quantify differences in evolvability between clades. Second, species diversity is not distributed evenly in this group - nearly 70% of cone snails are vermivorous (worm-earing). Thus, *Conus* provides a unique opportunity to test whether evolvability predicts the magnitude and rate of diversification.

To begin this work, I present preliminary results characterizing diet evolution in *Conus*. I generated a fossil-calibrated phylogeny of 222 species using six previously published loci. Then, I used phylogenetic comparative methods to characterize diet evolution and test whether diversification rates depend on diet. Finally, I propose future work to quantify the relationship between evolvability and diversification.

T19.P2

EXPERIMENTAL DROUGHT EFFECTS THE REPRODUCTION OF BROODING CLAUSILIID *A. BIPLICATA* (MONTAGU, 1803)

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A. biplicata is a viviparous land snail inhabiting Central Europe. Its distribution to the East seems to be limited by the increasingly continental climate (frosty winters and dry summers). To investigate the effect of drought on reproduction of the species we kept snails in dry boxes without any water supply. Control group of snails were kept under high constant humidity. For the experiment we collected snails in the field during their reproductive period.

The proportion of brooding snails in both groups exceeded 50% at the beginning of experiment. After 2 weeks all individuals were dissected and their reproductive activity was assessed (number of released neonates, intrauterine brood size, stages of embryo development). Embryos brooded in snails kept in dry boxes developed to the most advanced stage (shell with > 2 whorls) but were not released. 66% of snails brooded embryos at the end of experiment; 72% of brooded embryos were fully developed and already hatched in the uterus. New eggs did not appear in the uterus during laboratory treatment (3% of eggs without shelled embryo). Control group of snails kept under high constant humidity released neonates in the first and the second week of the experiment. 31% of these snails reproduced; litter size averaged 7.2 neonates (range 3 –

15). The individuals started to incubate new broods (65% of snails brooded at the end of experiment; 35% of brooded eggs were without shelled embryo; average brood size equaled 7.12 eggs/embryos (range 1-16).

The results of the experiment indicated that the period of drought hindered releasing the neonates and producing new broods while embryos already stored in uterus continued to develop. Two weeks long drought did not cause the mortality among adults nor brooded embryos but significantly influenced the reproductive success of individuals.

T19.P3

PREDICTING THE IMPACTS OF CLIMATE CHANGE ON THE DISTRIBUTION AND CONSERVATION OF ENDEMIC TERRESTRIAL SNAILS IN MADEIRA

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The studies regarding the impacts of climate change on global biodiversity have increased over the last years. However, a lot of evidences has suggested that the biological and ecological responses of a wide range of life forms require progressively more advanced tools in the creation of action plans and other conservation strategies. Recognized as a place of inarguable importance, Madeira archipelago encloses an important biological diversity, including several species of endemic terrestrial snails. In order to properly understand this issue and provide preliminary data for future studies concerning the archipelago's malacofauna, this study aims the evaluation of the performance of native species of terrestrial molluscs, facing a futuristic climate scenario, and the analysis of how the distribution of these populations can be affected.

To perform this study, several species of land snails were selected based on their ecological characteristics. The prediction of species' potential distribution, according to their future habitat suitability, was determined using climate data from CLIMAAT II project (2006), and a model of maximum entropy distribution (Maxent version 3.3.3a). This software has been recommended in recent model comparisons, and has been found to produce useful results with small sample sizes.

Climate change assumes an important role on species distribution. With a very particular distribution, some endemic species may face the extinction in a future warm environment. The use of predictive models demonstrates a high efficiency in the identification of the variables that limit the distribution of the target species, also providing important evidences about the assessment of the conservation status of their populations over the next 80 years. The results should provide an integrative platform for the development of action plans and establishment of mitigation procedures preventing the fragmentation of populations and habitats, and subsequently the loss of biodiversity in one of the world's most remarkable hotspots.

T19.P4

BEHAVIOUR OF *CEPAEA NEMORALIS* (L.): DIFFERENCES BETWEEN MORPHS AND EFFECTS OF ENVIRONMENTAL FACTORS

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Shell colour polymorphism of the land snail *Cepaea nemoralis* (L.) is a well-known model in evolutionary research. Nevertheless, the proximate and ultimate factors driving its evolution remain uncertain. One of the most important factors may be (micro) climatic selection and selective predation. However, many polymorphic species show differential behavioural responses to selective factors. Moreover, the knowledge on *C. nemoralis* behaviour is still deficient. Therefore, we investigated behaviour (frequency of aestivation and locomotion, tendency to climb and hide) of *Cepaea* morphs both in experimental and natural conditions, and estimated effects of environmental factors (temperature, humidity, food availability, habitat structure and predatory pressure). Morphs significantly differed in frequency of climbing tall objects and hiding in shaded places: unbanded morphs more often climbed and less often hid than banded ones. In conditions of high, constant humidity significant effect on these behaviours as well as on frequency of aestivation and locomotion had temperature. In natural colonies climbing frequency was significantly affected by humidity and percentage cover of trees and shrubs on colony area. Snails moved more frequently when food was available. Tendency of unbanded morphs to climb trees may have evolved under strong avian predatory pressure. On the other hand, strong tendency of banded ones to hide in shaded places may reflect prey preferences to cryptic background as well as to microhabitats marginally exposed to sunshine. The results implicate that differential behaviour of *C. nemoralis* morphs may compensate for their morphological and physiological limitations of adaptation to habitat.

T19.P5

MICROHABITAT REQUIREMENTS OF SNAIL SPECIES (GASTROPODA, PULMONATA) IN LOWLAND WETLANDS OF WESTERN POLAND

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Microhabitat requirements of 21 snail species inhabiting tall sedge swamps (All. *Magnocaricion*) were studied, in order to test how the abiotic (groundwater levels, soil moisture, shading, trophy) and biotic (plant species) factors influence the molluscs communities.

The study was conducted on two localities in the valleys of the Pliszka and Ilanka rivers (W Poland) in 2008-2009. Sampled habitats were located on alkaline substratum and overgrown mainly with sedges. Nevertheless, they differed according to character of microhabitats.

The abiotic factors had a larger impact on the molluscsan communities than the biotic ones. The within locality analyzes demonstrated that different abiotic factors played a leading role in shaping molluscs communities: in the "Ilanka" locality moisture was the only significant factor, whereas in the "Pliszka" locality shading had the strongest effect but also soil moisture, and abundance of *Urtica dioica* and *Lysimachia vulgaris* were significant.

GLM analyses allowed to distinguish three groups of species: (1) species which population density increased with increasing litter and soil moisture, (2) species which density decreased with increasing litter and soil moisture, and (3) species which density was not dependent on the substrate humidity. The snail species were assigned to these groups: (1) *Vertigo angustior, Vertigo moulinsiana, Vertigo antivertigo, Vallonia costata, Vallonia pulchella, Zonitoides nitidus, Cochlicopa lubrica, Euconulus trochiformis, Carychium minimum, Carychium tridentatum*; (2): *Vertigo substriata, Vertigo pygmaea, Columella edentula, Vitrea crystallina, Vitrina pellucida, Cepaea hortensis, Fruticicola fruticum*; (3): *Nesovitrea hammonis, Punctum pygmaeum, Perforatella bidentata* and *Arianta arbustorum*. Species of the first group often preferred large abundance of *Carex acutiformis* in microhabitat and avoid *Thelypteris palustris*, probably due to litter character: the litter of *C. acutiformis* was compact with high water retention, whereas leaves of *T. palustris* were twisting when drying, creating loose, easy drying litter.

T19.P6

STABLE ISOTOPE ANALYSIS OF *RAPANA VENOSA* (MURICIDAE: NEOGASTROPODA) FROM DIFFERENT SITES OF THE BLACK SEA: VERTICAL MIGRATIONS, AGE FLUCTUATIONS AND HABITAT IMPACT

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Stable isotope analysis is widely used for ecological studies of mollusks and other invertebrates. It is found, that concentrations of carbon and nitrogen stable isotopes in soft tissues and shell protein of gastropod mollusks reflect their ration and the depths of habitat. Invasive muricid *Rapana venosa*, spread all over the Black Sea, demonstrates outstanding ecological plasticity. Its alimentary preferences may vary during the life, and vertical migrations are observed. All this is supported by the data of stable isotope analysis.

Rapa whelks were collected in five sites along the eastern part of the Black Sea coast on 2-25 m depths. Summary carbon and nitrogen content, accumulated for a whole life of a mollusk, and isotope dynamics in different age zones of operculums were analyzed.

The content of $\delta^{13}C$ in shell protein of rapana from all sites decreased with depth.

Isotope content varied in different age zones of operculums. In the majority of sites, $\delta^{13}C$ increased with age, from the oldest zone of operculum corresponding to a juvenile whelk, to the youngest one. These data are in concordance with our previous results of $\delta^{18}O$ content in shell carbonates, which was the highest in the oldest part of the shell, thus pointing that juvenile rapa whelks lived in colder and deeper waters than adults. $\delta^{13}C$ contents of shell carbonates in rapa whelks of 3 and 4 years old from the same locality showed that mollusks of 3 years age lived deeper than those of 4 years.

A significant difference in $\delta^{13}C$ was present between small and large-sized whelks of the same age, probably due to the difference in their alimentary conditions. An average $\delta^{15}N$ meaning of the shells from the Black Sea coast was 6,5‰, while that of the Strait of Kerch –12,1‰. This may be explained by more eutrophicated waters of the strait, coming from the Sea of Azov.

T19.P7

THE EFFECT OF 3.11 TSUNAMI ON SHELL GROWTH OF THE INVASIVE NATICID GASTROPOD *EUSPIRA FORTUNEI*

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On 11 March 2011, the Pacific coast of Tohoku Earthquake occurred and it caused huge damage to the marine organisms along the Pacific coast of northern Japan. The invasive naticid gastropod *Euspira fortunei* (*Laguncula pulchella*) introduced with imported clam *Ruditapes philippinarum* from China and Korea has been found living after the earthquake. The growth break like the bivalve was observed on the shell surface. The object of this study was to examine inhabiting situation and shell growth of *E. fortunei* after the earthquake.

E. fortunei was becoming a new, strong predator of the clam stocks in Japan. The inhabitant and predation pressure of *E. fortunei* to the native mollusks in the tidal flats at Mangoku-ura Inlet and Matsushima Bay in Miyagi Prefecture and Matsukawa-ura Inlet in Fukushima Prefecture were investigated from May 2011 to March 2013. The size and weight were measured in all individuals collected. The roll length from aperture to growth break was also measured to estimate growth rate after the earthquake. We observed shell microstructure using Scanning Electron Microscope (SEM).

Population density of *E. fortunei* from May 2011 to March 2013 hardly exceeded the data of 2009. However, many juveniles had been collected in Matsushima Bay and Matsukawa-ura Inlet after February 2012. Although *E. fortunei* ate at least 15 species of mollusk, diets of the snail were heavily dominated by the infaunal bivalves mainly of *R. philippinarum*.

The growth rate of the roll length in Matsushima Bay was larger than that of Matsukawa-ura Inlet from May to October 2011. However, average size of the shell height in Matsukawa-ura Inlet was larger than that in Matsushima Bay. After forming the growth break, newly formed shell became thinner. It may be the result of rapid change of mineralization process including quick shell growth and/or repair.

T20

T20.O1

DON’T MISS THE TRAIT!: THE IMPORTANCE OF CONSIDERING BIOLOGICAL TRAITS FOR A BETTER UNDERSTANDING OF BENTHIC ASSEMBLAGES

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Temporal variation in benthic assemblages is usually a striking topic, as many factors influence it. Life cycles of each of the species or changes in sediment and other environmental factors overlap to determine the functioning of these communities. And we must add the difficulty to find the appropriate scale and periodicity, and the random factors affecting the samplings. Because of this, squeezing the results as much as possible, by considering different approaches, may constitute a reasonable procedure to obtain a more realistic view of this issue. One powerful tool is sorting the fauna by different biological traits, and look for their relationship with environmental factors. That was our aim in this study carried out in a small embayment, the Ría de Aldán (NW Iberian Peninsula). In its inner part, two sampling stations were studied from May 1998 to May 1999. At each station, five replicate samples were taken monthly by means of a Van-Veen grab and then sieved through a 0.5mm mesh. All the molluscs in the samples were sorted, identified and counted. The taxa found were grouped according to their trophic guild, life habits and the combination of both traits. An additional sample was taken to determine sediment characteristics, and physico-chemical variables of water and sediment were also measured.

For both stations, the abundance of some groups showed significant correlations with abiotic parameters which did not correlate significantly with the parameters of the whole assemblage. In other cases, we found that the significant correlations between certain abiotic factors and the whole assemblage were actually due to their correlation with only one or some of the groups. Some groups even contradicted the trends shown by the total assemblage, correlating with the same abiotic parameters but in the opposite direction. The results from certain groups suggest interesting trends, such as the possible influence of the upwelling dynamics in suspensivore molluscs.

T20.O2

GEOMALACUS MACULOSUS: WHY IS THIS LUSITANIAN SLUG SPECIES THRIVING IN A COMMERCIAL FORESTRY PLANTATION 200KM NORTH OF ITS PREVIOUSLY KNOWN DISTRIBUTION?

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The distribution of the Kerry Slug *Geomalacus maculosus*, a species protected under EU and Irish law, was, until recently, believed to be limited to northern Iberia and south-

west Ireland. Here it predominantly inhabits oak-dominated or mixed deciduous woodland and open moor or blanket bog. However, in July 2010, the slug was found in a commercial conifer plantation in county Galway (Ireland), about 200 km north of its previously known range and in a habitat formerly not associated with this species. This provided the incentive to undertake presence / absence surveys in 42 potentially suitable habitat sites situated between the original and the new distribution areas in Ireland, but the presence of *G. maculosus* could not be confirmed at any of the sites investigated. Given that the species was not found anywhere else, research focused on the recently discovered population in the conifer plantation in Co. Galway: The spatial distribution and habitat requirements of the Kerry Slug were investigated and positive correlations between the abundance of *G. maculosus* and bryophyte / lichen cover and tree circumference at breast height (CBH) were found. Preliminary feeding experiments indicated that lichens are the favoured food source of *G. maculosus*. Given its likely dependency on lichens which are generally more prolific on mature conifer trees, the effects of clearfelling on the species are discussed. Additionally, partial sequences of the mitochondrial 16S rDNA and COI genes were compared from Kerry Slug populations sampled from locations in county Galway and the south-west of Ireland and results suggest that the population in county Galway is introduced rather than being a unique population.

T20.O3

MOVEMENTS OF THE EUROPEAN FLAT OYSTER *OSTREA EDULIS* (LINNAEUS, 1758)

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The European flat oyster *Ostrea edulis* Linnaeus, 1758 has been identified as a threatened and declining species and habitat and is protected under the international European OSPAR Convention and nationally within the United Kingdom by a Species Biodiversity Action Plan. The devolved UK governments (England, Wales, Scotland, and Northern Ireland) now have to maintain and extend the abundance and distribution of *O. edulis* as a matter of conservation, but unusually they are also a commercially exploited species. Over the past 150 years oyster populations have declined mainly due to overexploitation and poor management but other extrinsic contributory factors have also been blamed, such as pollution, disease outbreaks, introduced predators, habitat loss and severe cold winters. The decline in oyster populations increased commercial movement for relaying or on-growing across the UK, Europe and to other parts of the world. Our new data suggest that oyster populations may be locally adapted to environmental factors, such as temperature, and have then led to a low success rate in their new relocated area; this may be a factor that is limiting restoration of the native oyster.

T20.O4

WASTE RECYCLING: POTENTIALS OF RICE BRAN IN CULTIVATION OF AFRICAN GIANT LAND SNAIL *ARCHACHATINA MARGINATA* (PULMONATA: STYLOMMATOPHORA)

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Investigation into utilization of agricultural waste -rice bran in compounding ration for snail was conducted. A 56 day feeding trial on *Archachatina marginata* placed on diets of different rice bran inclusion proved acceptance of the diet by the animal to be positive. Mean body weight gain of the snail at the end of the 56 days feeding trial was significantly similar (p>0.05). The results of the study proved that rice bran diet has positive influence on the growth of *Archachatina marginata*. This result encourages its use in animal production and through this the environment would be rid of of accumulated gaseous pollutants. The conversion of rice bran into snail flesh that is free of cholesterol would improve the health of hypertensive patients that consume it. Reducing accumulation of agricultural wastes in our environment and their use in formulating ration for animals under captive setting for optimum growth of the animals at a low cost has potentials of constant animal feed supply on a sustainable basis. Low mortality of 6% was recorded in this experiment and this might not be as a result of the diet. Most of these agricultural wastes (rice bran, cassava peel, maize offal, African breadfruit seed hull, cocoa pod husk, yam peel, sweet potato peel) employed in compounding rations for animals contain carbohydrates and minerals that the animals needed for their daily activities and body maintenance as well as effective meat yield. These agricultural waste as feedstuffs in the nutrition of snails aids in reducing cost of production as feed contributes up to 70% of cost of production in animal farming.

T20.O5

RESPONSE OF JUVENILE GIANT LAND SNAIL *ARCHACATINA MARGINATA* FED VARYING LEVELS OF COCOA POD HUSK

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Fresh cocoa husks were collected from cocoa farms near the Federal University of Technology, Akure. The cocoa pod husks were sun dried and milled thoroughly. It was then mixed at different levels to replace maize in the experimental diets. The proximte analysis was determined. The cocoa pod husk (CPH) was used to replace maize in the diets of juvenile giant land snails *Archachatina marginata*. 48 hatchlings of the snail were used for a feeding trial. There were four treatments with three replicates. There were four diets in which maize was replaces at 0, 20, 40 and 60% CPH. The animals were fed *ad libitum*. The snail pens were cleaned everyday while the soil in the snail pens was changed fortnightly. The experiment lasted 12 weeks. The following parameters were determined: feed intake, weight gain, feed conversion, empty shell weight, edible flesh weight and shell length. The results show that there was significant difference (P<0.05) in weight gain, feed conversion and weight of edible flesh only between the snails fed the 0 and 60% CPH diets. However, there was no significant difference between the control and the diets where CPH replaced up to 40% level of substitution in all the

parameters tested. Mortality was low in all the diets. It was concluded that cocoa pod husk like most other form of waste products, could easily replace maize in the diet of juvenile giant snail without any diverse effects on the animal.

T20.O6

DETECTION OF *HEXAMERMIS ALBICANS* NEMATODE IN *SUCCINEA PUTRIS* AMBERSNAIL IN HUNGARY

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Parasites of snails are unique organisms that develop only in them and do not infect other hosts. Mermithid nematodes are a special group of the so-called parasitoid organisms, which kill their hosts during their development. These parasites have not been investigated in Hungary so far. The research of these aquatic and terrestrial worms is extremely difficult because the adult specimens can only be found in soil, where they lay their eggs as well. Arthropods, snails and lumbricid worms take larvae of mermithids emerged from eggs and the parasitic larvae grow to adult stage inside them.

We detected the worm *Hexamermis albicans* that parasitizes *Succinea putris* land snails in the swampy area of Gemenc forestry in Hungary. With external inspection the infection of snails cannot be recognized in the affected host individuals. Specimens of snails were collected after a heavy summer rain, we preserved them in alcohol, and dissected their mantle cavity to detect the worms.

The identification of the worms was performed by morphological analysis of preadult stages using identification keys. Microscopic slide preparations were prepared suitable for morphological inspection and subsequent molecular analysis of worms which was removed from the bodies of hosts. The prevalence and intensity of parasites were calculated. Detection of the adult forms and eggs of *H. albicans* in soil has not been successful so far.

Sequence of 18S rDNS region of the worm showed low similarity with the DNA sequences of other Mermithid species available in GenBank. This proves the unique position of *H. albicans* among other Mermithid worms which develop in arthropods.

Remarkable feature of *H. albicans* is that unlike other parasites as trematodes, this worm does not damage the reproductive system of snails during its development. Thus, eggs can be formed by the host snail, despite of the fact that the parasite grows in it.

T20.P1

SUBTIDAL MOLLUSC DIVERSITY AND SEDIMENTARY FEATURES IN THE HIGHLY URBANIZED RÍA DE FERROL (GALICIA, NW IBERIAN PENINSULA)

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Distribution and composition of benthic assemblages depend on such factors as hydrodynamism or composition and organic matter content of the sediment. In addition, anthropogenic activities such as sewage disposal, dredging and urbanization of the shoreline often negatively affect benthic assemblages. For instance, the construction of structures protecting harbours and similar facilities may result in significant changes in local hydrodynamics and therefore in siltation and organic enrichment, which, finally, lead to major changes in the benthic structure (e.g. loss of diversity, dominance of opportunistic species).

The Galician rías (NW Iberian Peninsula) support high benthic biodiversity because of their peculiar hydrodynamic regimes, seasonal upwellings and diversity of subtidal habitats. Growing human concentration on their shorelines is, however, threatening the natural environment. For instance, the Ría de Ferrol is highly impacted because of the construction of the massive jetty to shelter the outer harbour facilities. The jetty has affected significantly the current patterns there and most sediment has nowadays turned from sand to mud.

To test the hypothesis that alteration in sedimentary conditions (i.e. increase in silt/clay from outer to inner ría) has resulted in impoverished benthic assemblages (fewer diversity; high numerical dominance), quantitative sampling was done in 2010 at 70 subtidal sites (3-32 m depth). This yielded more than 135 different molluscan taxa and ca. 22000 specimens. The main hypothesis was mostly supported; thus, there was higher mollusc diversity in the clean coarse and medium sand sediments still present along the main channel of the ría and outer areas than in inner areas corresponding to muddy sediments, which just supported few taxa (mostly thyasirid and semelid bivalves); the latter usually showed high numerical dominances. This highlights the need of carefully planning when building on the coastline to avoid as much as possible irreversible alterations of hydrodynamics patterns and therefore loss of biodiversity.

T20.P2

MOLLUSCS IN AZOREAN LAKES: WARNING FOR EUTROPHICATION

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Azorean freshwater malacofauna is poor, comprising six species not evenly recorded in all islands. In spite of the only recorded bivalve, *Pisidium casertanum* (Poli, 1791), being a threatened species according IUCN, all the other gastropods found in Azorean freshwater systems are either alien or naturalized. During the biological monitoring program of inland surface waters (2008-2012), it was observed the presence of *Physella acuta* (Draparnaud, 1805) and *Ferrissia fragilis* (Taylor 1981) only in the deep lakes displaying eutrophication evidences. Molluscs presence in lakes systems also has been linked to various water-chemistry variables (e.g. pH, conductivity, total phosphorus and nitrogen). In this work we explore this idea by relating these gastropods' presence and abundance in São Miguel lakes with the abiotic parameters used to determine eutrophication status in order to test the possibility of molluscs to be considered as eutrophication indicators in the Azores. The strongest correlations observed in the mean annual abundance for these two species were with total phosphorus ($R=0.76$; $p<0.001$; $n=17$) and nitrogen ($R=0.69$; $p<0.002$; $n=17$). The data suggest that these alien gastropods could be promise candidates to be included in a regional metric for ecological quality assessment.

T20.P3

GASTROPODS INDICATE SEAGRASS MEADOWS (AT SAN SALVADOR, BAHAMAS)

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Seagrass meadows are important marine ecosystems in terms of productivity, nutrient cycling and storage, and sediment stabilization. Furthermore, they provide habitat for a diverse assemblage of associated organisms. The recognition of seagrass vegetation in the geological record is problematic because marine angiosperms rarely fossilize. Thus, the presence of paleo-seagrass beds often has to be inferred from the occurrence of associated organisms with a higher potential for fossilization, for instance mollusks. Most mollusk taxa are not restricted to seagrass meadows, but might be particularly abundant in seagrass beds. Therefore, the species composition of whole mollusk faunas needs to be considered when distinguishing paleo-seagrass meadows from other marine habitats. In this study the utility of the faunal composition of gastropods as an indicator of seagrass vegetation was tested using present-day ecosystems. Gastropod death assemblages from shallow water seagrass meadows and unvegetated sand flats from San Salvador Island, Bahamas were bulk sampled in July 2012. Twenty four standardized ($n=200$) samples (114 identified species) were compared in terms of species composition. Multivariate analysis (NMDS and ANOSIM) show a significant difference between the species composition of assemblages from seagrass vegetated versus unvegetated areas. Furthermore, samples derived from seagrass meadows differ from those taken close-by the vegetated zone. These results suggest that gastropod assemblages may be a useful proxy of seagrass meadows in the fossil record.

T20.P4

THE LAND SNAILS OF A PARTIALLY RECLAIMED ABANDONED COAL MINE SITE

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The Monahan Outdoor Education Center (Crawford County, Kansas, USA) was developed on a former active coal mine and facility for washing and processing coal. At the time of reclamation, the site contained approximately 64 ha (160 ac) of barren refuse, a partly eroded coal slurry, mine spoils, a large strip pit lake and several small acidic pits. A portion of the site (32.4 ha, 80 ac) was recontoured and reclaimed in 1984-1985 with a planting of a mixture of native species and shrubs. Terrestrial gastropods were collected at 53 locations among reclaimed and unreclaimed areas from 2008-2013. The locations were grouped into 10 relatively homogeneous zones within three major habitats: four woody (naturally developed into a mixed oak/cedar woodland), four grassy (the active reclamation and some unreclaimed), and two mixed woody/shrub/grass zones (either encroaching or planted). At each location, a sample was collected by first examining coarse leafy or woody debris on the surface layer (1-2 m^2), then by gathering approximately 1 liter of surface sediment and organic matter for later sieving in the lab. A total of 27 taxa were collected. More taxa were collected from the woodland (25) compared to the grassland (4), with the mixed vegetation sites intermediate (17). The number of taxa varied among the wooded areas from 11-20, among grassed areas from 5-12, and among the mixed sites from 11-14. Only one taxon was found in an unreclaimed grassy area. *Glyphyalinia indentata* and *Gastrocopta armifera* were the most commonly collected species and were found in all three major habitats. *Pupoides albilabris*, and *Zonitoides arboreus, Euconulus trochulus* and members of the Succineidae were also common, but *Z. arboreus* and *E. trochulus* were only found in the wooded areas. Large polygrids were rare, limited to abandoned shells of *Mesodon clausus* and *M. thyroidus*.

T20.P5

ENVIRONMENTS AND DRILLING PREDATION IN THE PANAMA EASTERN PACIFIC COAST

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Predation and competition played a fundamental role throughout the history of life, influencing the distribution and abundance of organisms at the ecosystem level, as well as the diversity and structure of communities. Predator-prey interactions also provide a unique system to study natural selection at the individual level. Drilling predation is common among gastropods. Bore holes are abundant and easier to recognize

representing a good tool to study predator-prey relationships in marine mollusc communities and the influence of abiotic factors on predator-prey relationships.

The complexity found in modern eastern Pacific environments is reflected in the mollusc assemblages it supports. Earlier data showed a much higher trophic diversity and predation intensity in muddy substrate communities as compared with those from coralline algae. Here we were interested in the possible influence of substrate type on feeding habits of predatory snails in upwelling versus non-upwelling settings on the tropical eastern Pacific coast of Panama.

As expected, taxonomic distribution and substrate type are directly related. Predation intensity varies from 35.1% in mud substrates to13.0% in hard substrates for gastropods, and from 17.3% - 4.5% respectively for bivalves. On the other hand it seems that hydrology (i.e. upwelling / non upwelling) has no big influence in predation intensity. In both substrates gastropods show a much higher predation intensity. Prey selectivity seems to be present only concerning gastropods and scarcely on bivalves. Naticids are the dominant predator in both habitat types. Muricids are responsible for less than 10% of total drill holes found mostly on hard substrate.

T20.P6

SHELL VARIATION IN PATELLID LIMPETS: SCALES OF SPATIAL VARIABILITY

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Species of the genera *Patella* generally display a high degree of shell variation, which is thought to be an adaptation to environmental conditions. The present work examines the variation in the morphometry of the two patellid limpets present in the Azores (*Patella candei* and *P. aspera*) at multiple spatial scales. Individuals of both patellid species were collected on two sites in each of the nine islands of the Azores. All individuals were measured to estimate base ellipticity, base eccentricity, conicity and cone eccentricity. Shell variation in *P. candei* was consistent among groups of islands (eastern, central, western) but there was significant variation in shell morphometry at the scales of islands and sites. Components of variation showed that a substantial proportion of variation was associated with the scale of individuals. Shell variation in *P. aspera* was consistent at the scale of island groups and islands but there was significant variation among sites. Analysis of the components of variability showed that variability in shell morphometry was mostly associated with differences among individuals. Overall, these results suggest that variation in shell morphometry in the two patellid is not influenced by large scale processes as would be expected given that *P. candei* and *P. aspera* both have a pelagic larvae. In addition, this study suggests that shell variation in these species is likely to be a result of an adaptation to local conditions (e.g. microhabitats).

T20.P7

MALACOFAUNA ASSOCIATED WITH MARINE SPONGES IN THE AZORES ARCHIPELAGO

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Marine sponges (Porifera) provide habitat, refuge and food to a wide variety of organisms thus playing key ecological roles in benthic communities. The macrofauna associated with three sponge species, viz. *Haliclona fistulosa* (Bowerbank, 1866), *Myxilla macrosigma* Boury-Esnault, 1971 and *Tedania anhelans* (Lieberkühn, 1859), was studied and compared with that inhabiting the adjoining algal cover.

Molluscs were shown to constitute the second and third most abundant group associated with the algae and the sponges, respectively. A total of 2079 individuals were identified and assigned to 68 taxonomic units (TUs), representing 52 genera, 35 families, 12 orders, and 3 classes. The algal-associated molluscan assemblages were more abundant but equally speciose (N=1575; S= 53) than the sponge-associated assemblages (N=504; S=52). Sixteen TUs were found exclusively on the algal cover, whereas 15 TUs were only found associated with the sponges. Thirty-seven TUs were shared among hosts. The species *Ammonicera rota* (Forbes & Hanley, 1850), *Bittium nanum* (Mayer, 1864) and *Tricollia pullus azorica* (Dautzenberg, 1889) strongly dominated both assemblages. Half of the species occurred in very low frequencies (less than 3 individuals).

These findings highlight the important role that sponges play as habitat for the littoral malacofauna of the archipelago.

T20.P8

HOW AND WHY GASTROPOD SHELLS BECOME REMODELED HOMES FOR TERRESTRIAL HERMIT CRABS

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Gastropod shells represent a critical resource that hermit crabs occupy as homes. However, terrestrial hermit crabs do not merely occupy gastropod shells they also architecturally remodel them through a process of niche construction. Here I detail the before-to-after changes in these remodeled shells (*Nerita scabricosta* as well as other species) and I present an ecological, evolutionary, and behavioral synthesis of how and why terrestrial hermit crabs perform this niche construction of gastropod shells. I report data from my long-term study population in the field (*Coenobita compressus* in Osa Peninsula, Costa Rica), the results of laboratory experiments, and a novel synthesis of information from the broader literature.

Compared to their marine ancestors, terrestrial hermit crabs faced a radically different suite of predators as well as substantially altered locomotion costs in their new terrestrial environment. In particular, the transition from sea to land dramatically relaxed

predation pressures on hermit crabs, while at the same time increased the cost for crabs of traveling with their portable home—the gastropod shell. Natural selection therefore favored crabs that remodeled their shells, creating thinner, less protective shells that were lighter to carry.

Mechanistically, crabs seem to accomplish remodeling via a chemical-mechanical sculpting of the shell interior, which erodes the columella as well as much of the inner calcium-carbonate matrix.

Ultimately, crabs' niche construction has created novel evolutionary pressures on them, specializing them to inhabit remodeled shells and consequently ratcheting up their level of sociality for stealing the remodeled products of fellow conspecifics.

Gastropod shells represent the central ecological theatre for this evolutionary play among hermit crabs, a theatre that the hermit crabs themselves redesigned to their own specifications.

T20.P9

OLD HOSTS, NEW GUESTS - EUROPEAN SNAILS HOSTING AMERICAN LIVER FLUKES. AN INTERIM REPORT

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The giant liver fluke *Fascioloides magna*, an invasive trematode (Digenea) species originating from North America, was recorded in Europe first time in 1875 in Italy. In Austria it was detected in the wild for the first time in the year 2000 at River Danube. The lesser pond snail *Galba truncatula*, an autochthonous snail, evidenced to act as snail intermediate host in Austria; cervids were reported as final hosts. For assessing the risks of spreading it is essential to get data about abundance and ecology of hosts and epidemiology of worms. Approximately 14,000 *G. truncatula* snails have been investigated parasitological by dissecting. Morphology and genotyping was used for species delimitation.

G. truncatula is abundant in all parts of the investigated Danube flood plain area, preferably at shores of slow running branches of the river. Main cercarial shedding of *F. magna* happens in mid-sized individuals and occurs in mid-summer. Prevalence of *F. magna* in snails is low (0.03-0.2%) compared with prevalence in deer (20-100%). *G. truncatula* occurs also in adjacent areas at River Leitha, but no fasciolids were found in appr. 1,000 individuals collected there. Until now, only *G. truncatula* has been verified as intermediate host species in Austria. But a number of other lymnaeid species are known as hosts from the literature. Since snail hosts must be considered to play an important role in parasite dispersal, other potential hosts have been investigated. First investigations of *Lymnaea stagnalis, Stagnicola* sp. and *Radix* sp. did not evidence fascioloids, neither in Danube flood plains nor in neighbouring areas. Nevertheless these native species, but also potential invaders like *Pseudosuccinea columella* should be considered as intermediate hosts. Investigations will be continued.

T20.P10

SHELLS OF THE LIMPET *PATELLA ASPERA* AS HABITAT FOR EPIBIONTS

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Although limpets can control the abundance and distribution of algae and other organisms, their shells can offer a refuge for the establishment of diverse assemblage that would otherwise be excluded. In this study, we make a preliminary analysis of the epibiota growing on shells of the limpet *Patella aspera*. Individuals of *P. aspera* were collected in all islands of the Azores and the biota on their shells was identified and quantified to species level. A total of 144 species was identified. The composition of the epibiota assemblage varied among islands and among locations within islands. There was also significant variation in epibiota richness at the scale of locations, but not at the scale of islands. A positive and highly significant correlation was also found between epibiota richness and shell length. This study adds to the literature by showing that the shells of *P. aspera*, an over-exploited species in the Azores, support a very rich community of algae and invertebrates and that this is controlled by processes operating at multiple spatial scales ranging from metres (among individuals) to 100's of kilometres (among islands).

T20.P11

WHEN MALACOLOGY MEETS MYCOLOGY: MICROFUNGAL COLONISATION OF EMPTY *CEPAEA* SHELLS

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Soil and litter colonizing fungi can degrade many natural materials, including highly resilient proteinaceous compounds of animal origin. The shells of terrestrial gastropods are formed from such a compound combined with inorganic calcium carbonate. Nevertheless, the colonization of empty shells by fungi has been hitherto overlooked.

We investigated fungal communities colonizing empty shells of the terrestrial gastropod *Cepaea hortensis*. Shells were cultivated on the surface of litter from four different forest types under identical conditions, and the fungi were surveyed and identified in four 3-month periods.

We found and identified 35 fungal species and one genus of filamentous bacterium colonizing the shells. Multivariate analysis revealed a significant effect of the litter type on the fungal community. Known cellulolytic and nonspecific degraders dominated over keratinophilic species. Humidity and pH at the locality are likely to be more important for determining the fungal community than the proteinaceous material of the shell.

During the survey, a new fungal genus represented by a new species *Pentaster cepaeophilus* (Pezizomycotina inc. sed.) was described. This species is characterized by melanized, multiseptate staurosporous conidia with five arms. The conidia are unique in that two arms form a central axis and three arms stretch from its centre.

T20.P12

IMPACT OF EXTRACT OF *EUPHORBIA PULCHERIMA* AND *ATRIPLEX NUMMULARIA* ON THE INFECTIVITY OF *SCHISTOSOMA HAEMATOBIUM* TO *BULINUS TRUNCATUS* SNAILS AND HISTOLOGICAL STRUCTURE OF HOST SNAIL

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The effect of extract of *Euphorbia pulcherima* and *Atriplex nummularia* on infection rate and cercarial production of *Bulinus truncatus* infected with *Schistosoma haematobium*, as well as on the free living stages of *the parasite* (miracidia and cercariae) was studied through the histological structure of the digestive and hermaphrodite glands of the host snail.

The results showed that LC_{25} of extract of *E. pulcherima* and *A. nummularia* caused a considerable reduction in the infectivity of *S. haematobium* miracidia to the snail. It caused reduction in number of cercariae per snail during the patent period and the period of cercarial shedding. The mortality rates of miracidia and cercariae were elevated gradually by increasing the exposure period to extract of these plants.

Exposure of snails to LC_{25} of extract of *E. pulcherima* and *A. nummularia* for 2 weeks caused a great damage in the epithelial tissues of *Bulinus truncatus*, cells lost their regular shape, appeared empty of cytoplasm, showing several vacuolations, disappearance of secretory cells from the digestive tubules and the connective tissue between shrunk acini was damaged. The present results showed severe damages, obvious degeneration of most gametogenic stages and inhibition of spermatogenesis and oocytes in the hermaphrodite gland of *Bulinus truncatus* after 2 weeks of exposure to LC_{25} of extract of two plants. It was concluded that the application of LC_{25} of extract of *E. pulcherima* and *A. nummularia* may be helpful in snail control as it interferes with the snails' histology.

T20.P13

DETECTION OF *HEXAMERMIS ALBICANS* NEMATODE IN *SUCCINEA PUTRIS* AMBERSNAIL IN HUNGARY

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Parasites of snails are unique organisms that develop only in them and do not infect other hosts. Mermithid nematodes are a special group of the so-called parasitoid organisms, which kill their hosts during their development. These parasites have not been investigated in Hungary so far. The research of these aquatic and terrestrial worms is extremely difficult because the adult specimens can only be found in soil, where they

lay their eggs as well. Arthropods, snails and lumbricid worms take larvae of mermithids emerged from eggs and the parasitic larvae grow to adult stage inside them.

We detected the worm *Hexamermis albicans* that parasitizes *Succinea putris* land snails in the swampy area of Gemenc forestry in Hungary. With external inspection the infection of snails cannot be recognized in the affected host individuals. Specimens of snails were collected after a heavy summer rain, we preserved them in alcohol, and dissected their mantle cavity to detect the worms.

The identification of the worms was performed by morphological analysis of preadult stages using identification keys. Microscopic slide preparations were prepared suitable for morphological inspection and subsequent molecular analysis of worms which was removed from the bodies of hosts. The prevalence and intensity of parasites were calculated. Detection of the adult forms and eggs of *H. albicans* in soil has not been successful so far.

Sequence of 18S rDNS region of the worm showed low similarity with the DNA sequences of other Mermithid species available in GenBank. This proves the unique position of *H. albicans* among other Mermithid worms which develop in arthropods.

Remarkable feature of *H. albicans* is that unlike other parasites as trematodes, this worm does not damage the reproductive system of snails during its development. Thus, eggs can be formed by the host snail, despite of the fact that the parasite grows in it.

T20.P14

TOXICITY OF PARAQUAT HERBICIDE TO SOME PHYSIOLOGICAL AND MOLECULAR ASPECTS OF *BULINUS TRUNCATUS* SNAILS AS A BIOINDICATOR

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Paraquat has been demonstrated to be a highly toxic compound for humans and animals and many cases of acute poisoning and death have been reported over the past few decades. The present study was undertaken to evaluate toxicity Paraquat to biochemical and molecular aspects of *Bulinus truncatus* snails. It was found that, the glucose level in hemolymph of exposed snails was elevated while the glycogen showed a decrease in soft tissues when compared with the control group. In addition, the activity level of some enzymes representing glycolytic enzymes as hexokinase (HK), pyruvate kinase (PK), ,phosphofructokinase (PFK), lactate dehydrogenase (LDH),and glucose phosphate isomerase (GPI). The changes in the number, position and intensity of DNA bands induced by Paraquat herbicide may be attributed to the fact that herbicide can induce genotoxicity through DNA damage. Thus the present study indicated that the genotoxicity products at low concentration and for long time treatment showed the hazard of herbicide addiction on man life.

T21

T21.O1

HYPOXIA TOLERANCE OF JUMBO SQUIDS (*DOSIDICUS GIGAS*) IN THE EASTERN PACIFIC OXYGEN MINIMUM ZONES: PHYSIOLOGICAL AND BIOCHEMICAL MECHANISMS

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The Humboldt (jumbo) squid, *Dosidicus gigas*, is a large oceanic squid endemic off the Eastern Tropical Pacific that undertakes diel vertical migrations into mesopelagic oxygen minimum zones (OMZs) and, thereby, encounters oxygen levels below its critical oxygen partial pressure. To better understand the biochemical and physiological strategies to survive such harsh conditions, we exposed *D. gigas* to oxygen levels found in the OMZ (1 kPa, 10ºC) and investigated (i) oxygen uptake and ventilatory mechanisms, (ii) oxygen consumption rate, (iii) anaerobic metabolic pathways, and (iv) the potential of metabolic suppression.

Under early hypoxia (<160 min), jumbo squid breathe "deeply", with more powerful contractions and enlarged inflation period (reduced contraction frequency). Such deep-breathing behavior and a reduced relaxed mantle diameter optimize oxygen extraction efficiency (up to 82%) by favoring diffusion pathways. Further, deep-breathing enabled *D. gigas* to pass the same amount of water through the mantle cavity per period of time (i.e. stable ventilatory volume per minute) that might explain its high activity under such unfavorable O_2 conditions. At progressing hypoxia (> 180 min), all ventilatory processes were significantly reduced except for O_2 extraction efficiency (up to 40%), probably by using the collar-flap system, and followed by a lethargic state, a common strategy to safe energy expenditure and extend residence time in OMZs. Anaerobic energy production via energy reserve store and glycogen depletion increased (70%), but could not compensate the energy loss due to reduced oxygen consumption rates (70-80%) resulting in metabolic suppression (45-60%). Total protein concentrations decreased non-significantly, yet, our present findings indicate that *D. gigas* degrade, at least under progressing hypoxia, specific muscle proteins (i.e. α-actinin) anaerobically. Moreover, the ubiquitin-proteasome system and the heat shock protein 90 machinery seem to play an important role in hypoxia tolerance, but further investigations are necessary to discover their full potentials and pathways.

T21.O2

EVALUATION OF THE GLUTATHIONE S TRANSFERASE RESPONSE TO SEASONALITY, POLYCYCLIC AROMATIC HYDROCARBON (PAH) AND HEAVY METAL POLLUTANTS IN *SACCOSTREA CUCULLATA* (BIVALVIA: OSTREIDAE), ALONG THE IRANIAN COAST OF THE PERSIAN GULF

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Bivalves are one of the most well-known bioindicators used for assessing the aquatic environmental pollution. Although the animals are able to highly accumulate contaminants without any poisonous effects but they usually employ some detoxification mechanisms to cope with the adverse influences of such chemicals. In the study, we assayed the level activity of biotransformation enzyme, Glutathione S transferase (GST) for the first time in rock oyster, *Saccostrea cucullata*, to determine if it could be a suitable biomarker for polycyclic aromatic hydrocarbons (PAHs) and heavy metals. For this, the PAHs concentration as well as cadmium (Cd), chromium (Cr) and copper (Cu) levels were analyzed in whole tissue of the species in three stations and two seasons (warm and cold) along the Iranian coast of Persian Gulf. Our results indicated the GST activity had the maximum and minimum correlation with Cu (r = 0.83) and PAHs (r = 0.078), respectively. It was observed that the concentration of heavy metals in winter and summer is paralleled with the GST activity in the seasons. On the other hand, PAH compounds level was indirectly relevant to GST in both seasons. Taking into account of all the data, it seems that GST could be perceived as a more appropriate biomarker for heavy metals pollution than PAH contaminants.

T21.O3

OXIDASES AND DEHYDROGENASES METABOLIZING MANNITOL AND OTHER ALCOHOLS IN THE DIGESTIVE GLAND OF GASTROPODS

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Mannitol is a 6 carbon polyalcohol present in algae, fungi and plants, being one of the most abundant sugar alcohols in nature. In many species this compound is a storage substance, but it is also important for osmoregulation and may act as a scavenger of reactive oxygen species. Thus, enzymes capable of converting mannitol present in algae and plants into sugar will be valuable for herbivorous gastropods. Mannitol

oxidase, an enzyme that catalyses the oxidation of D-mannitol using molecular oxygen as hydrogen acceptor generating mannose and hydrogen peroxide, was previously reported in the digestive gland and crop of herbivorous land snails (Heterobranchia, Stylommatophora) and in the digestive gland of the marine herbivore *Aplysia depilans* (Heterobranchia, Euopisthobranchia). The current study also revealed mannitol oxidase activity in the digestive gland of other herbivores, namely the caenogastropod *Littorina littorea* and the heterobranchs *Siphonaria pectinata* and *Planorbarius corneus*. This enzyme was neither detected in the digestive gland of the carnivorous caenogastropods *Nucella lapillus, Nassarius reticulatus* and *Ocenebra erinacea*, nor in the herbivores *Patella vulgata* (Patellogastropoda) and *Osilinus lineatus* (Vetigastropoda). Nevertheless, these two last species contained a high mannitol dehydrogenase activity in the digestive gland. In this case, NAD^+ is the hydrogen acceptor. Moreover, mannitol dehydrogenase activity was detected in the digestive gland of several other gastropods. Enzymatic activities were also investigated with other alcohols. Significant oxidase and dehydrogenase activities were recorded with the aromatic cinnamyl alcohol in all species tested so far. Ethanol oxidase activity was detectable only in some species. Dehydrogenase activities could also be detected with D-sorbitol, 2-butanol, glycerol and ethanol as substrates. Available data suggest that mannitol oxidase is present in the digestive gland of herbivorous caenogastropods and heterobranchs, but mannitol dehydrogenase has a wider phylogenetic distribution. In gastropods, alcohol dehydrogenases metabolize a wider range of substrates than alcohol oxidases.

T21.O4

PLATINUM-INDUCED SHELL INTERNALIZATION IN THE RAMSHORN SNAIL *MARISA CORNUARIETIS*

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Toxic substances like heavy metals can inhibit and disrupt the normal embryonic development of organisms. High platinum concentrations can prevent the formation of an external shell during *Marisa cornuarietis* embryogenesis. Pt-exposed embryos and controls held at 26 °C show similar development until 70 to 82 h postfertilization when in controls the anlage of both shell gland and mantle spreads across the visceral sac. During this developmental process, the growth of the tissue on the left side of the visceral sac normally exceeds that of the right side, leading to a horizontal rotation of the visceral sac and an enfolding of the tissue on its right side into the mantle cavity. In Pt-exposed embryos, platinum inhibits the growth of shell gland and mantle edge during embryogenesis. The visceral sac rotates vertically instead of horizontally, and the shell-secreting tissue is displaced to the ventral side of the visceral sac. Without the growth of shell gland and mantle edge, the mantle tissue invaginates into the embryo, causing an internalization of the mantle and, thus, also of the shell. The resulting snails show a "sluggish" appearance with an anterior anus and posterior gills. However, cultivation at higher temperatures induces a re-start of shell gland and mantle edge growth after a period of inactivity in Pt-exposed individuals. These embryos exhibit a broad spectrum of shell forms ranging from fully internal shells to partly-external to normal shells. These intermediate and internal shells have some characteristics in common with internal shells that can be found in other molluscan clades: primarily, the shell is external and is then partly overgrown and internalized. Furthermore, like in many cephalopods, the Pt-induced internal shells are surrounded by shell-secreting tissues which has consequences for the shells´ anatomy.

T21.P1

UPTAKE, ACCUMULATION, TRANSFORMATION AND DEPURATION OF PARALYTIC SHELLFISH TOXINS IN COMMON OCTOPUS (*OCTOPUS VULGARIS*)

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Harmful algal bloom (HAB)-related marine toxins can be accumulated by primary consumers and work their way through the food web, creating a chain of vectors that transfer the toxin to higher trophic levels. Cephalopods, namely the common octopus (*Octopus vulgaris*), prey mostly on common vectors of HAB toxins, such as bivalves and crustaceans. On the other hand, these mollusks are included in the diets of marine mammals and top predator fish. Octopuses are known to retain high levels of marine toxins in the digestive gland, including paralytic shellfish toxins (PSTs), during and even after the bloom. However, no studies on the depuration rates and toxin kinetics have been performed within this mollusk group. In the present study, octopuses (*O. vulgaris*) were subjected to a diet of naturally contaminated clams (*Donax sp.*) with PST produced by *Gymnodinium catenatum* for a period of 6 days and non-contamined diet afterwards. Toxin concentrations in the digestive gland progressively increased throughout the uptake period, with B1 (sulfocarbamoyl toxin) and dcSTX (decarbamoyl toxin) being the most abundant saxitoxin (STX) derivatives found. Octopus are metabolically active organisms and have high food conversion, digestion and excretion rates, and when they were fed with non-toxic diet it was observed a rapid depuration of PSTs. By the end of the experimental time (16 days) the levels of STX derivatives were already non-detected. With the present findings we clearly demonstrated the uptake, accumulation, transformation and depuration of PSTs in this key (vector) group of the food web and the fate of these compounds in the marine ecosystem.

T22

T22.O1

SNAIL BEHAVIOUR: WHAT COMPUTER SIMULATIONS CAN TELL US ABOUT DECISION-MAKING AND EVOLUTION

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High shore littorinid snails often live in more-or-less two dimensional habitats and have few predators. This makes modelling their behaviour relatively easy on the basis of simple theoretical rules. Outputs of models closely match observed distribution patterns on the shore, which gives us confidence in their applicability. Aside from replicating nature, these models can be used to manipulate the virtual environment to understand decision-making and evolution in these neurologically relative simple animals.

When emersed, snails form complex static patterns that involve aggregations and crevice-occupation, which can be considered as emergent properties or features of self-organisation. Using *in silico* experimentation that is palpably impossible we show that a few simple rules can generate complex spatial patterns and how such self-organisation, which looks suspiciously like co-operation, can be initiated and sustained over evolutionary periods. Using evolutionary algorithms we thus we propose a mechanism for the evolution of co-operative behaviour. The self-organisation appears to be relatively insensitive to changes at the individual agent (organism) level and so is largely self-perpetuating.

But are the behaviours purely co-operative or do 'cheats' evolve in the system? We show in a two-species scenario that cheats can exist in high proportion before the system collapses, indicating inter-specific differences in selection pressure.

In silico studies can give us new insights into snail behaviour. The (only?) problem lies in whether we believe the models or not, since our manipulations cannot be tested in reality.

T22.O2

INFLUENCE OF SIMULATED EXPLOITATION ON THE SEX CHANGE AND POPULATION DYNAMICS IN *PATELLA VULGATA*

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We describe a field experiment designed to simulate human exploitation of limpets in order to evaluate the effects of human exploitation on the ecology of *Patella vulgata* (the target species). *P. vulgata* is not a major target species for human consumption today, but due to the occurrence of sex change was considered an appropriate model for investigating the consequences of predation by humans upon the sex change phenomenon. Limpet populations were exploited by systematic removal for 18 months, during which records were kept of limpet density, size frequency and sex ratios, and shore macro-community structure. The hypothesis tested was that selective removal through time of largest limpets would influence the timing and magnitude of several biological processes, including sex change, growth, migration and density regulation. There was strong evidence that the size at sex change (L_{50}) decreased in response to the exploitation treatment, given by analysis of the averaged L_{50} extracted from the logistic regression on each treatment plot. The observed L_{50} at controls (50.54 ± 6.38 mm) suggested that sex change was occurring at a bigger size than expected from the overlap in male and female size classes. The study sites located in the south-west of England had considerable differences in community structure: Trevone was a moderately exposed shore with barnacles and *Fucus* spp. dominated community while Constantine can be considered an exposed shore with a *Mytilus* spp. dominated shore community. Thus the sex change response could be context-dependent and influenced by the community on the rest of the shore. To further understand the sex change in *P. vulgata* it is essential to design experiments that consider differences among patches. The knowledge of sex change dynamics in exploited sex changing limpet populations would allow management procedures to counter population decline being essential to rocky shore conservation and resource management.

T22.O3

POPULATION STRUCTURE IN HIGH SHORE LITTORINIDS: A CONTRAST BETWEEN RIPRAP AND ROCKY SHORES

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The number of anthropogenic structures deployed in coastal areas has increased markedly in recent times and many studies have now shown that these structures seldom mimic the natural habitats they replace. To date, however, most such studies have focused on the numbers and relative abundance of species and little is known about how these structures affect the patterns of species aggregation and size structure, despite the fact that variations in these parameters may have important ecological consequences at population and community levels. Here we compare the relative abundance, patterns of aggregation and size structure of two high shore gastropod littorinids (*Tectarius striatus* and *Melarhaphe neritoides*) on riprap and adjacent rocky shores. While the relative abundance of *T. striatus* was similar on riprap and natural rocky shores, *M. neritoides* was significantly more abundant on rocky shores. At small spatial scales (cm's) both littorinids species showed more aggregated distributions on riprap. At larger scales (m's), both littorinids were also more aggregated on riprap although this was only significant for *T. striatus*. Habitat type influenced the size structure with both species attaining a significantly larger size on riprap. Here we add to the wider literature by showing that anthropogenic structures can affect intertidal assemblages in ways other than richness or the relative abundance of organisms alone.

The here documented variation in patterns of aggregation and size structure between habitats likely influence the population dynamics of these species and may have wider community level consequences.

T22.O4

mtDNA SUGGESTS STRONG GENETIC DIFFERENTIATION AT UNEXPECTEDLY FINE-SCALES IN A HIGH-DISPERSAL MARINE PERIWINKLE

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Marine invertebrates with long-lived planktonic larvae are assumed to have high dispersal potential and broad-scale gene flow. They are thought to disperse over long distances and to be genetically homogeneous over large areas. The periwinkle *Melarhaphe neritoides* which ranges along much of the European coastline, is such a species. Its long-lived planktonic larval phase lasts 4-8 weeks and previous allozyme studies have shown very little to no population genetic differentiation along the European coast, even over distances of thousands of kilometers. However, a growing number of studies based on DNA markers suggest that there is a poor correlation between pelagic larval duration (PLD) and the level of population genetic differentiation ($r^2 = 0.29$). Nevertheless, recent work reaffirms that PLD might still be a good predictor of population genetic differentiation as a function of geographic scale, if based on unbiased F_{ST} estimates and appropriate sampling sizes. We explored these conflicting views by assessing mtDNA (COI, 16S, Cytb) differentiation among five intensively-sampled populations of *M. neritoides* in the Azores. In contrast with previous allozyme data, our mtDNA data reveal remarkably high genetic diversity and differentiation among *M. neritoides* populations, even those as close as 50 km. Even at this scale, populations do not seem to share haplotypes, despite the assumed high potential of broad-scale gene flow in *M. neritoides*. Hence, the relationship between PLD and dispersal potential or the level of population genetic differentiation, is indeed not straightforward.

T22.O5

INDIVIDUAL AND POPULATION LEVEL DIETARY BREADTH OF *CONUS MILIARIS* AT EASTER ISLAND

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Understanding the processes associated with changes in resource utilization can illuminate the factors affecting niche expansion. *Conus miliaris* is a broadly distributed Indo-West Pacific predatory marine snail that was previously found to exhibit ecological

release and concomitant increased dietary breadth at Easter Island where congeners that typically co-occur with this species elsewhere are largely absent. In addition, past investigations of the venom of *C. miliaris* (that is used to capture prey) have revealed that several venom components are substantially differentiated between Easter Island and other Indo-West Pacific populations of this species. Here I examined and identified prey items of individuals of *C. miliaris* at Easter Island that were recovered from separate feeding bouts through a mark-recapture approach and DNA barcoding of fecal materials. I used these data to determine whether the increased dietary breadth of the population reflects (i) increased niche breadth of individuals or (ii) individual-level resource specialization and increased inter-individual variation in diet. As observed previously, I found that *C. miliaris* at Easter Island preys on a diversity of polychaetes, including at least eight eunicid, one nereid and one notomastid species, and that diets are associated with shell length. Based on comparisons of observed and expected frequencies of instances of feeding on the same and different prey item during separate feeding bouts, individuals of *C. miliaris* at Easter Island do not exhibit preferences for particular prey and diets of the population and individuals are equally broad. These results imply that the previously observed divergence in venom components of *C. miliaris* at Easter Island was driven by selection from increased dietary breadth. Moreover, I predict that venoms of *C. miliaris* at Easter Island affect a greater diversity of potential prey species than at other locations in the Indo-West Pacific where dietary breadth of *C. miliaris* is more narrow.

T22.P1

BROAD-SCALE PATTERNS OF SEX RATIOS OF *PATELLA* SPP.: A COMPARISON OF THE BRITISH ISLES AND PORTUGAL

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A broad-scale survey of limpets by sex and size classes covering a range of latitudes from Zambujeira do Mar (southern Portugal) to Jennycliff (southern England) is presented here. The primary aim of the survey was to explore changes in sex ratio within the range of the species studied: *P. vulgata* (southern limit in Portugal, range centre in the British Isles) and *Patella depressa* (poleward limit in the British Isles, range centre in Portugal). As a protandric population approaches its range boundary, the alternative hypotheses to test are: (i) sub-optimal conditions (due to the environment or increased interspecific competition) delay promotion from male to female resulting in fewer females; (ii) relaxation of resource limitation resulting from reduced intraspecific competition will enhance promotion from males to females resulting in higher number of females; (iii) at range edges recruitment is intermittent leading to more older larger animals which are female. Evidence was found for the occurrence of protandry in non-harvested *P. vulgata* populations from the south of England, with females predominating in larger size classes; cumulative frequency distributions of males and females were different; sex ratios were biased towards the first sex and smallest sizes of males were smaller than the smallest sizes of females. In *P. depressa* populations from England and Portugal: females were interspersed across most size classes; cumulative frequency distributions of males and females and smallest sizes of males and females did not differ. This was also displayed in *P. vulgata* populations from Portugal. *P. depressa*, however, also showed some patterns indicating the possibility of slight protandry occurring in Portugal. The test of sex ratio variation with latitude revealed that *P. vulgata* sex ratios could be involved in determining the species range limit, since the likelihood of being male rises with latitude from Alentejo (Portugal) through to Plymouth (England).

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